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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 13:24:39 ; Search time 602.28 Seconds  
(Without alignments)  
10059.976 Million cell updates/sec

Title: US-10-027-923-1

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Gapop 60.0 , Gapext 60.0

Searched: 2201672 seqs, 1661799599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1823	100.0	1823	14	US-10-027-923-1	Sequence 1, Appl
2	1784	97.9	1788	10	US-09-822-830A-61	Sequence 61, Appl
3	1110	60.9	1110	14	US-10-027-923-3	Sequence 3, Appl
4	222	12.2	2826	13	US-10-346-241-1	Sequence 1, Appl
5	222	12.2	3129	13	US-10-346-241-5	Sequence 1, Appl
6	222	12.2	4518	15	US-10-225-567A-177	Sequence 177, Appl
7	33	1.8	55	15	US-10-245-988-9	Sequence 9, Appl
8	33	1.8	111	10	US-09-960-352-7296	Sequence 7296, Ap
9	33	1.8	116	9	US-09-770-696-726	Sequence 726, App
10	33	1.8	166	10	US-09-867-701-9576	Sequence 9576, Ap
11	33	1.8	174	9	US-09-925-299-750	Sequence 750, App
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13	33	1.8	190	10	US-09-867-701-9295	Sequence 9295, Ap
14	33	1.8	200	10	US-09-960-352-4816	Sequence 4816, Ap
15	33	1.8	212	10	US-09-867-701-9190	Sequence 9190, Ap

16	33	1.8	241	9	US-09-604-287A-334	Sequence 334, App
17	33	1.8	241	11	US-09-551-621-334	Sequence 334, App
18	33	1.8	241	11	US-10-124-805-334	Sequence 334, App
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36	33	1.8	420	15	US-10-074-475-127	Sequence 127, App
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42	33	1.8	464	11	US-09-918-995-13312	Sequence 13312, A
43	33	1.8	465	15	US-10-198-846-11931	Sequence 11931, A
44	33	1.8	503	10	US-09-995-494-26	Sequence 26, Appl
45	33	1.8	515	15	US-10-198-846-9933	Sequence 9933, Ap

## ALIGNMENTS

RESULT 1  
US-10-027-923-1  
; Sequence 1, Application US/10027923  
; Publication No. US20020142330A1  
; GENERAL INFORMATION:  
; APPLICANT: Brian Galtner Bates  
; APPLICANT: Kamalaka Gulukota  
; APPLICANT: Yuhong Xie  
; APPLICANT: Janet Elizabeth Paulsen  
; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
; FILE REFERENCE: GNN-024  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR  
; CURRENT APPLICATION NUMBER: US/10/027,923  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,589  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1823  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4)..(1110)  
; US-10-027-923-1

Query Match 100.0%; Score 1823; DB 14; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB GCACAGCTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 120

OY		CTCCTTTTCGTGTAATCAACAGCCATCTGTGGACGAAGTCAATGAGGAACTGTGGGGACA	180
Dd	121	CTCTTTCTGTTCATCATCACAGCTACTGTGACGAAGTTCAATGAGGAATGTGGGGACA	180
OY	181	GTCGCGTGAACAGTATGCGATTCAAGAGTGAAGGCCATGCTGCATACCCTGAAAAGATC	240
Dd	181	GTCGCGTGAACAGTATGCGATTCAAGAGTGAAGGCCATGCTGCATACCCTGAAAAGATC	240
OY	241	AATTCAAGCCCCAACACTTTGGCCCACATCAACTGGGGCTGTGAATAAGGAAITTCCTGCG	300
Dd	241	AATTCAAGCCCCAACACTTTGGCCCACATCAACTGGGGCTGTGAATAAGGAAITTCCTGCG	300
OY	301	TGGCATTTGGGCTGTGGCCCTAGAGCAGACAAATGAGTTCATAAAGATITCCCTCATTTCT	360
Dd	301	TGGCATTTGGGCTGTGGCCCTAGAGCAGACAAATGAGTTCATAAAGATITCCCTCATTTCT	360
OY	361	TGCGAAGAAGAAAGAGGCTTGATGCTGTGTGATGGCTCCTCTCTTCTCTTCGCGCTCC	420
Dd	361	TGCGAAGAAGAAAGAGGCTTGATGCTGTGTGATGGCTCCTCTCTTCTCTTCGCGCTCC	420
OY	421	AAGAAGCCCATAGTAGGGGTGATTTGGGGCTGGTCCAATCTTTAGCCATTCAGGCTCCAG	480
Dd	421	AAGAAGCCCATAGTAGGGGTGATTTGGGGCTGGTCCAATCTTTAGCCATTCAGGCTCCAG	480
OY	481	AATTGTCTCAGCTTTTCAACATCCTGCAATGGCTTACTGACGAAACCATATGATCTG	540
Dd	481	AATTGTCTCAGCTTTTCAACATCCTGCAATGGCTTACTGACGAAACCATATGATCTG	540
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Dd	541	AGTGCACAGACTCTGTCTCAAATATTTCTAGAGGGTGTGCTCTCAGATGCTCAGCAGGCA	600
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Dd	601	AGGTCATAGTGAACATAGTGAAGAGTGAACAACTGATCTATGATCAAGCGGTACACACA	660
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Dd	841	GGCATGACGGGTGAAGAGTCTGTGTATGGCCATGAGGCGCTGGGGTCTATAGTGGAGAAATTT	900
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Dd	901	CTGCTTTGGGCGAGGAAACAGATCCATCTTTATTTAGATCTCAAGAACAGACATCCTA	960
OY	961	TGGGAAGACAGAGAAAAATGCCAAGGTGCTTCTTCAAGGGTTTTGAGACATATTCAC	1020
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DB	1261	CAGACTTTCACCTCTGGCAAGTATTACTGGAGGTCATGTGGGGGACTCTTGGAAATYGG	1320
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DB	1501	GATTGTGAAGTAAATCTGGAAGTTTGGTGAAGTTATCAAAAGTCCCTCATATACACC	1560
QY	1561	ATCCCTAATGCTCTTCTCAACCTCTCAAGGCTATCTTGTGCTATATCATCTCTGA	1620
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QY	1621	CCAGAGCAAAATCAGAAGAATGTATTATCTGTGTGGAAACCCCTTATATCCCATTAAGCCC	1680
DB	1621	CCAGAGCAAAATCAGAAGAATGTATTATCTGTGTGGAAACCCCTTATATCCCATTAAGCCC	1680
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QY	1741	CTAATGTTATTAATACTCATTTATGTGTATCTATTAATGTGTGTAAMACACAAAAAA	1800
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RESULT 2
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/ Sequence 61, Application US/09822830A
/ Patent No. US20020142952A1
/ GENERAL INFORMATION:
/ APPLICANT: Genetics Institute, Inc.
/ APPLICANT: Mong, Gordon G.
/ APPLICANT: Clark, Hilary
/ APPLICANT: Rechtel, Kim
/ APPLICANT: Agostino, Michael J.
/ APPLICANT: Howes, Steven H.
/ APPLICANT: Resnick, Richard J.
/ APPLICANT: Guhokota, Kamalakar
/ APPLICANT: Graham, James R.
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
/ FILE REFERENCE: GIN 6402
/ CURRENT APPLICATION NUMBER: US/09/822,830A
/ CURRENT FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/195,604
/ PRIOR FILING DATE: 2000-04-06
/ NUMBER OF SEQ ID NOS: 631
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 61
/ LENGTH: 1788
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-822-830A-61

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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 241 AGAGCCCACTCTTGGCCCAACATCACTGGGCTGTGAGATTAAGGATTCCTGCTGGCA 300

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QY 1746 GTTATTAAACTCAATTTATGTTTACTTAAATGTTGTAATAA 1789

DB 1741 GTTATTAAACTCAATTTATGTTTACTTAAATGTTGTAATAA 1784

RESULT 3  
 US-10-027-923-3  
 ; Sequence 3, Application US/10027923  
 ; Publication No. US20020142330A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brian Galtner Bates  
 ; APPLICANT: Kamalaka Gulukota  
 ; APPLICANT: Yuhong Xie  
 ; APPLICANT: Janet Elizabeth Paulsen  
 ; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
 ; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
 ; FILE REFERENCE: GNN-024  
 ; CURRENT FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: 60/257,589  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1110  
 ; TYPE: DNA

ORGANISM: Homo sapiens  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: (1)..(1110)  
 US-10-027-923-3

Query Match 60.9%; Score 1110; DB 14; Length 1110;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 481 TTGCTCAGCTTTTCAACATCACTCAGATGCTTCACTCAGAACATCATGATGATG 540
QY 544 GACAAAGCTCTGTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 603
DB 541 GACAAAGCTCTGTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 604 TCCATGCTGAGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
DB 601 TCCATGCTGAGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 664 GGCACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723
DB 661 GGCACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 724 TGCATGCCCACTCTTCAAAATCTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAG 783
DB 721 TGCATGCCCACTCTTCAAAATCTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 784 CTGAAGAGAGCTCAGAGATCACTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
DB 781 CTGAAGAGAGCTCAGAGATCACTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 844 ATGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
DB 841 ATGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 904 CTTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 963
DB 901 CTTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

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QY 964 GAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023
DB 961 GAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1024 AGTGAAGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
DB 1021 AGTGAAGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1084 ATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1113
DB 1081 ATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110

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## RESULT 4

```

US-10-346-241-1
; Sequence 1, Application US/10346241
; Publication No. US20030157647A1
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STOROHANN, LAURA G.
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: NRS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/10/346, 241
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US/09/695,481
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2826)
US-10-346-241-1

```

Query Match 12.2%; Score 222; DB 13; Length 2826;

Best Local Similarity 99.1%; Pred. No. 2.4e-102; Indels 0; Gaps 0;

Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 464 TAGCCATTCAGTCCAGAGATTTGCTCAGCTTTCAACATCACTCAGATGCTTACTCAG 523
DB 461 TAGCCATTCAGTCCAGAGATTTGCTCAGCTTTCAACATCACTCAGATGCTTACTCAG 520
QY 524 CAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583
DB 521 CAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
QY 584 CAGATGCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
DB 581 CAGATGCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
QY 644 TATCAGCCGTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
DB 641 TATCAGCCGTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
QY 704 TGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
DB 701 TGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
QY 764 AGCAGAGCTTTGATTAAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 823
DB 761 AGCAGAGCTTTGATTAAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 820
QY 824 TGCCCTACTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 883

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DB 821 TGGCTGCTCTGTGAGGGCATGACGGTGTGATGATGATGAGGGGCTTG 880  
QY 884 GTCTAG 889  
DB 881 GTCTAG 886

## RESULT 5

US-10-346-241-5  
; Sequence 5, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: STORMANN, LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241  
; PRIOR FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US/09/695,481  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 3129  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric  
; OTHER INFORMATION: molecule comprising portions of human mGluR5 and  
; OTHER INFORMATION: the human calcium receptor.  
; NAME/KEY: CDS  
; LOCATION: (1)..(3129)  
US-10-346-241-5

Query Match 12.2%; Score 222; DB 13; Length 3129;

Best Local Similarity 99.1%; Pred. No 2,4e-102; Indels 0; Gaps 0;

Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
DB 461 TACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 520  
QY 524 CAACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 583  
DB 521 CAACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 580  
QY 584 CAGATGTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 643  
DB 581 CAGATGTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 640  
QY 644 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 703  
DB 641 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 700  
QY 704 TGTCAAGGAAAGGAGGATTTGATGCGCCCACTTTTCAAAATCTTCAAGTAATGCAAGGG 763  
DB 701 TGTCAAGGAAAGGAGGATTTGATGCGCCCACTTTTCAAAATCTTCAAGTAATGCAAGGG 760  
QY 764 AGCAGAGCTTGTATAGCTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGG 823  
DB 761 AGCAGAGCTTGTATAGCTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGG 820  
QY 824 TGGCTGCTCTGTGAGGGCATGACGGTGTGATGATGATGAGGGGCTTG 883  
DB 821 TGGCTGCTCTGTGAGGGCATGACGGTGTGATGATGATGAGGGGCTTG 880

QY 884 GTCTAG 889  
DB 881 GTCTAG 886

## RESULT 6

US-10-225-567A-177  
; Sequence 177, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 177  
; LENGTH: 4518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-177

Query Match 12.2%; Score 222; DB 15; Length 4518;

Best Local Similarity 99.1%; Pred. No 2,4e-102; Indels 0; Gaps 0;

Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
DB 611 TACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 670  
QY 524 CAACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 583  
DB 671 CAACCATTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 720  
QY 584 CAGATGTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 643  
DB 731 CAGATGTCAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 720  
QY 644 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 703  
DB 791 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 850  
QY 704 TGTCAAGGAAAGGAGGATTTGATGCGCCCACTTTTCAAAATCTTCAAGTAATGCAAGGG 763  
DB 851 TGTCAAGGAAAGGAGGATTTGATGCGCCCACTTTTCAAAATCTTCAAGTAATGCAAGGG 910  
QY 764 AGCAGAGCTTGTATAGCTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGG 823  
DB 911 AGCAGAGCTTGTATAGCTGCTGAAGAGCTCAAGTCACTTGGCCCAAGCCCGGGTGG 970  
QY 824 TGGCTGCTCTGTGAGGGCATGACGGTGTGATGATGATGAGGGGCTTG 883  
DB 971 TGGCTGCTCTGTGAGGGCATGACGGTGTGATGATGATGAGGGGCTTG 1030  
QY 884 GTCTAG 889  
DB 1031 GTCTAG 1036

## RESULT 7

US-10-245-988-9  
; Sequence 9, Application US/10245988  
; Publication No. US20030108921A1  
; GENERAL INFORMATION:  
; APPLICANT: Jucker, Markus T.  
; APPLICANT: Brenlano, Steven T.

APPLICANT: Delgado, Francisco D.  
APPLICANT: Cleuziat, Philippe  
TITLE OF INVENTION: DETECTION OF RPOB SEQUENCES OF MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: GPI08-02.UT  
CURRENT APPLICATION NUMBER: US/10/245,988  
CURRENT FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: 60/323,485  
PRIOR FILING DATE: 2001-09-18  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 55  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: capture  
US-10-245-988-9

Query Match 1.8%; Score 33; DB 15; Length 55;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823  
Db 23 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 55

RESULT 8  
US-09-960-352-7296/C  
Sequence 7296, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathilagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 7296  
LENGTH: 111  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 31-LIB34-055-Q1-E1-H3  
US-09-960-352-7296

Query Match 1.8%; Score 33; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823  
Db 103 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 71

RESULT 9  
US-09-770-696-726/C  
Sequence 726, Application US/09770696  
Patent No. US2001004940A1  
GENERAL INFORMATION:  
APPLICANT: Goriach, Jorn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy

APPLICANT: Mathew, Abraham V.  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Woessner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Kricke, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.  
APPLICANT: Allen, Keith  
APPLICANT: Hoffman, Neil  
APPLICANT: Hurban, Patrick  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: 2031US (PARA-020PRV)  
CURRENT APPLICATION NUMBER: US/09/770,696  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,278  
PRIOR FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 911  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 726  
LENGTH: 116  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-770-696-726

Query Match 1.8%; Score 33; DB 9; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823  
Db 56 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 10  
US-09-867-701-9576  
Sequence 9576, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9576  
LENGTH: 166  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-9576

Query Match 1.8%; Score 33; DB 10; Length 166;  
Best Local Similarity 100.0%; Pred. No. 4.6e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823  
Db 78 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 110

RESULT 11  
US-09-925-299-750  
Sequence 750, Application US/09925299  
Patent No. US20020055627A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA102

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; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 750
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (155)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (159)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (165)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (173)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-750
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Query Match      1.8%; Score 33; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      46 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 78
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RESULT 12
; US-09-925-299-750
; Sequence 750, Application US/09925299
; Publication No. US2003040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 750
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (155)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (159)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (165)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
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```

; LOCATION: (173)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-750
```

```

Query Match      1.8%; Score 33; DB 11; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      46 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 78
```

```

RESULT 13
; US-09-867-701-9295
; Sequence 9295, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Agiata, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9295
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-867-701-9295
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Query Match      1.8%; Score 33; DB 10; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      146 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 178
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RESULT 14
; US-09-960-352-4816/c
; Sequence 4816, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Kengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathiasagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4816
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 21-LIB3057-015-Q1-K1-F1
; US-09-960-352-4816
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Query Match      1.8%; Score 33; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823
DB      42 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 10
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RESULT 15

US-09-867-701-9190  
 ; Sequence 9190, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agiate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9190  
 ; LENGTH: 212  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-867-701-9190

Query Match 1.8%; Score 33; DB 10; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-06;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1791 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1823  
 Db 166 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 198

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 Job time : 606.28 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:02:02 : Search time 366.72 seconds  
(without alignments)  
10059.976 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110

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18: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1110	14	US-10-027-923-3
2	1110	100.0	1823	14	US-10-027-923-1
3	1108	99.8	1788	10	US-09-822-830A-61
4	888.4	80.0	2826	13	US-10-346-241-1
5	888.4	80.0	3129	13	US-10-346-241-5
6	888.4	80.0	4518	13	US-10-346-241-5
7	458.2	41.3	3295	13	US-09-826-509-346
8	458.2	41.3	3295	13	US-09-826-509-346
9	458.2	41.3	6619	15	US-10-101-510-258
10	449.2	40.5	3219	15	US-10-225-567A-169
11	449.2	40.5	3384	15	US-10-300-473-1
12	444.4	40.0	3219	15	US-10-300-473-1
13	145.8	13.1	2736	10	US-10-255-149-1
14	143.6	12.9	2736	10	US-09-817-464-1
15	143.6	12.9	2736	15	US-10-331-289-1

16	143.6	12.9	3884	10	US-09-820-809-14	Sequence 14, Appl
17	143.6	12.9	3884	15	US-10-225-567A-175	Sequence 175, App
18	138.6	12.5	6122	15	US-10-225-567A-179	Sequence 179, App
19	131.6	11.9	2621	13	US-10-251-661-3	Sequence 3, Appl
20	131.6	11.9	2621	15	US-10-225-567A-171	Sequence 171, App
21	124	11.2	2830	10	US-09-900-714A-1	Sequence 1, Appl
22	123.6	11.1	3410	15	US-10-225-567A-173	Sequence 173, App
23	118.8	10.7	2745	15	US-09-817-464-11	Sequence 11, Appl
24	118.8	10.7	2745	15	US-10-331-289-11	Sequence 11, Appl
25	118.8	10.7	2748	15	US-10-083-168-7	Sequence 7, Appl
26	118.8	10.7	2748	15	US-10-083-168-66	Sequence 66, Appl
27	118.8	10.7	2748	15	US-10-083-168-68	Sequence 68, Appl
28	118.8	10.7	2748	15	US-10-083-168-70	Sequence 70, Appl
29	118.8	10.7	2748	15	US-10-083-168-72	Sequence 72, Appl
30	118.8	10.7	2766	15	US-09-817-464-13	Sequence 13, Appl
31	118.8	10.7	2766	15	US-10-331-289-13	Sequence 13, Appl
32	118.8	10.7	3804	15	US-09-817-464-3	Sequence 3, Appl
33	118.8	10.7	3804	15	US-10-331-289-3	Sequence 3, Appl
34	118.8	10.7	4312	15	US-10-225-567A-181	Sequence 181, App
35	114.8	10.3	3321	13	US-10-353-690-85	Sequence 85, Appl
36	114.8	10.3	3321	15	US-10-225-567A-183	Sequence 183, App
37	92	8.3	2595	15	US-10-151-208-13	Sequence 13, Appl
38	85.8	7.7	600	13	US-10-029-386-9681	Sequence 9681, Ap
39	84	7.6	227	13	US-10-002-854-1	Sequence 2381, A
40	83.8	7.5	3361	14	US-10-270-333-5	Sequence 1, Appl
41	82.8	7.5	2456	15	US-10-151-208-1	Sequence 5, Appl
42	82.4	7.4	2877	15	US-10-151-208-1	Sequence 1, Appl
43	82.2	7.4	2925	15	US-10-346-241-3	Sequence 3, Appl
44	82.2	7.4	3783	15	US-10-225-567A-117	Sequence 117, App
45	82.2	7.4	4000	15	US-10-300-473-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-10-027-923-3  
Sequence 3, Application US/10027923  
Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Brian Galtner Bates  
APPLICANT: Kamalaka Gulukota  
APPLICANT: Yuhong Xie  
APPLICANT: Janet Elizabeth Paulsen  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
FILE REFERENCE: NUCLEIC ACID MOLECULES AND USES THEREFOR  
CURRENT APPLICATION NUMBER: US/10/027,923  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,589  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1110  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1110)  
US-10-027-923-3  
Query Match 100.0%; Score 1110; DB 14; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTCTCTGTATCTCTGTCAGCTCTTAACTTTGAAAGAGATGTCCTGGAGATGCA 60  
DB 1 ATGCTCTCTCTGTATCTCTGTCAGCTCTTAACTTTGAAAGAGATGTCCTGGAGATGCA 60  
QY 61 CAGTTCAGTGAAG 120  
DB 61 CAGTTCAGTGAAG 120



Db	664	GGCAACTGTGAGAAAGTGGGATGGAAACCTTTCAAAAGTATGTCAGCCAAGGAAGGATTT	723
Qy	721	TGCATGCGCCACTCTTTACAAAATTACAGTAAATGCAAGGAGAGACAGAGCTTTGATAGCTG	780
Db	724	TGCATGCGCCCACTCTTTACAAAATCTACAGTAAATGCAAGGAGAGACAGAGCTTTGATAGCTG	783
Qy	781	CTGAAGAAAGCTCACAAGTCACTTGTGCCCAAGGCCCGGGTGTGTGGCTACTTCTGTGAGGGC	840
Db	784	CTGAAGAAAGCTCACAAGTCACTTGTGCCCAAGGCCCGGGTGTGTGGCTACTTCTGTGAGGGC	843
Qy	841	ATGACGGTAGAGGGCTGCTGTGATGCGCATGAGGAGCGCTGGGCTGTAGTGGAGAAATTTCTG	900
Db	844	ATGACGGTAGAGGGCTGCTGTGATGCGCATGAGGAGCGCTGGGCTGTAGTGGAGAAATTTCTG	903
Qy	901	CTTCTGGGACAGGAAACAGATGCGCATCTTTATTAGATCTCAAGAAACAGGATCCTATGG	960
Db	904	CTTCTGGGACAGGAAACAGATGCGCATCTTTATTAGATCTCAAGAAACAGGATCCTATGG	963
Qy	961	GAAGACAGAGAAATAATGCCAAGTGCCTTCTTCAGGGTTTTGGAGACATATTACACAGA	1020
Db	964	GAAGACAGAGAAATAATGCCAAGTGCCTTCTTCAGGGTTTTGGAGACATATTACACAGA	1023
Qy	1021	AGTAGTCCCGTCTGCTGCAATGCCCCAGGCTCTGAATCTAGAGCTCAAGTTCAAGGCC	1088
Db	1024	AGTAGTCCCGTCTGCTGCAATGCCCCAGGCTCTGAATCTAGAGCTCAAGTTCAAGGCC	1091
Qy	1081	ATCACTGAGCTGAGGAGCAGGCTCATCTTAA	1110
Db	1084	ATCACTGAGCTGAGGAGCAGGCTCATCTTAA	1113

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RESULT 3
US-09-822-830A-61
: Sequence 61, Application US/09822830A
: Patent No. US20020142952A1
: GENERAL INFORMATION:
: APPLICANT: Genetics Institute, Inc.
: APPLICANT: Wong, Gordon G.
: APPLICANT: Clark, Hilary
: APPLICANT: Fechtel, Kim
: APPLICANT: Agostino, Michael J.
: APPLICANT: Howes, Steven H.
: APPLICANT: Resnick, Richard J.
: APPLICANT: Gulukota, Kamalakara
: APPLICANT: Graham, James R.
: TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
: FILE REFERENCE: GIN 6402
: CURRENT APPLICATION NUMBER: US/09/822, 830A
: CURRENT FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/195,604
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 631
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 61
: LENGTH: 1788
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-822-830A-61

Query Match          99.8%; Score 1108; DB 10; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTCTTCTGTGTAACCTGTCAGTCTTACTTTGAAAGAAGATGCGGTGGAGATGCACA 62
Db 1 GGTCTTCTGTGTAACCTGTCAGTCTTACTTTGAAAGAAGATGCGGTGGAGATGCACA 60
QY 63 GTCCAGTAGAGAGAGGTGTGTGCTCACATGCTGGGTGACATCATTTATTTGAGCTCTCTT 122
Db 61 GTCCAGTAGAGAGAGGTGTGTGCTCACATGCTGGGTGACATCATTTATTTGAGCTCTCTT 120
QY 123 TTCTGTTTCATACACAGCTTACTGTGTGACGAAGTTTCATGAGAGGAAGTGTGGGCGAGTCCG 182

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Db	121	TTCTGTTTCATACCAAGCTACTGTGGACGAAGTTCAATGAGAGAAAGTGTGGGCAAGTCCG	180
QY	183	TGAACAGTATGGCAATTCAAGAGTGGAGAGGCATGCTGCATACCTGGAAAGATCAATTG	242
Db	181	TGAACAGATATGGCAATTCAGAGATGGAGAGGCATGCTGCATACCTGGAAAGATCAATTG	240
QY	243	AGACCCCAACATCTTGGCCCAATCAACAATGGGGCTGGAGATAAGGGATTCTGTGGCA	302
Db	241	AGACCCCAACATCTTGGCCCAATCAACTGGGCTGGAGATAAGGGATTCTGTGGCA	300
QY	303	TTGCGCTGTGGCCCTTAGAGCAGAGCAATTAAGATTCTAATAAGATTCCCTCATTTCTTGGCA	362
Db	301	TTGCGCTGTGGCCCTTAGAGCAGAGCAATTAAGATTCTAATAAGATTCCCTCATTTCTTGGCA	360
QY	363	AGAGAAAGAGGGCTTTGGTAATGCTGTGGATAGGCTCTCTCTCTCTCTCTCTGGCTCAAGAA	422
Db	361	AGAGAAAGAGGGCTTTGGTAATGCTGTGGATAGGCTCTCTCTCTCTCTCTCTGGCTCAAGAA	420
QY	423	GCCCATAGTAGGGGTCAATTGGGCTGGTCCAGTCTTTAGCCCAATGAGTCCAGAAATTT	482
Db	421	GCCCATAGTAGGGGTCAATTGGGCTGGTCCAGTCTTTAGCCCAATGAGTCCAGAAATTT	480
QY	483	GCTCCAGCTTTTCAACATACCTCAAGATTGCTTACTCAAGCAACAATATGATCTTGAATGA	542
Db	481	GCTCCAGCTTTTCAACATACCTCAAGATTGCTTACTCAAGCAACAATATGATCTTGAATGA	540
QY	543	CAAGACTCTGTTCAAAATATTTCAAGAGGGTGTGCTTCAGATGCTCAGAGCGAGCAAGGTC	602
Db	541	CAAGACTCTGTTCAAAATATTTCAAGAGGGTGTGCTTCAGATGCTCAGAGCGAGCAAGGTC	600
QY	603	CATGATGACATATAGTGAAGAGTACAATGGAACCTATGTATCAGCCGTTACACAGAAAG	662
Db	601	CATGATGACATATAGTGAAGAGTACAATGGAACCTATGTATCAGCCGTTACACAGAAAG	660
QY	663	CAACTATAGGAAGAGTGGATGGAAGCCTTCAAAAGATATGTCAGCGAAGAGGAAGGATTTG	722
Db	661	CAACTATAGGAAGAGTGGATGGAAGCCTTCAAAAGATATGTCAGCGAAGAGGAAGGATTTG	720
QY	723	CATGCGCCACTCTTACAAATCTACAGTAATGACGGGAGCAGAGCTTGTATTAAGTCT	782
Db	721	CATGCGCCACTCTTACAAATCTACAGTAATGACGGGAGCAGAGCTTGTATTAAGTCT	780
QY	783	GAAGAAGTCAACAGTCACTTGGCCCAAGGCCCCGGGTGGTGGCTTAATTTCTGTAGGGCAT	842
Db	781	GAAGAAGTCAACAGTCACTTGGCCCAAGGCCCCGGGTGGTGGCTTAATTTCTGTAGGGCAT	840
QY	843	GACGGTGAAGAGTGTGCTGATAGGCTCATGAGGCGGCTGGTCTTATGGGAGAAATTTCTGCT	902
Db	841	GACGGTGAAGAGTGTGCTGATAGGCTCATGAGGCGGCTGGTCTTATGGGAGAAATTTCTGCT	900
QY	903	TCTGGGCAAGGAAACAAGATGCATCTTATTTAGATCTCAAGAAACAGCATCTATGGGA	962
Db	901	TCTGGGCAAGGAAACAAGATGCATCTTATTTAGATCTCAAGAAACAGCATCTATGGGA	960
QY	963	AGACAGAAAGAAATAGCAAGGTGCTCTCTTCAAGGTTTGGAGACATATTAACAGAG	1022
Db	961	AGACAGAAAGAAATAGCAAGGTGCTCTCTTCAAGGTTTGGAGACATATTAACAGAG	1020
QY	1023	TGAGTCCGTGCTGTGCACATGCCCCAGGCTCTGAATCTAAGGCTCAAGTTCAGGGCCCAT	1082
Db	1021	TGAGTCCGTGCTGTGCACATGCCCCAGGCTCTGAATCTAAGGCTCAAGTTCAGGGCCCAT	1080
QY	1083	CACATGACATAAGGGAACAGGCTCAATCTTAA	1110
Db	1081	CACATGACATAAGGGAACAGGCTCAATCTTAA	1108

RESULT 4  
US-10-346-241-1  
; Sequence 1, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:

```

; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHANN, LAURA
; APPLICANT: HAMERLAND, LANCE G.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: NPS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/10/346,241
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US/09/695,481
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2826)
; US-10-346-241-1

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Query Match 80.0%; Score 888.4; DB 13; Length 2826;

Best Local Similarity 98.2%; Pred. No. 2.8e-286; Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy 1 ATGGTCCTTCTGTGATCTGTCACTCTTACTTTTGAAGAAGATGTCGGGAGTGCA 60
Db 1 ATGGTCCTTCTGTGATCTGTCACTCTTACTTTTGAAGAAGATGTCGGGAGTGCA 60
Qy 61 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 61 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Qy 121 TTTTCTGTTATATACCAAGCCTACTGTGGAAGAGTTATAGAGAAAGTGCGGAGTC 180
Db 121 TTTTCTGTTATATACCAAGCCTACTGTGGAAGAGTTATAGAGAAAGTGCGGAGTC 180
Qy 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Qy 241 TCAGAACCCCACTCTTGGCCCAATATCACTGGGCTGTGAGATTAAGGAGTTCTGCTGG 300
Db 241 TCAGAACCCCACTCTTGGCCCAATATCACTGGGCTGTGAGATTAAGGAGTTCTGCTGG 300
Qy 301 CATTGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 CATTGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 361 GAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 GAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 421 AAGGCCATAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 421 AAGGCCATAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Qy 481 TTGCTCAGCTTTTCAACATATTTTCAATATTTTCAATATTTTCAATATTTTCAATAT 540
Db 481 TTGCTCAGCTTTTCAACATATTTTCAATATTTTCAATATTTTCAATATTTTCAATAT 540
Qy 541 GACAAAGCTCTGTTCAATATTTTCAATATTTTCAATATTTTCAATATTTTCAATAT 600
Db 541 GACAAAGCTCTGTTCAATATTTTCAATATTTTCAATATTTTCAATATTTTCAATAT 600
Qy 601 TCCATGCTGACATATGTAAGAGGAGTCACTGAGCTATGATATAGCCGTTACACAGAA 660
Db 601 TCCATGCTGACATATGTAAGAGGAGTCACTGAGCTATGATATAGCCGTTACACAGAA 660

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Qy 661 GGCACATATGAGAAAGTGGATGGAAGCCTTCAAAAGATATGTACAGGAAGAGGATT 720
Db 661 GGCACATATGAGAAAGTGGATGGAAGCCTTCAAAAGATATGTACAGGAAGAGGATT 720
Qy 721 TGCAATGCGCCACTTTTCAAAATTTTCAATATTTTCAATATTTTCAATATTTTCAAT 780
Db 721 TGCAATGCGCCACTTTTCAAAATTTTCAATATTTTCAATATTTTCAATATTTTCAAT 780
Qy 781 CTGAAGAAGCTCAAGTCACTTGGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db 781 CTGAAGAAGCTCAAGTCACTTGGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Qy 841 ATGACGCTGAGAGGAGTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 841 ATGACGCTGAGAGGAGTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Qy 901 CTTCCTGGGAGGGA 914
Db 901 CTTCCTGGGAGGGA 914

```

# RESULT 5

US-10-346-241-5

Sequence 5, Application US/10346241

Publication No. US20030157647A1

GENERAL INFORMATION:

APPLICANT: STORMANN, THOMAS M.

APPLICANT: LEVINTHAL, CYNTHIA

APPLICANT: STORJOHANN, LAURA

APPLICANT: HAMERLAND, LANCE G.

APPLICANT: KRAPCHO, KAREN J.

APPLICANT: NPS PHARMACEUTICALS, INC.

TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR

FILE REFERENCE: 1094.2.6

CURRENT APPLICATION NUMBER: US/10/346,241

CURRENT FILING DATE: 2003-01-17

PRIOR APPLICATION NUMBER: US/09/695,481

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: 60/161,481

PRIOR FILING DATE: 1999-10-25

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 3129

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Chimeric

OTHER INFORMATION: molecule comprising portions of human mglur5d and

OTHER INFORMATION: the human calcium receptor.

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(3129)

US-10-346-241-5

Query Match 80.0%; Score 888.4; DB 13; Length 3129;

Best Local Similarity 98.2%; Pred. No. 2.9e-286; Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy 1 ATGGTCCTTCTGTGATCTGTCACTCTTACTTTTGAAGAAGATGTCGGGAGTGCA 60
Db 1 ATGGTCCTTCTGTGATCTGTCACTCTTACTTTTGAAGAAGATGTCGGGAGTGCA 60
Qy 61 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 61 CAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Qy 121 TTTTCTGTTATATACCAAGCCTACTGTGGAAGAGTTATAGAGAAAGTGCGGAGTC 180
Db 121 TTTTCTGTTATATACCAAGCCTACTGTGGAAGAGTTATAGAGAAAGTGCGGAGTC 180
Qy 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

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Db 181 CGTGAACAGTANGCATTGAGAGTGAAGGCCATGCTGATCACTCGTGAAGATCAAT 240  
Qy 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATAAGGATTCCTGCTGG 300  
Db 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATAAGGATTCCTGCTGG 300  
Qy 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGATTCATAAAGATTCCTCATTTCTTGG 360  
Db 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGATTCATAAAGATTCCTCATTTCTTGA 360  
Qy 361 GAAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGGCTCTCTCTTCTTCCGCTCAAG 420  
Db 361 GAAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGGCTCTCTCTTCTTCCGCTCAAG 420  
Qy 421 AAGCCCATGTAGAGGCTCATTTGGGCTGGTTCAGTTCTTTAGCCATTGAGCTCCAGAT 480  
Db 421 AAGCCCATGTAGAGGCTCATTTGGGCTGGTTCAGTTCTTTAGCCATTGAGCTCCAGAT 480  
Qy 481 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCAATCATGATCTGAGT 540  
Db 481 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCAATCATGATCTGAGT 540  
Qy 541 GACAAAGACTCTGTTCATAATTTTATGAGGCTTGTGCTTCAAGTCTCAGAGCAGCAAG 600  
Db 541 GACAAAGACTCTGTTCATAATTTTATGAGGCTTGTGCTTCAAGTCTCAGAGCAGCAAG 600  
Qy 601 TCCATGTTGAGACATGATGAAGAGGTACAATGAGCCTATGATACAGCCGTCACACAGAA 660  
Db 601 TCCATGTTGAGACATGATGAAGAGGTACAATGAGCCTATGATACAGCCGTCACACAGAA 660  
Qy 661 GGCACCTATGAGAAAGTGGATGAGAGCCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 720  
Db 661 GGCACCTATGAGAAAGTGGATGAGAGCCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 720  
Qy 721 TGCATGCCCCACTCTTCAAAATTTACAGTATGACAGGAGAGCAGCTTTGATTAAGCTG 780  
Db 721 TGCATGCCCCACTCTTCAAAATTTACAGTATGACAGGAGAGCAGCTTTGATTAAGCTG 780  
Qy 781 CTGAAGAGCTCAAGATCACTTGGCCCAAGGCCCGGGGTGTGGCTTACTTCTGTAGGGC 840  
Db 781 CTGAAGAGCTCAAGATCACTTGGCCCAAGGCCCGGGGTGTGGCTTACTTCTGTAGGGC 840  
Qy 841 ATGACGGTGAAGAGTGTGCTGATGAGCAGATGAGGCGCTGGGTCTAGTGGGAGAAATTTCTG 900  
Db 841 ATGACGGTGAAGAGTGTGCTGATGAGCAGATGAGGCGCTGGGTCTAGCAGGAGAAATTTCTG 900  
Qy 901 CTTCTGGGAGGAGA 914  
Db 901 CTTCTGGGAGGAGA 914

RESULT 6  
US-10-225-567A-177  
; Sequence 177, Application US/10225567A  
; Publication No.: US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 177  
; LENGTH: 4518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-177

Query Match 80.0%; Score 888.4; DB 15; Length 4518;  
Best Local Similarity 98.2%; Pred. No. 3 6e-286;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
Qy 1 ATGCTCTTCTGTGTGATTCCTGTCAGTCTTACTTTTGAAGAAAGATTCCTGGAGTGA 60  
Db 151 ATGCTCTTCTGTGTGATTCCTGTCAGTCTTACTTTTGAAGAAAGATTCCTGGAGTGA 210  
Qy 61 CAGTCCAGTGAAGAGAGGCTGTGCTCAATGCTGGGTGAATCATTTATGGAGCTCTC 120  
Db 211 CAGTCCAGTGAAGAGAGGCTGTGCTCAATGCTGGGTGAATCATTTATGGAGCTCTC 270  
Qy 121 TTTTCTGTTCAATCAGCAGCTTACTGTGAGCAAGATTATGAGAGAAAGTGGGGGAGTC 180  
Db 271 TTTTCTGTTCAATCAGCAGCTTACTGTGAGCAAGATTATGAGAGAAAGTGGGGGAGTC 330  
Qy 181 CGTGAACAGTATGGAATTCAGAGAGTGAAGGCCATGCTGCATACCTGGAAGATCAAT 240  
Db 331 CGTGAACAGTATGGAATTCAGAGAGTGAAGGCCATGCTGCATACCTGGAAGATCAAT 390  
Qy 241 TCAGACCCCACTCTTGGCCCAATCACAATGAGGCTGTGAGATAAGGATTCCTGCTGG 300  
Db 391 TCAGACCCCACTCTTGGCCCAATCACAATGAGGCTGTGAGATAAGGATTCCTGCTGG 450  
Qy 301 CATTGGGCTGTGGCCCTAGAGCAGAGCATTGATTCATAAAGATTCCTCATTTCTTGG 360  
Db 451 CATTGGGCTGTGGCCCTAGAGCAGAGCATTGATTCATAAAGATTCCTCATTTCTTGA 510  
Qy 361 GAAAGAGAAAGAGGCTTGGTATGCTCTGTGATGAGTGGCTCTCTCTTCTTCCGCTCAAG 420  
Db 511 GAAAGAGAAAGAGGCTTGGTATGCTCTGTGATGAGTGGCTCTCTCTTCTTCCGCTCAAG 570  
Qy 421 AAGCCCATGTAGAGGCTCATTTGGGCTGTTCAGTCTTTTGAACATTCAGGTCAGAAAT 480  
Db 571 AAGCCCATGTAGAGGCTCATTTGGGCTGTTCAGTCTTTTGAACATTCAGGTCAGAAAT 630  
Qy 481 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCAATCATGATCTGAGT 540  
Db 631 TTGCTTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCAATCATGATCTGAGT 590  
Qy 541 GACAAAGACTCTGTTCATAATTTTATGAGGCTTGTGCTTCAAGTCTCAGAGCAGCAAG 600  
Db 691 GACAAAGACTCTGTTCATAATTTTATGAGGCTTGTGCTTCAAGTCTCAGAGCAGCAAG 750  
Qy 601 TCCATGTTGAGACATGATGAAGAGGTACAATGAGCCTATGATATCAGCCGTCACACAGAA 660  
Db 751 TCCATGTTGAGACATGATGAAGAGGTACAATGAGCCTATGATATCAGCCGTCACACAGAA 810  
Qy 661 GGCACCTATGAGAAAGTGGATGAGAGCCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 720  
Db 811 GGCACCTATGAGAAAGTGGATGAGAGCCTTCAAAAGATATGTCAAGCAAGAAAGGATTT 870  
Qy 721 TGCATGCCCCACTCTTCAAAATTTACAGTATGACAGGAGAGCAGCTTTGATTAAGCTG 780  
Db 871 TGCATGCCCCACTCTTCAAAATTTACAGTATGACAGGAGAGCAGCTTTGATTAAGCTG 930  
Qy 781 CTGAAGAGCTCAAGATCACTTGGCCCAAGGCCCGGGGTGTGGCTTACTTCTGTAGGGC 840  
Db 931 CTGAAGAGCTCAAGATCACTTGGCCCAAGGCCCGGGGTGTGGCTTACTTCTGTAGGGC 990  
Qy 841 ATGACGGTGAAGAGTGTGCTGATGAGCAGATGAGGCGCTGGGTCTAGCAGGAGAAATTTCTG 900  
Db 991 ATGACGGTGAAGAGTGTGCTGATGAGCAGATGAGGCGCTGGGTCTAGCAGGAGAAATTTCTG 1050  
Qy 901 CTTCTGGGAGGAGA 914  
Db 1051 CTTCTGGGAGGAGA 1064

RESULT 7  
US-09-826-509-346  
; Sequence 346, Application US/09826509





Db 961 GTACAAATCTCTGAGGGTGTCCCTTGTGACATTTGCAAGGCAAGGCCATGCTTGA 1020  
Qy 612 CATAGTGAAGAGGTACAACTGACCTATGTATGAGCGGTACACAGAGGCAACTATGG 671  
Db 1021 CATAGTGAAGAGGTACAACTGACCTATGTATGAGCGGTACACAGAGGCAACTATGG 1080  
Qy 672 AGAAGTGGAGTGAAGGCTTCAAGATATGTACAGCAAGAGGAGGATTTGCAATCGCCA 731  
Db 1081 GGAGAGGGAATGGAAGCTTTCAAGAGCTGCGTCCAGAGGAGGCTCTGTATCGCCA 1140  
Qy 732 CTCTTCAAAATCTACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 791  
Db 1141 TTCTGCAAAATCTACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
Qy 792 CACAAGTCACTTCCCAAGGCGCGGTGTGCTTCTTGTGAGGAGGAGGAGGAGGAGGAGG 851  
Db 1201 CCGAGAGAGGCTTCCCAAGGCTGAGTGTGCTTCTTGTGAGGAGGAGGAGGAGGAGG 1260  
Qy 852 AGGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 911  
Db 1261 AGGACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
Qy 912 GGA 914  
Db 1321 TGA 1323

## RESULT 9

US-10-225-567A-169  
; Sequence 169, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 169  
; LENGTH: 6619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-169

Query Match 41.3%; Score 458.2; DB 15; Length 6619;  
Best Local Similarity 72.5%; Pred. No. 6.5e-142;  
Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

Qy 81 GGTGGCTCAGCATGCTGGGAGCATATTATGAGGCTCTTTTCTGTGATCAACCGCC 140  
Db 346 GGTGGCTCAGCATGCTGGGAGCATATTATGAGGCTCTTTTCTGTGATCAACCGCC 405  
Qy 141 TACTGTGAGCAAGTTCATGAGAGGAGTGTGGGAGTCCGTGAACATATGATGATCA 200  
Db 406 TCCGGCCGAAAGTGTCCGAGGAGGAGTGTGGGAGTCCGTGAACATATGATGATCA 465  
Qy 201 GAGAGTGGAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 260  
Db 466 GAGAGTGGAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 525  
Qy 261 CACATCACTGGGCTGTGAGATTAAGAGATTCCTGTGGGATTCGGCTGGGCGCTAGA 320  
Db 526 CACATCACTGGGCTGTGAGATTAAGAGATTCCTGTGGGATTCGGCTGGGCGCTAGA 380  
Qy 321 GAGAGATTAAGATTAAGAGATTCCTGTGGGATTCGGCTGGGCGCTAGA 380  
Db 586 ACAGAGATTAAGATTAAGAGATTCCTGTGGGATTCGGCTGGGCGCTAGA 645

Qy 381 ATGC-----TGTGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 431  
Db 646 CACCGGTGTCT 705  
Qy 432 AGGGGTATTTGGGCTGTGTTCAGATCTTATGAGGATTCAGTCCAGATTTGCTCCAGCT 491  
Db 706 GGGAGTATGGGTCCGGGCTCCAGCTCTGTAGCAATTAAGTCAAGAACTGCTCCAGCT 765  
Qy 492 TTTCACATACCTCAATTTGCTTACTGAGCAACATCATGATGATGATGATGATGATGAT 551  
Db 766 CTTCGACATCCCAATGCTTATTCAGCAACATCATGATGATGATGATGATGATGATGAT 825  
Qy 552 GTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCT 611  
Db 826 GTACAAATATCTCTAGAGGTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885  
Qy 612 CATAGTGAAGAGGTACAACTGACCTATGATGATGATGATGATGATGATGATGATGATG 671  
Db 886 CATAGTGAAGAGGTACAACTGACCTATGATGATGATGATGATGATGATGATGATGATG 945  
Qy 672 AGAAGTGGAGTGAAGGCTTCAAGATATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 731  
Db 946 GAGAGCGGAGTGAAGGCTTCAAGAGGCTGCTGCCAGGAGGAGGAGGAGGAGGAGGAG 1005  
Qy 732 CTCTTCAAAATCTACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 791  
Db 1006 TTCTGCAAAATCTACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1065  
Qy 792 CACAAGTCACTTCCCAAGGCGCGGTGTGCTTCTTGTGAGGAGGAGGAGGAGGAGGAGG 851  
Db 1066 CCGAGAGAGGCTTCCCAAGGCTGAGTGTGCTTCTTGTGAGGAGGAGGAGGAGGAGG 1125  
Qy 852 AGGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 911  
Db 1126 AGGACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1185  
Qy 912 GGA 914  
Db 1186 TGA 1188

## RESULT 10

US-10-300-473-3  
; Sequence 3, Application US/10300473  
; Publication No. US20030113873A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: FULLER, FORREST H.  
; APPLICANT: KAPCHO, KAREN J.  
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING  
; TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE  
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE  
; FILE REFERENCE: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES  
; CURRENT APPLICATION NUMBER: US/10/300,473  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 09/435,897  
; PRIOR FILING DATE: 1999-11-08  
; PRIOR APPLICATION NUMBER: 08/687,289  
; PRIOR FILING DATE: 1996-07-25  
; PRIOR APPLICATION NUMBER: 60/001,526  
; PRIOR FILING DATE: 1995-07-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthesized rat







; PRIOR FILING DATE: 1993-09-20  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2736  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2736)  
US-10-331-289-1

Query Match 12.9%; Score 143.6; DB 15; Length 2736;  
Best Local Similarity 55.7%; Pred. No. 1,1e-36;  
Matches 322; Conservative 0; Mismatches 244; Indels 12; Gaps 2;

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DB 199 TGTGGAGAACTTAAGAAAGAAAGGGGATCCACCGGCTGGAGGCCATGTGTGCGCCTG 258  
QY 229 GAAAGATCAATTCAAGCCCCACACTTGGCCCAACATCACTGGGCTGTGATTAAG 288  
DB 259 GATGGCATCAACAGACCCGACCTGTGCTTAACATCAAGCTGGGCGCCGCAATTCTG 318  
QY 289 GATTCCCTGTGGCATTCGGCTGTGGCCCTAGAGCAGAGCATTTGAGTTCATAGAGATTCC 348  
DB 319 GACACCTGTCTCCAGGAGACACCCATGCTTCAGAGCATGCGCTTGTGTGAGGGCCTC 378  
QY 349 CTGATTTCTTTCGGAAGAGAGAGGGCTTGTAATGCTGTGTGAATGGCTCTCTCTTC 408  
DB 379 ATC-----GAGAAAGATGGCAGAGAGTCCGCTGTGGCAGTGGCGGCCACCATC 429  
QY 409 TTCCGCTCCAGAAAGCCCATAGTAGGGGTCAATGGGGCTGTGCTTCAATTTTAGCCATT 468  
DB 430 ATCAACCAAGCTGAACGTGTGTGTGTGTCATCGGTCTCAGGAGCTGGTCTCCATC 489  
QY 469 CAGGTCAGAAATTGTCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATC 528  
DB 490 ATGTGGCCCAACATCTTCCCTCTTCAAGATACCCAGATCACTACGCTTCCACAGCG 549  
QY 529 ATGGATCTGAGTACAAAGACTCTGTTCAAATATTTCATGAGGGTGTGCTTCAATGCT 588  
DB 550 CCAGACTGTAGTACAAACAGCCGCTACGACTTCTTCCCGGCGTGGGCCCTCGACACG 609  
QY 589 CAGCAGGCAAGTCCATGTGTGACATATGTGAAGATCACTGAGCTTATATACGCC 648  
DB 610 TACCAAGGCCAGGCAATGTGTGACATGTCCGCTCAAGTGAACATAATGTGTCCCA 669  
QY 649 GTACACACAGAAAGCAACTATGAGAAAGTGGAGTGAAGCCTTCAAGAATATGTACGCG 708  
DB 670 GTGGCTTCGAGGCGAGCTATGTGTGAAGCGGTGTGAGGCTTTCATCCAGAAATCCCGT 729  
QY 709 AAGGAAGG---ATTGTCATGCCCCACTTTACAAAT 743  
DB 730 GAGGACGGGGCGTGTGCATGCCAGTCGCTGAAGAT 767

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Run on: December 14, 2003, 21:52:04 ; Search time 415 Seconds  
(Without alignments)  
2955.200 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA:\*

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- 3: /cg2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 12: /cg2\_6/ptodata/2/pubpna/US09\_PUB.seq:\*
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- 16: /cg2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1873	100.0	1110	14	US-10-027-923-3	Sequence 3, Appl1
2	1873	100.0	1823	14 <td>US-10-027-923-1</td> <td>Sequence 1, Appl1</td>	US-10-027-923-1	Sequence 1, Appl1
3	1868	99.7	1788	14 <td>US-09-822-830A-61</td> <td>Sequence 61, Appl1</td>	US-09-822-830A-61	Sequence 61, Appl1
4	1484.5	79.3	2826	13 <td>US-10-346-241-1</td> <td>Sequence 1, Appl1</td>	US-10-346-241-1	Sequence 1, Appl1
5	1484.5	79.3	3129	13 <td>US-10-346-241-5</td> <td>Sequence 5, Appl1</td>	US-10-346-241-5	Sequence 5, Appl1
6	1484.5	79.3	4518	13 <td>US-10-225-567A-177</td> <td>Sequence 177, Appl1</td>	US-10-225-567A-177	Sequence 177, Appl1
7	1118.5	59.7	2634	13 <td>US-09-826-509-346</td> <td>Sequence 346, App</td>	US-09-826-509-346	Sequence 346, App
8	1118.5	59.7	3295	13 <td>US-10-101-510-258</td> <td>Sequence 258, App</td>	US-10-101-510-258	Sequence 258, App
9	1118.5	59.7	4639	13 <td>US-10-225-567A-159</td> <td>Sequence 159, App</td>	US-10-225-567A-159	Sequence 159, App
10	1117.5	59.7	3219	15 <td>US-10-300-473-3</td> <td>Sequence 3, Appl1</td>	US-10-300-473-3	Sequence 3, Appl1
11	1117.5	59.7	3219	15 <td>US-10-300-473-4</td> <td>Sequence 4, Appl1</td>	US-10-300-473-4	Sequence 4, Appl1
12	1117.5	59.7	3384	15 <td>US-10-300-473-1</td> <td>Sequence 1, Appl1</td>	US-10-300-473-1	Sequence 1, Appl1
13	550	29.4	2830	10 <td>US-09-900-714A-1</td> <td>Sequence 1, Appl1</td>	US-09-900-714A-1	Sequence 1, Appl1
14	548	29.3	3321	13 <td>US-10-353-699-85</td> <td>Sequence 85, Appl1</td>	US-10-353-699-85	Sequence 85, Appl1
15	548	29.3	3321	13 <td>US-10-225-567A-183</td> <td>Sequence 183, App</td>	US-10-225-567A-183	Sequence 183, App
16	546.5	29.2	2736	10 <td>US-09-817-464-1</td> <td>Sequence 0, Appl1</td>	US-09-817-464-1	Sequence 0, Appl1
17	546.5	29.2	2736	10 <td>US-10-331-289-1</td> <td>Sequence 1, Appl1</td>	US-10-331-289-1	Sequence 1, Appl1
18	546.5	29.2	3884	15 <td>US-09-820-809-14</td> <td>Sequence 14, Appl1</td>	US-09-820-809-14	Sequence 14, Appl1
19	546.5	29.2	3884	15 <td>US-10-225-567A-175</td> <td>Sequence 175, App</td>	US-10-225-567A-175	Sequence 175, App
20	544.5	29.1	3867	15 <td>US-10-255-149-1</td> <td>Sequence 1, Appl1</td>	US-10-255-149-1	Sequence 1, Appl1
21	538.5	28.8	2745	10 <td>US-09-817-464-11</td> <td>Sequence 11, Appl1</td>	US-09-817-464-11	Sequence 11, Appl1
22	538.5	28.8	2745	15 <td>US-10-331-289-11</td> <td>Sequence 11, Appl1</td>	US-10-331-289-11	Sequence 11, Appl1
23	538.5	28.8	2748	15 <td>US-10-083-168-7</td> <td>Sequence 7, Appl1</td>	US-10-083-168-7	Sequence 7, Appl1
24	538.5	28.8	2748	15 <td>US-10-083-168-66</td> <td>Sequence 66, Appl1</td>	US-10-083-168-66	Sequence 66, Appl1
25	538.5	28.8	2748	15 <td>US-10-083-168-66</td> <td>Sequence 68, Appl1</td>	US-10-083-168-66	Sequence 68, Appl1
26	538.5	28.8	2748	15 <td>US-10-083-168-70</td> <td>Sequence 70, Appl1</td>	US-10-083-168-70	Sequence 70, Appl1
27	538.5	28.8	2748	15 <td>US-10-083-168-72</td> <td>Sequence 72, Appl1</td>	US-10-083-168-72	Sequence 72, Appl1
28	538.5	28.8	2766	10 <td>US-09-817-464-13</td> <td>Sequence 13, Appl1</td>	US-09-817-464-13	Sequence 13, Appl1
29	538.5	28.8	2766	10 <td>US-10-331-289-13</td> <td>Sequence 13, Appl1</td>	US-10-331-289-13	Sequence 13, Appl1
30	538.5	28.8	4312	15 <td>US-10-225-567A-181</td> <td>Sequence 181, App</td>	US-10-225-567A-181	Sequence 181, App
31	532	28.4	2621	13 <td>US-10-251-661-3</td> <td>Sequence 3, Appl1</td>	US-10-251-661-3	Sequence 3, Appl1
32	532	28.4	2621	15 <td>US-10-225-567A-171</td> <td>Sequence 171, App</td>	US-10-225-567A-171	Sequence 171, App
33	525.5	28.1	6122	15 <td>US-10-225-567A-179</td> <td>Sequence 179, App</td>	US-10-225-567A-179	Sequence 179, App
34	522	27.9	3410	15 <td>US-10-225-567A-173</td> <td>Sequence 173, App</td>	US-10-225-567A-173	Sequence 173, App
35	511.5	27.3	3804	15 <td>US-09-817-464-3</td> <td>Sequence 3, Appl1</td>	US-09-817-464-3	Sequence 3, Appl1
36	511.5	27.3	3804	15 <td>US-10-331-289-3</td> <td>Sequence 3, Appl1</td>	US-10-331-289-3	Sequence 3, Appl1
37	381.5	20.4	2295	13 <td>US-10-346-241-3</td> <td>Sequence 3, Appl1</td>	US-10-346-241-3	Sequence 3, Appl1
38	381.5	20.4	3351	14 <td>US-10-002-851-1</td> <td>Sequence 1, Appl1</td>	US-10-002-851-1	Sequence 1, Appl1
39	381.5	20.4	3783	15 <td>US-10-225-567A-117</td> <td>Sequence 117, App</td>	US-10-225-567A-117	Sequence 117, App
40	381.5	20.4	4000	15 <td>US-10-300-473-2</td> <td>Sequence 2, Appl1</td>	US-10-300-473-2	Sequence 2, Appl1
41	379.5	20.3	3237	9 <td>US-09-727-205-1</td> <td>Sequence 1, Appl1</td>	US-09-727-205-1	Sequence 1, Appl1
42	362.5	19.4	2877	15 <td>US-10-151-208-1</td> <td>Sequence 1, Appl1</td>	US-10-151-208-1	Sequence 1, Appl1
43	361	19.3	3824	15 <td>US-10-125-776-11</td> <td>Sequence 11, Appl1</td>	US-10-125-776-11	Sequence 11, Appl1
44	361	19.3	3824	15 <td>US-10-125-776-11</td> <td>Sequence 11, Appl1</td>	US-10-125-776-11	Sequence 11, Appl1
45	361	19.3	3824	15 <td>US-10-125-772-11</td> <td>Sequence 11, Appl1</td>	US-10-125-772-11	Sequence 11, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-027-923-3  
Sequence 3, Application US/10027923  
Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Brian Galtner Bates  
APPLICANT: Kamataka Gutukota  
APPLICANT: Yuhong Xie  
APPLICANT: Janet Elizabeth Paulsen  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
FILE REFERENCE: GNM-024  
CURRENT APPLICATION NUMBER: US/10/027, 923  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257, 589  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1110  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

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US-10-027-923-3

Alignment Scores:
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Score: 1873.00 Matches: 369
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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Qy 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40
Db 61 CAGTCCAGTGAAGAGAGGTGGTGCACATGCTGGTGACATATTATGAGCTCTC 120
Qy 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgGlySerGlyAlaVal 60
Db 121 TTTTCTGTTATCATCACCGCTACTGTGAGCAAGTTTCATGAGAGAGTGTGGGCGAGTC 180
Qy 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80
Db 181 CGTGAACAGTATGGCATTCACAGAGGTGAGGCACTGCTGCACTCGAAGAGATCAAT 240
Qy 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
Db 241 TCAGACCCCACTCTTGCCCAACATCACCTGGGCTGTGAGATTAAGGATTCCTGCTGG 300
Qy 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120
Db 301 CATTCGGCTGTGGCCCTTACAGAGCATTAAGTTCATTAAGATTCCTCATTTCTTTCG 360
Qy 121 GluGluGlnGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerIle 140
Db 361 GAAGAGGAGAGGGCTGTGTATGCTGTGTGATGAGCTCTCTTCTCTCCGCTCCAG 420
Qy 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160
Db 421 AAGCCCATATAGGGGCTCATTTGGGCTGTTCAGTTCTTTAGCCATTCAGTCCAGAT 480
Qy 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180
Db 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGAGATCTGAGT 540
Qy 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnIleAlaArg 200
Db 541 GACAAAGCTGTTCATAATATTCATATGAGGATGTGGCTTCAGATGCTCAGGCAAGG 600
Qy 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220
Db 601 TCCATGGTGAACATAGAGAGAGTACACTGAGCCATATGATACGCCATACACAGAA 660
Qy 221 GlyAsnTyrGlyGlySerGlyMetGluAlaPheLysAspMetSerAlaLysGlyGlyTle 240
Db 661 GGCACACTATGAGAAAGTGGAGTGAAGCTTCATAAATATGTCAGAGGAAGAGGATTT 720
Qy 241 CysIleIleHisSerTyrLysIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260
Db 721 TGCATGCCCACTCTTACAAATTCATACATGCAAGAGGAGGAGCTTTGATTAAGCTG 780
Qy 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGlyGly 280
Db 781 CTGAAGAAGCTCACAACTCTTGCCCAAGGCCCGGTGTGGCTTACTTCTGTAGAGGC 840
Qy 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300
Db 841 ATGACGGTGAAGAGTGTGATGAGCATGAGGAGGCTGGGTCTAGTGGAGAAATTTCTG 900

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Qy 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerTyrAsnSerIleLeuTrp 320
Db 901 CTTCTGGGCAAGGAAACCATGATGCCATCTTATTGAATCTCAAGAACACATCTATGG 960
Qy 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340
Db 961 GAAGACAGAAAGAAATGCCAAAGTCCCTTCTCAGGGTTTGGACATATTACACAGA 1020
Qy 341 SerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyPro 360
Db 1021 AGTGAAGTCCGTGTGCTGCAATGCCCCAGCTTGAATCTAAGGCTCAGTTCAAGGCC 1080
Qy 361 IleThrGlyLeuArgAspArgLeuIle 369
Db 1081 ATCATGAGACTGAGGACAGGCTCATC 1107

RESULT 2
US-10-027-923-1
: Sequence 1, Application US/10027923
: Publication No. US2002014230A1
: GENERAL INFORMATION:
: APPLICANT: Brian Gaither Bates
: APPLICANT: Kamalaka Gulukota
: APPLICANT: Yuhong Xie
: APPLICANT: Janet Elizabeth Paulsen
: TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
: FILER REFERENCE: GNM-024
: CURRENT APPLICATION NUMBER: US/10/027,923
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/257,589
: PRIOR FILING DATE: 2000-12-22
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1823
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (4) ..(1110)
: US-10-027-923-1

Alignment Scores:
Pred. No.: 9,94e-231 Length: 1823
Score: 1873.00 Matches: 369
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-027-923-2 (1-369) x US-10-027-923-1 (1-1823)
Qy 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuLeuValArgGlySerAla 20
Db 4 ATGGTCTTGTGTGATCTGCTGAGTCTTACTTTTGAAGAAGATGCTGGGAGTGC 63
Qy 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40
Db 64 CAGTCCAGTGAAGAGAGGTGGTGCACATGCTGGTGAACATTAATTGAGCTCTC 123
Qy 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgGlySerGlyAlaVal 60
Db 124 TTTTCTGTTATCATCACCGCTACTGTGAGCAAGATTCATGAGAGAGTGTGGGCACTC 183
Qy 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80
Db 184 CGTGAACAGTATGGCATTCACAGAGGTGAGGCACTGCTCATTCCTGGAAGAGATCAAT 243
Qy 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
Db 244 TCAGACCCCACTCTTGCCCAACATCACCTGGGCTGTGAGATTAAGGATTCCTGCTGG 303

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QY 101 HsSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120
DB 304 CATTGGCTGTGGCCCTAGAGGAGACATTGATTCATTAAGAAATCCCTCATTTCTTGG 363
QY 121 GluGluGluGluGluValCysSerValAspGlySerSerSerPheArgSerIlys 140
DB 364 GAAGAGGAAGAGGGCTGGATGCTCTGGATGGCTCCCTCTCTCTCCCTCCCAAG 423
QY 141 LysProIleValAlaIleGlyProGlySerSerSerLeuAlaIleGlnValGlnIle 160
DB 424 AAGCCCATGTAAGGGGCTGAGGCTGGCTGGCTTCAGATTCCTTACCAATTCAGGTCAGAAAT 483
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleAlaIleAlaIleAlaIleAlaIle 180
DB 484 TTGCTCCAGCTTTTCAACATCTCAGATTGCTTACTCAGCAACATTCATGATTCGAGT 543
QY 181 AspIleThrLeuPheIlePheIlePheIlePheIlePheIlePheIlePheIlePheIle 200
DB 544 GACAGAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAATGCTCAGAGCTCAGCAGG 603
QY 201 SerMetValAspIleValIleValIleValIleValIleValIleValIleValIleValIle 220
DB 604 TCATGCTGACATGATGTAAGAGTACCACTGAGCTTATGATCAGCCGTAACACAGAGA 663
QY 221 GlyAsnIleGlyGluSerGlyMetGluAlaPheIleAspMetSerAlaIleValGluGlyIle 240
DB 664 GGCACCTATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCACGCAAGAGAGGAGAT 723
QY 241 CysIleAlaHisSerIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 260
DB 724 TCATGCGCCACTCTTACAAATCTACAGTAATGACGAGGAGGAGGAGGAGGAGGAGGAGG 783
QY 261 LeuIleValLeuIleThrSerIleLeuProIleAlaIleValIleValIleValIleValIle 280
DB 784 CGAAGAAAGCTCAAGATCACTTCCCAAGGCGCGGCTGGCTGCTCTCTCTCTCTCTCTCT 843
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu 300
DB 844 ATGACGCTAGAGGCTGCTGATGAGGCAAGAGGCTGGCTTATGGAGAAATTTCTG 903
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTrp 320
DB 904 CTTCTGGGAGGAAACCAATGCTCTTATGAGATCTCAAAAGAACGATCTATG 963
QY 321 GluAspArgArgIleGlySerGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340
DB 964 GAAGACAGAAAGAAAGCAAGGTCCTTCTCAGGGTTTGGAGACATATTACACAGA 1023
QY 341 SerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyPro 360
DB 1024 AGTGAAGTCCGCTGCTGCAATGAGCCCGAGCTCTGAATCTAGAGCTCAGTTCAAGGAGCC 1083
QY 361 IleThrGlyLeuArgAspArgLeuIle 369
DB 1084 ATCACTAGAGTGAAGGAGCAAGGCTCATC 1110

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RESULT 3
US-09-822-830A-61
; Sequence 61, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A

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; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-61

Alignment Scores:
Pred. No.: 4,25e-230 Length: 1788
Score: 1868.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.73% Indels: 0
DB: 10 Gaps: 0

US-10-027-923-2 (1-369) x US-09-822-830A-61 (1-1788)
QY 2 ValLeuLeuLeuIleLeuSerValLeuLeuLeuValArgGlySerAlaGln 21
DB 2 GTCTTCTGTGATCTCTGCACTTACTTTGAAAGAAAGATCCGCTGGAGTGACAG 61
QY 22 SerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleValAlaLeuPhe 41
DB 62 TCATGAGAGAGAGGGGTGGCTGCATGCTGGGAGATCATATTAATTAAGCTCTCTT 121
QY 42 SerValHisHisGlnProThrValAspGluValHisGluArgIleCysGlyAlaValArg 61
DB 122 TCTGTTTATCACCAGCTCTGTGACAGAGTTTCAAGAGAGAGTGGGCAATCCCT 181
QY 62 GluGlnIleGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluIleAsnSer 81
DB 182 GAACAGTATGAGCATTCAGAGAGTGGAGGCTGATGCTGATACCTGGAAAGATCAATTC 241
QY 82 AspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrpHis 101
DB 242 GACCCCACTCTTGGCCCAATCACTGAGCTGTGAATTAAGGATTCCTGCTGGCA 301
QY 102 SerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSerGlu 121
DB 302 TCGGCTGTGGCCCTAGAGAGACATTAAGTTCTAAGAGATTCCTCATTTCTCGAA 361
QY 122 GluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIlys 141
DB 362 GAAGAAAGAGGCTGGTATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCT 421
QY 142 ProIleValAlaIleGlyProGlySerSerSerLeuAlaIleGlnValGlnIle 161
DB 422 CCATATGAGAGGATGATGGGCTGCTTCAATTTCTTTCAGATTCAGAGTTCAGAAATTTG 481
QY 162 LeuGlnLeuPheAsnIleProGlnIleAlaIleAlaIleAlaIleAlaIleAlaIle 181
DB 482 CTCAGCTTTTCAACATTCATCTCAATGCTTACTGCAACATTCATGATTCGATGAGC 541
QY 182 LysThrLeuPheIlePheIlePheIlePheIlePheIlePheIlePheIlePheIle 201
DB 542 AAGAGCTCTGTTCAAAATATTTCAATGAGGCTGTGCTTCAAGATGCTCAGCAGGAGAGTCC 601
QY 202 MetValAspIleValIleValArgGlyAsnIlePheIleValSerAlaHisThrGluGly 221
DB 602 ATGGTGGACATGATGTAAGAGTACCACTGGACCTTGTATCAGCCCTTACACAGAAAGCC 661
QY 222 AsnIleGlyGluSerGlyMetGluAlaPheIleAspMetSerAlaIleValGluGlyIleCys 241
DB 662 AACTATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGCAGAAAGAGGAGATTTCC 721
QY 242 IleAlaHisSerIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 261
DB 722 ATCGCCCACTTTACAAATATTCAGATATGACGAGGAGGAGCAAGGCTTATTAAGCTCTG 781

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Qy	262	ysylvslleuThSeHileuProlysaIlaArgvalValAlaThyPheCyegluglYmet	281
Db	782	AAGAAGCTCAACAAGTCACTTGCCCAAGGCGGAGTGTGAGCTTCTGTGTAGGGCCATG	841
Qy	282	ThrValaArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeuLeu	301
Db	842	ACGGTGAAGGCTCTCTGATAGGCCATGAGCCGCTGGCTAGTGGAGAAATTTCGCTT	901
Qy	302	LeuGlyArgGluProAspAlaIlePheIleGluIleSerIlyAsnSerIleuTPGlu	321
Db	902	CTGGGCAAGGAAACAGATGCCATCTTTATTGAGATCTCAAGAACAGCATCTCATGGAA	961
Qy	322	AspArgArgGlyCyegluglYArgPheLeuGlnIlyPheGlyAspIleIleuHisArgSer	341
Db	962	GACGAAAGAAATATGCAAGAGTGGCTCTTCAAGGTTTGGACACATATTACCAAGAGT	1022
Qy	342	GluSerValLeuLeuHisMetProGlnProLeuAsnLeuGlyIleuSerSerGlyProIle	361
Db	1022	GAGTCCGTCGCTCTGCACTGCCCCAGCCTCTGAACTGAGGCTCAAGGCTCAGGCCCCATC	108
Qy	362	ThrGlyLeuArgAspArgLeuIle	369
Db	1082	ACTGAGCTGAGGAGCAGGCTCATC	1105
RESULT 4			
US-10-346-241-1			
; Sequence 1, Application US/10346241			
; Publication No. US20030157647A1			
; GENERAL INFORMATION:			
; APPLICANT: STORMANN, THOMAS M.			
; APPLICANT: LEVINTHAL, CYNTHIA			
; APPLICANT: STORJOHANN, LAURA			
; APPLICANT: HAMMERLAND, LANCE G.			
; APPLICANT: KRAPCHO, KAREN J.			
; APPLICANT: NPS PHARMACEUTICALS, INC.			
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR			
; FILE REFERENCE: 1094.2.6			
; CURRENT APPLICATION NUMBER: US/10/346,241			
; PRIOR FILING DATE: 2003-01-17			
; PRIOR APPLICATION NUMBER: US/09/695,481			
; PRIOR FILING DATE: 2000-10-24			
; PRIOR APPLICATION NUMBER: 60/161,481			
; PRIOR FILING DATE: 1999-10-25			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 2826			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1) .. (2826)			
US-10-346-241-1			
Alignment Scores:			
Pred. No.: 2,626-180 Length: 2826			
Score: 1484.50 Matches: 306			
Percent Similarity: 87.22% Conservative: 8			
Best local Similarity: 85.00% Mismatches: 22			
Query Match: 79.25% Indels: 24			
DB: 13 Gaps: 2			
US-10-027-923-2 (1-369) x US-10-346-241-1 (1-2826)			
Qy	1	MetValleuLeuLeuIleLeuSerValLeuLeuLeuGluAspValaArgGlySerAla	20
Db	1	ATGGCTCTTCTGTATCTGTCAGCTTACTTTTGAAGAAGATGCTCCGTGGAGTGC	60
Qy	21	GlnSerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu	40
Db	61	CAGTCAATGAGAGAGAGGTGTGCTGCATACGCCGGTGAACATATTATTGAGCTCTC	120
Qy	41	PheSerValHisHisGlnProThrValaAspGluValHisGluArgGlyCyegluAlaVal	60

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Db      121 TTTTCTGTTCAATCACCAAGCTTCTGTGACAAAGTTCATGAGAGAACTGTGGGCGCTC 180
        61 ArgGInGInTGTGlyLeGInaArgValGInuJameLeuHiGthrLeuGInaArgLeaSn 80
        181 CGTGAACAGATATGGCACTTCAGAGAGTGGAGGCGCATGTGCTCATACCTCGTGAAGAGATCAAT 240
Qy      81 SerAspProThrLeuLeuProAsnHLehrLeuGInCyArguHLeaArgAspSerCyTrp 1000
        241 TCGAGACCCACACTCTTGCCCAACATCACACTGGGCGTGTGAGTAAGAGAGACTCTGCTGG 3000
Qy      101 HisSerAlaValAlaLeuGInGInSerLeGInuPheHLeaArgAspSerLeuHLeSerSer 120
        301 CATTCGGCTGTGGCCCTTAGAGAGAGCATTTGATTTCAATAGATTCCTCATTTCTTCA 3600
Db      121 GInGInGInGInGInGInValCySerSerValAspGlySerSerSerSerPheArgSerLyS 140
        361 GAAGAGAGAAAGGCTTGATGATCGCTGTGTGATGGCTCTCTCTCTCTCCGCTCCAG 4200
Qy      141 LysProTrIleValGlyValHLeGlyProGlySerSerSerSerLeuAlaHLeGInValGInAsn 1600
        421 AACCCCATAGTGGGGGTCAATTGGGCTGGCTGCACAGTTCTTAGGCATTACAGGTCCAAAT 4800
Qy      161 LeuLeuGInLeuPheAsnHLeProGInHLeaATyrSerSerAlaThrHLeMetAspLeuSer 1800
        481 TTCTCTCAGCTTTTCAACATACCTAGATTTGCTTACTAGACACAGCATGATCTGAT 5400
Db      181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGInGInuAlaArg 2000
        541 GACAAAGCTCTGTAAATATTTCAATGAGGGTGTGGCTTCAGATGTCTCAGACAGCAAG 6000
Qy      201 SerMetValAspHLeValLysArgTyrAsnThrPheTyrValSerAlaValHLeThrGlu 2200
        601 GCCATGTGTGACATGTGTGAAGAGTACCACTGACATATGATACGCCGGTGCACACAGAA 6600
Qy      221 GLeAsnTyrGInGInSerGInuMetGInuAlaPheLysAspMetSerAlaLysGInGlyHLe 2400
        661 GGCACACTATGAGAAAGTGGAGTGGAGGCTTCAAGATATGTCAAGAGAGAAAGGGATTT 7200
Db      241 CyeHLeAlaHLeSerTyrLysHLeTyrSerAsnAlaGlyGInGInSerPheAspLysLeu 2600
        721 TGCATGGCCCACTTCAAAATCTACAGTATGAGGGAGGAGCAGAGACTTTGATMACTG 7800
Qy      261 LeuLysLysLeuThrSerHLeuProLysAlaArgValValAlaTyrPheCysGInGly 2800
        781 CTGAAGAACTCAACAAGTCACTTGCCCAAGGCCCGGGGTGGTGGCTCTCTGTGAAGGCG 8400
Qy      281 MetThrValArgGlyLeuLeuMetHLeMetArgHArgLeuGInLysLeuValGInuPheLeu 3000
        841 ATACACGTAGAGAGTGTGTATGGCCATGAGAGCGCTGGGTCTTAGCGGAGAAATTTCTG 9000
Qy      301 LeuLeuGInValArgGInProAsnAlaHLePheHLeGInuHLeSerLysAsnSerLeuLeuTrp 3200
        901 CTTCTGGGACAGATGCG-----TGG 921
Db      321 GInuAspArgArgLysCysGInGlyArgPheLeuGInGInuPheGInuAspHLeuHLeuVar 3400
        922 GCTGACAGAGTATGATGTGACAG-----ATGATAT 951
Qy      340 gSerGInuSerValLeuLeuHLeMetProGInProLeuAsnLeuGInuLeuSerSerGly 359
        952 CACCGAGAAAGCTGTGTGGTGGCATCAATCAAGCTCAATCTCCGATGTCAAGTGGT 1009

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APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346,241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US/09/695,481  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
OTHER INFORMATION: molecule comprising portions of human mGluR3d and  
FEATURE:  
NAME/KEY: CDS  
LOCATION: ( )..(3129)  
US-10-346-241-5

Alignment Scores:  
Pred. No.: 3,09e-180 Length: 3129  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
DB: 13 Gaps: 2

US-10-027-923-2 (1-369) x US-10-346-241-5 (1-3129)

QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuGluAspValAlaArgIysSerAla 20  
DB 1 ATGGTCCTTCTGTGATCCTGTCAGTCTTACTTTTGAAGAAGATGTCGGTGGAGTGA 60  
QY 21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 61 CAGTCCAGTGAAGAGGAGGTGGCTGCACATGCCGGTACATCATTTATTTGAGCTCTC 120  
QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgIysGlyAlaVal 60  
DB 121 TTTTCTTCTATACCAAGCTTACTGTGACAAAGTTTCATAGAGAGTGTGGGCGCTC 180  
QY 61 ArgGluGlnIysGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
DB 181 CGTGAACAGATGAGCATTCAGAGATGAGGCGCATGCTCATACCTGGAAAGATCAAT 240  
QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
DB 241 TCAGACCCCACTCTTCCCAACATCACTGGGCTGTAGATTAAGGAGCTCTGTGG 300  
QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
DB 301 CATTCGGCTGTGGCCTTAAGCAGAGCATTAAGTTCATTAAGATTCCTCATTTCTTCA 360  
QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerIys 140  
DB 361 GAAGAGGAAAGAGGTGTGACCTGTGTGATGTGGCTCTCTCTCTCCCTCCGCTCAAG 420  
QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
DB 421 AAGCCCATGATGAGGAGTTCATTTGGGCTCCAGTTCATCTGTACCATTCAGTCCAGAAAT 480  
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIysSerAlaThrIleMetAspLeuSer 180  
DB 481 TTGCTCCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACAGCATGAGATTCGAGT 540  
QY 181 AspLysThrLeuPheLeuIysIysPheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
DB 541 GACAAAGCTCTGTCAAAATATTCATGAGGGTGTGTGCTTCAGATGCTCAGCAGGCAAG 600

QY 201 SerMetValAspIleValIysArgTyrAsnTrpThrTyrValSerAlaValHisTrnGlu 220  
DB 601 GCCATGTGACATCATTAAGAGGTACACTGACCTTAATGATACAGCCGTGCACAGAA 660  
QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaIysGluGlyIle 240  
DB 661 GGCAACTATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTACAGAAAGAAAGGATTT 720  
QY 241 CysIleAlaHisSerTyrIysIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
DB 721 TGCATGCCACCTCTTACAAATCTACAGTAATGACGAGGAGAGAGCTTTGATAGCTG 780  
QY 261 LeuLysValLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGluGly 280  
DB 781 CTGAAGAAGCTCAACAGTCACTTCCCAAGGCCGGGGTGTGGCTGTCTGTGTGAGGGC 840  
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
DB 841 ATGACGCTGAGAGGTCTGCTGANTGCCATGAGGCGCTGGGTCTACGGGAGAAATTTCTG 900  
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320  
DB 901 CTTCTGGCAGTATGCGC-----TGG 921  
QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
DB 922 GCTGACAGGTATGANTGTGACAG-----ATGGAATAT 951  
QY 340 GSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
DB 952 CAGCGAAGAGCTGTGTGTGGCATCACATCAAGCTCCATCTCCGATGTCAAGTGGT 1009

RESULT 6  
US-10-225-567A-177  
Sequence 177, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biociences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenn C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 177  
LENGTH: 4518  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-225-567A-177

Alignment Scores:  
Pred. No.: 5.6e-180 Length: 4518  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
DB: 15 Gaps: 2

US-10-027-923-2 (1-369) x US-10-225-567A-177 (1-4518)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValAlaArgIysSerAla 20  
DB 151 ATGGTCCTTCTGTGATCCTGTCAGTCTTACTTTTGAAGAAGATVTCGGTGGAGTGA 210  
QY 21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
DB 211 CAGTCCAGTGAAGAGGAGGTGGCTGCACATGCCGGTACATCATTTATTTGAGCTCTC 270

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Qy 41 PheSerValHisIsgInProThrValAspGluValHisGluArgLysCysGluAlaVal 60
Db 271 TTTTCTTCTTATCAACGCTTCTGTCGACAAATTCATAGAGAAAGTGGGGCGCTC 330
Qy 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80
Db 331 CGTGAACAGATGAGCATTCAGAGAGTGGAGCCCATGCTGCATACCTCGAAAGATCAAT 390
Qy 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
Db 391 TCAGACCCCACTCTGCTCCCAACATCACTGGCTGTGATAGATAGAGAGACTCTGCTGG 450
Qy 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120
Db 451 CATTCGCTGTGGCCCTTACAGACAGATTCAGATTCATTAAGATTCCTCATTTCTTCA 510
Qy 121 GluGluGluGluGluValCysSerValAspGlySerSerSerSerPheArgSerLys 140
Db 511 GAAGAGAGAAAGAGCTTGTACGCTGTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 570
Qy 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160
Db 571 AAGCCCATAGTACGGGTCTATGGGCTGCTGCCAGTTCTGTAGCCATTCAGATTCAGAAAT 630
Qy 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180
Db 631 TTGCTCCAGCTTTTCAACATACCTCAGATTCCTTACTCAGACACACACATGATCTAGT 690
Qy 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200
Db 691 GACAGAGCTCTGTTCAAAATTTTCATAGAGGTTGTGCTTCAGATGCTCAGCAGGCAAG 750
Qy 201 SerMetAlaAspIleValLysArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220
Db 751 GCCATGTGTGACATAGTGAAGAGGTACATCGACCTATGATCAGCGTGACACAGAA 810
Qy 221 GluAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240
Db 811 GGCACATATGAGAAAGTGGGATGGAAGCTTCAAAATATGTACGAGGAAGAGAGATTT 870
Qy 241 CysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260
Db 871 TGCATCGCCCACTTCAAAATCTACATGATCAGAGGAGCAGACTTGTATTAAGCTG 930
Qy 261 LeuLysLysLeuPheSerHisLeuProLysAlaArgValAlaAlaTyrPheCysGluGly 280
Db 931 CTGAGAGAGCTCAACAGTCACTTGCCAGAGGCCCGGGTGTGGCTCTCTGTGAGGAGC 990
Qy 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValIleGlyLysPheLeu 300
Db 991 ATAGACGTGAGAGGTCTGCTGATGCGCATAGAGCGCTTGAGTCAAGGAGAAATTTCTG 1050
Qy 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320
Db 1051 CTCTCGGAGCATGATGAGC-----TGG 1071
Qy 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340
Db 1072 GCTGACGAGTATGATGACAG-----ATGCAATAT 1101
Qy 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359
Db 1102 CAGCGAGAAAGCTGTGTGTGCGATCAATCAAGCTCCAAATCTCCGATGTCAAAGTGT 1159

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; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIORITY FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 346
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-346

Alignment Scores:
Pred. No.: 3,78e-133 Length: 2634
Score: 1118.50 Matches: 226
Percent Similarity: 81.10% Conservative: 40
Best Local Similarity: 68.90% Mismatches: 45
Query Match: 59.72% Indels: 17
DB: 13 Gaps: 5

US-10-027-923-2 (1-369) x US-09-826-509-346 (1-2634)
Qy 20 AlaGlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAla 39
Db 88 GCGAGAGCGTCTGCTCAACGCGCTGTCGCAATGACAGAAATGATCATATGAGAGCC 147
Qy 40 LeuPheSerValHisIsgInProThrValAspGluValHisGluArgLysCysGlyAla 59
Db 148 CTCTTCTCAGTCCATCAACAGCTCCGCGCGAGAAAGTCCGAGAGAAAGTGGGAG 207
Qy 60 ValArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIle 79
Db 208 ATCAGGAGACAGATGAGATCCAGAGGGTGGAGCCATGTTCCACAGCTGATAGATC 267
Qy 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCys 99
Db 268 AACGGAGCCCGGTCTCTGCGCCCAATCACTCCGCGAGTAAAGATCCGGAGCTCTGC 327
Qy 100 TrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSer 119
Db 328 TGGCACTCTTCCGTGCTCTGGAACAGAGATTCATTAAGAGCTCTGATTTCC 387
Qy 120 ---SerGluGluGluGluGlyLeu---ValCysSerValAspGlySerSer---SerSer 136
Db 388 ATTCGAGATGAGAGATGAGATCAACCGGTGTCTCTGACCGGCAAGTCCCTCCGCCA 447
Qy 137 PheArgSerLysLysProIleValIleGlyValIleGlyProGlySerSerSerSerLeuAlaIle 156
Db 448 GGCAGAGACTAAGAGCCCATGTGGGAGTATGTGCTCCGCTCCAGCTCTGTAGCAAT 507
Qy 157 GluValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176
Db 508 CAGGTGCAAGACTGCTCAGCTCTTCCAGATCCCAATCCCTTATTCAGCAAGC 567
Qy 177 MetAspLeuSerAspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAla 196
Db 568 ATGACCTGAGTACAAACTTTGTCAAAATCTCTGAGGGGTGTCTCTTGTGACACT 627
Qy 197 GlnGlnAlaArgSerMetValAspIleValLysArgTyrAsnTrpThrTyrValIleSerAla 216
Db 628 TTGCAAGCAAGGCGCATGTCATAGTCAAAAGTTACATTTGACATGCTCTGCA 667
Qy 217 ValHisThrGluGluValAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAla 236
Db 688 GTCCACACGAGAGGAAATTTATGGGAGAGCGGAATGAGCCTTCAAAAGCTGCGCTGCC 747
Qy 237 LysGluGlyIleCysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGluGlnSer 256

```



Db	748	CAGAAAGCCCTCGTATGCGCCATTCTGACAAAATCTACAGACAGCCGTGGGAGAGAGGC	807
Qy	257	PheAspIysLeuLeuLysValPheLeuThrsSerHisLeuProValAlaArgValAlaAlaTrp	276
Db	808	TTTATCCGACCTCTTGCCGMAATCCGAGAGAGCGCTTCCCAAGCGCTAGAGTGATGCTTGC	867
Qy	277	PheCysGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuVal	296
Db	868	TTCTGTGAGGCATGACAGTGCAGAGGATCTCTGAGCGCCATGCGCGCTTGGGCGTCTG	927
Qy	297	GlyGluIleLeuLeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsn	316
Db	928	GGCAGGTTCTCATTGATGAAGTGATGA-----	957
Qy	317	SerIleLeuTrpGluAspArgArgLys---CysGlnGlyArgPheLeuGlnGlyPheGly	335
Db	958	-----TCGGCAGACAGAGATGAACTATTGAGCGTGAAGCGCAAGCGG	1008
Qy	336	AspIleLeuHisArgSerGlnSer	343
Db	1009	GGAATCACGATAAAGCTGCAGGCT	1032

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RESULT 8
US-10-101-510-258
; Sequence 258. Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT : MAN, JACKSON
APPLICANT : MANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 258
LENGTH: 3295
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-258

Alignment Scores:
Pred.: 5,44e-133 Length: 3295
Score: 1118.50 Matches: 226
Percent Similarity: 81.10% Conservative: 40
Best Local Similarity: 68.90% Mismatch: 45
Query Match: 59.72% Indels: 17
DB: 13 Gaps: 5

US-10-027-923-2 (1-369) x US-10-101-510-258 (1-3295)
QY 20 AAGGAGGGCGCTGTCAATCCAGAGGCGTGCACAAATGAGCATGTCATATTGAGGCC 39
   :::::|||||
Dy 458 GCAGGAGCGCTGTCAATCCAGAGGCGTGCACAAATGAGCATGTCATATTGAGGCC 517
   :::::|||||
QY 40 LeuPheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAla 59
   CTTCTTCTCAGTCATCACACAGCCCTCGGCGCCAGAAGGCCCGAGAGGAAGTGCGGAG 577
   :::::|||||
QY 60 ValArgGluGlnIleThrGlyLeuGlnArgValGluAlaMetLeuHisIleThrLeuGluArgIle 79
   :::::|||||
Db 578 ATCAGGAGAGCATGATGATCCATCCAGAGGCGTGCACAAATGAGCATGTCATATTGAGGCC 637
   :::::|||||
QY 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCys 99
   AACGGCGAGCCCGGCTCTCTCGCCCAAATCACCTCGGCGAGTGAAGATCCGCGACTCTGC 697
   :::::|||||
Db 638 AACGGCGAGCCCGGCTCTCTCGCCCAAATCACCTCGGCGAGTGAAGATCCGCGACTCTGC 697
   :::::|||||
QY 100 TrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSer 119
   TGGCAGCTCTTCCTGCTGTGGAACGAGCATTTGAGGACTCTCTGATTTCC 757
   :::::|||||
Db 698 TGGCAGCTCTTCCTGCTGTGGAACGAGCATTTGAGGACTCTCTGATTTCC 757

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[illegible]

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RESULT 9
US-10-225-567A-169
; Sequence 169, Application US/10/225567A
; Publication No. US20030113796A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 6619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-169

Alignment Scores:
1.69e-132 Length: 6619

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Db 472 GGCAGAGCTAAGAGCTATTGCTGAGATGATCGCCCTGCTCAGCTCTGTGGCAAT 531
Qy 157 GlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176
Db 532 CAAGTCCAAATTTTTCAGCTGTTTCAGATCCACAGATCCCTTAATTCCTGACAGAG 591
Qy 177 MetAspLeuSerAspIleThrLeuPheLeuTyrPheMetArgValAlaProSerAspAla 196
Db 592 ATGAGACTGAGTGACAAACTTTGTACAAATACTTCTGAGGGTGGCTTCTGACACT 651
Qy 197 GlnGlnAlaArgSerMetValAspIleValArgTyrAsnThrThrTyrValSerAla 216
Db 652 TTGCAGGCAAGGCGGATGCTCGACATATGCAACGTTTACAACTGACCTATGTCTGACA 711
Qy 217 ValHisThrGlnGluValAsnTyrGlnGlnSerGlnMetGlnAlaPheLeuAspMetSerAla 236
Db 712 GTCCACACGAGAGGAAATTTACGGCGAGATGAGATGATGCTTTCAAGAACTGGCTGCC 771
Qy 237 LysGlnGluTyrLeuCyseIleAlaHisSerTyrLysIleTyrSerAsnAlaGlnGlnGlnSer 256
Db 772 CAGGAAGGCTCTGATTCGACATCGACATCGGACAAATCTACAGCAATCTGCGGAGAAAGC 831
Qy 257 PheAspLysLeuLeuLeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyr 276
Db 832 TTGACCGGCTCTGCGTAAACTCCGGAGCGGCTTCCCAAGGCGAGGGTTGTGTCTGC 891
Qy 277 PheCyGlnGluMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlnGlyLeuVal 296
Db 892 TTCTGGAGGGCAATGACAGCGGGCTTACTAGTGCATGCGCGGCTGCGGCGTGTG 951
Qy 297 GlyGlnPheLeuLeuGlnGlyArgGlnProAspAlaIlePheIleGlnIleSerLysAsn 316
Db 952 GGGAGTTCTCACTCATTTGAAAGTATGCA----- 991
Qy 317 SerIleLeuTyrGlnAspArgArgLys--CyseGlnGlyArgPheLeuGlnGlnGly 335
Db 982 -----TGCGCAGACAGAGATGAAGTCATGCAAGGCTATGAGTGGAGCCAGCA 1032
Qy 336 AspIleLeuHisArgSerGlnSer 343
Db 1033 GGGATCACAATMAAGCTTCACTCT 1056

RESULT 11
US-10-300-473-4
; Sequence 4, Application US/10300473
; Publication No. US20030113873A1
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: STORJOHANN, LAURA L.
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: FULLER, FORREST H.
; APPLICANT: KAPCHO, KAREN J.
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE
; TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES
; FILE REFERENCE: 072827/0909
; CURRENT APPLICATION NUMBER: US/10/300,473
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 09/435,897
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 08/687,289
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: 60/001,526
; PRIOR FILING DATE: 1995-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized human

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; OTHER INFORMATION: mGluR and human calcium receptor
US-10-300-473-4
Alignment Scores:
Pred. No.: 7,05e-133 Length: 3219
Score: 1117.50 Matches: 226
Percent Similarity: 81.10% Conservative: 40
Best Local Similarity: 68.90% Mismatches: 45
Query Match: 59.66% Indels: 17
DB: 15 Gaps: 5
US-10-027-923-2 (1-369) x US-10-300-473-4 (1-3219)
Qy 20 AlaGlnSerSerGlnLysArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAla 39
Db 112 GCAAGTCTCTCTCCACAGCTCTCTGCGAGAAATGACAGAGATGTCATCTGAGAGCC 171
Qy 40 LeuPheSerValHisHisGlnProThrValAspGluValHisGlnLysArgLysCyseGlyAla 59
Db 172 CTCTTCTGATGTCATCACAGGCTCCAGCCGAGAAAGTATCCGAAAGAAAGTGTGGAG 231
Qy 60 ValArgGlnGlnTyrGlyIleGlnArgValGlnAlaMetLeuHisThrLeuGlnArgIle 79
Db 232 ATCAGGGAACAGATGTATCCAGAGGTGGAAGGCGCATGTCCACACGTTGATTAAGATT 291
Qy 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCyseGlnIleArgAspSerCyse 99
Db 292 AACGGGACCCGAGTGTCTCTGCGCAACATCACTCGGAGTGAAGTCCGAGCTCTGC 351
Qy 100 TrpHisSerAlaValAlaLeuGlnGlnSerIleGlnPheIleArgAspSerLeuIleSer 119
Db 352 TGGCACTCTTCACTGAGCTCTGCAACAGACATCGAATTCATGAGAACCTCCGATTCC 411
Qy 120 ---SerGlnGlnGlnGlnGlyLeu--ValCyseValAspGlySerSer---SerSer 136
Db 412 ATCCAGATGAGAAAGATGGCTGAAACCATGCTCTGCAATGCGCAGACCTGCCCT 471
Qy 137 PheArgSerLysLysProIleValGlnValIleGlnProGlnIleSerSerSerLeuAlaIle 156
Db 472 GGCAGAGCTAAGAGCTATGCTGAGATGATGGCGCTGCGCTCCAGCTCTGTGGCAATT 531
Qy 157 GlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176
Db 532 CAAGTCCAAATTTTTCAGCTGTTTCAGATCCACAGATCCCTTAATTCCTGACAGAG 591
Qy 177 MetAspLeuSerAspIleThrLeuPheLeuTyrPheMetArgValAlaProSerAspAla 196
Db 592 ATGAGACTGAGTGACAAACTTTGTACAAATACTTCTGAGGGTGGCTTCTGACACT 651
Qy 197 GlnGlnAlaArgSerMetValAspIleValArgTyrAsnThrThrTyrValSerAla 216
Db 652 TTGCAGGCAAGGCGGATGCTCGACATATGCAACGTTTACAACTGACCTATGTCTGACA 711
Qy 217 ValHisThrGlnGluValAsnTyrGlnGlnSerGlnMetGlnAlaPheLeuAspMetSerAla 236
Db 712 GTCCACACGAGAGGAAATTTACGGCGAGATGAGATGATGCTTTCAAGAACTGGCTGCC 771
Qy 237 LysGlnGluTyrLeuCyseIleAlaHisSerTyrLysIleTyrSerAsnAlaGlnGlnGlnSer 256
Db 772 CAGGAAGGCTCTGATTCGACATCGGACAAATCTACAGCAATCTGCGGAGAAAGC 831
Qy 257 PheAspLysLeuLeuLeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyr 276
Db 832 TTGACCGGCTCTGCGTAAACTCCGGAGCGGCTTCCCAAGGCTGAGTGTGTCTGC 891
Qy 277 PheCyGlnGluMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlnGlyLeuVal 296
Db 892 TTCTGGAGGGCAATGACAGCGGGCTTACTAGTGCATGCGCGGCTGCGGCGTGTG 951
Qy 297 GlyGlnPheLeuLeuGlnGlyArgGlnProAspAlaIlePheIleGlnIleSerLysAsn 316
Db 952 GGGAGTTCTCACTCATTTGAAAGTATGCA----- 981

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QY 317 SerLeuTrpGluAspArgValys---CysGlnGlyArgPheLeuGlnGlyPheGly 335  
 Db 982 -----TGGGACAGACAGATGAAGTCAATGAGGTTATGAGGTGAGAACCAAGGG 1032  
 QY 336 AspiLeuHisArgSerGlySer 343  
 Db 1033 GGAATCACGATTAAGCTGCAGTCT 1056  
 RESULT 12  
 US-10-300-473-1  
 ; Sequence 1, Application US/10300473  
 ; Publication No. US20030113873A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STORMANN, THOMAS M.  
 ; APPLICANT: STORJOHANN, LAURA L.  
 ; APPLICANT: HAMMERLAND, LANCE G.  
 ; APPLICANT: FULLER, FOREST H.  
 ; APPLICANT: KAPACHO, KAREN J.  
 ; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING  
 ; TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE  
 ; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE  
 ; TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES  
 ; FILE REFERENCE: 072827/0909  
 ; CURRENT APPLICATION NUMBER: US/10/300,473  
 ; PRIOR FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: 09/435,897  
 ; PRIOR FILING DATE: 1999-11-08  
 ; PRIOR APPLICATION NUMBER: 08/687,289  
 ; PRIOR FILING DATE: 1996-07-25  
 ; PRIOR APPLICATION NUMBER: 60/001,526  
 ; PRIOR FILING DATE: 1995-07-26  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 3384  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthesized rat  
 ; OTHER INFORMATION: mGluR and human calcium receptor  
 US-10-300-473-1  
 Alignment Scores:  
 Pred. No.: 7.65e-133 Length: 3384  
 Score: 1117.50 Matches: 226  
 Percent Similarity: 81.10% Conservative: 40  
 Best Local Similarity: 68.90% Mismatches: 45  
 Query Match: 59.66% Indels: 17  
 Gaps: 5  
 US-10-027-923-2 (1-369) x US-10-300-473-1 (1-3384)  
 QY 20 AlGlnSerSerGluArgValAlaHisMetLeuGlyAspiLeuIleIleGlyAla 39  
 Db 95 GCGAGTCCCTCCGCCAGCCCTCGTGGCGAGATGACGAGATGTCATCATCGGAGCC 154  
 QY 40 LeuPheSerValHisGlnProThrValAspGluValHisGluArgValysGlyAla 59  
 Db 155 CTCTTCTCAGTCACTCCAGCCCTCCAGCCGAGAGGTACCCGAAAGAGAGTGTGGGAG 214  
 QY 60 ValArgGlnGlnTrpGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIle 79  
 Db 215 ATCAGGAAACAGATGTATCCAGAGGTGAGGCTTCATGTTCCACACGTTGGAATAAGATT 274  
 QY 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCys 99  
 Db 275 AACGGGACCCGGGCTCTCCGCCCAACATCATCTTGCGGAGTGAATCCGCGACTCTGTC 334  
 QY 100 TrpHisSerAlaValAlaLeuGlnSerIleGluPheIleArgAspSerLeuIleSer 119  
 Db 335 TGGCACTCTTCAGTGGCTCTCGAACAGACATCAATTCATCAGAGCTCCCTGATTTCC 394  
 QY 120 ---SerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 136

Db 395 ATCCGAGATGAGAGATGGGCTGAACCCAGATGCTCTGATGAGCCAGCCCTGCCCT 454  
 QY 137 PheArgSerIleYsPheProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIle 156  
 Db 455 GGCAGACATGAAGGCTATGCTGAGATGATGGCCCTGGCTGACGCTCTGTGGCAATT 514  
 QY 157 GlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaIleYsSerAlaThrIle 176  
 Db 515 CAAGTCCAGATTTCTCCAGCTGTTGCACATCCACAGATGCCATTTCTGCACAGC 574  
 QY 177 MetAspLeuSerAspIleYsThrLeuPheIleYsTrpPheMetArgValAlaProSerAspAla 196  
 Db 575 ATGACCTGAGTGAACAACTTTGTACAAATCTTCTGAGGGTGTGCTCTTGTGACACT 634  
 QY 197 GlnGlnAlaArgSerMetValAspIleValIleArgTrpAsnThrPheTrpValIleSerAla 216  
 Db 635 TTGCAGGCAAGGGGCTGCTGCACATAGTCACAGCTTACAACTGACCTATGTCTAGCA 694  
 QY 217 ValHisThrGlnGlyAsnTrpGlyGlnSerGlyMetGluAlaPheIleAspMetSerAla 236  
 Db 695 GTCCACACAGAGGGAATTTACGCGAGAGTGAATGATGCTTTCAAAAGACTGGCTGCC 754  
 QY 237 LysGlnGlyIleCysIleAlaHisSerTrpIleYsTrpSerAsnAlaGlyGlnGlnSer 256  
 Db 755 CAGGAAGGCTCTGATCCGACACCTGCAACAAATCTACAGCAATCTGGCGAGAGAGC 814  
 QY 257 PheAspLeuLeuLeuLeuYsIleYsLeuThrSerHisLeuProIleValIleArgValAlaIleYs 276  
 Db 815 TTGACCGGCTCTGTGGTAACTCCGAGAGCGGCTTCCAGAGCCAGGGTGTGGTCTGC 874  
 QY 277 PheCysGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuVal 296  
 Db 875 TTCTGAGAGGCGATGACAGTGGCGGCTTACTGAGTGCATGGCCGCGCTGGCGCTG 954  
 QY 297 GlyGlnPheLeuLeuLeuGlyArgGlnProAspAlaIlePheIleGluIleSerIleYsAsn 316  
 Db 935 GCGAGTCTTCACTCATGGAAGTGAAGA----- 964  
 QY 317 SerLeuTrpGluAspArgValys---CysGlnGlyArgPheLeuGlnGlyPheGly 335  
 Db 965 -----TGGGACAGACAGATGAAGTCAATGAGGTTATGAGGTGAGAACCAAGGG 1015  
 QY 336 AspiLeuHisArgSerGlySer 343  
 Db 1016 GGAATCACATTAAGCTGCAGTCT 1039  
 RESULT 13  
 US-09-900-714A-1  
 ; Sequence 1, Application US/09900714A  
 ; Patent No. US20020162133A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Allen, Keith D.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MGLUR  
 ; TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTOR GENE DISRUPTIONS  
 ; FILE REFERENCE: R-657  
 ; CURRENT APPLICATION NUMBER: US/09/900,714A  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: US 60/216,252  
 ; PRIOR FILING DATE: 2000-07-06  
 ; PRIOR APPLICATION NUMBER: US 60/221,490  
 ; PRIOR FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: US 60/262,138  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,928  
 ; PRIOR FILING DATE: 2000-07-26  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2830  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-900-714A-1

**Alignment Scores:**

Pred. No.:	9,08e-60	Length:	2830
Score:	550.00	Matches:	125
Percent Similarity:	60.82	Conservative:	52
Best Local Similarity:	49.96	Mismatches:	98
Query Match:	29.36	Indels:	16
DB:	10	Gaps:	7

US-10-027-923-2 (1-369) X US-09-900-714A-1 (1-2830)

QY	21	GlnSerSerGluArgValValAlaHisMetLeu-----GlyAspIleIle	37
		:::	
Db	155	CANAAGACTCACGACGAGATATGCCATTCCATCCCGCTGAGTGGGAGATCATTTTG	214
QY	38	GlyAlaLeuPheSerValHisHisGlnProThrValaAspGluValHisGluArg----	55
		:::	
Db	215	GGGGGCTTTTCTCTGTTCAATGCCA-----GGAGAAAGAGGGGTG	256
QY	56	LysCysGlyValaValArgGluGlnTrpGlyIleGlnArgValGluAlaMetLeuHisThr	75
		:::	
Db	257	CCTTGTTGGGACCTGAAGAGAGAAAGGGCATCTCACAGCTTGAGCGCATCTTTAAGCA	316
QY	76	LeuGluArgIleAsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIle	95
		:::	
Db	317	ATGCACACAGCTAATAAAGACCCCATCTCTCTCCATATCATCTCGGTGTCGGATC	376
QY	96	ArgAspSerCysTrpHisSerAlaValaAlaLeuGluGlnSerIleGluPheIleArgAsp	115
		:::	
Db	377	CTTGACACAGTGTCCAGGACACCTATGCTTTGGAGCAGTCACTAACCTTGTCAG--	433
QY	116	SerLeuIleSerSerGluGluGluGluGluValaCysSerValaAspGlySerSerSer	135
		:::	
Db	434	GCACTGTA-----GAGAAAGACGGGTGTACGTGAAGTGTCTAATGAAGACCCACC	487
QY	136	SerPheArgSerLysLysArgProIleValaGlyValaIleGlyProGlySerSerSerLeuAla	155
		:::	
Db	488	ATATTCACCAAGCCGCAAGATTTCTGTGTGCATAGGTCGTCGACGACAGAGCTCGTGTC	547
QY	156	IleGlnValaGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaIleTyrSerAlaThr	175
		:::	
Db	548	ATCATGGTGGCTTAACCTTTTAAAGACTTTTAAAGATACCTCAGATTAGCTATGACATCA	607
QY	176	IleMetAspLeuSerAspLysThrLeuPheLysTrpPheMetArgValaValProSerAsp	195
		:::	
Db	608	GCCCCAGAGCTAAGTACAAACACAGATATGATTTCTTTCTCGGGTGTCCCGCTGAC	667
QY	196	AlaGlnGlnAlaArgSerMetValAspIleValaLysArgTyrAsnTrpThrTyrValSer	215
		:::	
Db	668	TCTCAACCAAGCCCAAGCCAGTGGTGACATTTGACAGAGCCCTGGATGAAATTATGTGCA	722
QY	216	AlaValaHisThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	235
		:::	
Db	728	ACACTGGCTTCCAGGGGAACTATGAGAGAGTGTGTGGAGCCCTTCACTCAAGATCTCA	787
QY	236	AlaLys-----GluGlyIleCysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGlu	254
		:::	
Db	788	AGGAGAGTTGT	847
QY	255	GlnSerPheAspLysLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys	274
		:::	
Db	848	GGAGAAATTCGAAAAAATTATCAACGCGCTGTG--GAGACACCAACGCTCGGACGCTG	904
QY	275	AlaTyrPheCysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	294
		:::	
Db	905	ATTATGTTTGGCAATGAGATGACAGAGGGGATATTTGGAAGACGCAAAAAAATTAAAC	964
QY	295	LeuValaGlyGluPheLeuLeuLeuGluGlyArgGlu	305
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Db	965	CAGAGTGGGCAATTTCTATGAGATGTGCTCAGAT	997

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; Publication 85 Application US/10353690
; Publication No. US20030215840A1
GENERAL INFORMATION:
APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Myoung
APPLICANT: Galvin, Katherine M.
APPLICANT: Healy, Allen
APPLICANT: Acton, Susan L.
APPLICANT: Donoghue, Mary
APPLICANT: Stagliano, Nancy
APPLICANT: Rodriguez, Jacquelin
APPLICANT: Rodriguez-Way, Amelie
TITLE OF INVENTION: Methods and compositions for treating
TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395
TITLE OF INVENTION: 29002, 3316, 43726, 69292, 26156, 32427, 2402, 7747, 1120
TITLE OF INVENTION: 9131, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
TITLE OF INVENTION: 14445, 58848, 1870, 25856, 32394, 3484, 9252, 9135,
TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
TITLE OF INVENTION: 51130, 19489, 21833, 2317, 55990, 15992, 2094, 2252, 3474,
FILE REFERENCE: MP102-018P1RNMNMIM
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/10/353,690
PRIOR APPLICATION NUMBER: 60/353,224
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/364,529
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/373,861
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/376,287
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: 60/388,080
PRIOR FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: 60/390,971
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/394,130
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/394,797
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: 60/404,904
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 60/405,450
PRIOR FILING DATE: 2002-08-23
Remaining PRIOR Application data removed - see File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 85
LENGTH: 3321
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-353-690-85
Alignment Scores:
Pred. No.: 2,13e-59 Length: 3321
Score: 548.00 Matches: 125
Percent Similarity: 60.82% Conservative: 52
Best Local Similarity: 42.96% Mismatches: 98
Query Match: 29.26% Indels: 16
DB: 13 Gaps: 7
US-10-027-923-2 (1-369) x US-10-353-690-85 (1-3321)
QY 21 GlnSerGergLunrgArGVAlValAlAhMeLeu-----GLyApIlelle 37
Db 142 CAAGAAGCTACAGCCCAAGAGTATGCCCATTCATCGGGGTGATGGAGACATTATTGG 201
QY 38 GLyAlAleuPheserValInHsiGInProThVAlAspGIuValInHsiGluArg----- 55
Db 202 GGCGGCTCTTTCCCTGTGCACGCAAG-----CGAGAGAGAGCGCGTG 243
QY 56 LyAcGagLIyAlValrGlugInTrYGlyILegLnArGVAlGluAlMeLeuHsr 75

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Db 244 CCTGTGTGGAGCTGAAGAAAGGAGGATTCACAGACTGAGCCATGCTTTATGCA 303  
Qy 76 LeuGluArgIleAsnSerAppProThrLeuLeuProAsnIlePheLeuGlyCysGluIle 95  
Db 304 ATTAGCCAGATTAAACAAGACCCTGATCTCTTCCAACTACATCTGGGGTCCGATC 363  
Qy 96 ArgAspSerCysTrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAsp 115  
Db 364 CTCGACACGTCCTAGAGACACCTATGCTTTGGAGAGCTTCAACATTCGTGCAG--- 420  
Qy 116 SerLeuIleSerSerGluGluGluGluGluValCysSerValAspGlySerSerSer 135  
Db 421 GCATTATA-----GAGAAAGATGCTTCGATGTGAAGTGTGATGAGATCCACC 474  
Qy 136 SerPheArgSerIleValAlaValAlaValIleGlyProGlySerSerSerSerLeuAla 155  
Db 475 ATTTTACCAAGCCCGACAGATTTCTGGGCTCATAGGTCTGACGACAGCTCCGTCTC 534  
Qy 156 IleGlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaIleYrSerAlaThr 175  
Db 535 ATCATGCTTGTCAATTTTAAGCTTTTAAGTACCTCAATCAGCTATGATCCACACA 594  
Qy 176 IleMetAspLeuSerAspIleThrLeuPheIleYrPheMetArgValAlaProSerAsp 195  
Db 595 GCCCCAGAGCTAAGTGAATACACAGAGGTATGATTTCTCTCGAGGTGCTCCGCTGAC 654  
Qy 196 AlaGlnGlnAlaArgSerMetValAspIleValIleValIleValIleValIleValSer 215  
Db 655 TCCATCAACAGCCCAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 714  
Qy 216 AlaValHisThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 235  
Db 715 ACACTGCTCTGAGGGAACTATGATGATGATGATGATGATGATGATGATGATGATG 774  
Qy 236 AlaIleYr---GluGlyIleCysIleAlaHisSerYrIleYrSerAsnAlaGlyGlu 254  
Db 775 AGGAGATGCTGTGTGCTTTCATTTGCTCAGTCAAGAAATCCACCTGACCAAGACCT 834  
Qy 255 GlnSerPheAspIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 274  
Db 835 GAGGATTTGAAATAATTAATCAAGCCCTGCTA---GAAACACTTAATGCTCGAGCATG 891  
Qy 275 AlaIleYrPheCysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 294  
Db 892 ATTATGTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951  
Qy 295 LeuValGlyGluPheLeuLeuLeuGlyArgGlu 305  
Db 952 CAAAGTGGCATTTTCTCTGATTTGCTCAGAT 984

RESULT 15  
US-10-225-567A-183  
Sequence 183, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burmer, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: Patent version 3.1  
SEQ ID NO 183  
LENGTH: 3321  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-225-567A-183

Alignment Scores:  
Pred. No.: 2,13e-59 Length: 3321  
Score: 548.00 Matches: 125  
Percent Similarity: 60.82% Conservative: 52  
Best Local Similarity: 42.96% Identities: 98  
Query Match: 29,26% Indels: 16  
DB: 15 Gaps: 7

US-10-027-923-2 (1-369) x US-10-225-567A-183 (1-3321)

Qy 21 GlnSerSerGluArgArgValValAlaHisMetLeu-----GlyAspIleIleIle 37  
Db 142 CAAAGATCAACAGCCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 201  
Qy 38 GlyAlaLeuPheSerValHisGlnProThrValAspValHisIleGluArg----- 55  
Db 202 GGGGGTCT 243  
Qy 56 IlyCysGlyAlaValArgGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 75  
Db 244 CCTGTGTGGAGCTGAAGAAAGGAGATTCACAGACTGAGCCATGCTTTATGCA 303  
Qy 76 LeuGluArgIleAsnSerAppProThrLeuLeuProAsnIlePheLeuGlyCysGluIle 95  
Db 304 ATTAGCCAGATTAAACAAGACCCTGATCTCTTCCAACTACATCTGGGGTCCGATC 363  
Qy 96 ArgAspSerCysTrpHisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAsp 115  
Db 364 CTCGACACGTCCTAGAGACACCTATGCTTTGGAGAGCTTCAACATTCGTGCAG--- 420  
Qy 116 SerLeuIleSerSerGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 135  
Db 421 GCATTATA-----GAGAAAGATGCTTCGATGTGAAGTGTGATGAGATCCACC 474  
Qy 136 SerPheArgSerIleValAlaValAlaValIleGlyProGlySerSerSerSerLeuAla 155  
Db 475 ATTTTACCAAGCCCGACAGATTTCTGGGCTCATAGGTCTGACGACAGCTCCGTCTC 534  
Qy 156 IleGlnValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaIleYrSerAlaThr 175  
Db 535 ATCATGCTTGTCAATTTTAAGCTTTTAAGTACCTCAATCAGCTATGATCCACACA 594  
Qy 176 IleMetAspLeuSerAspIleThrLeuPheIleYrPheMetArgValAlaProSerAsp 195  
Db 595 GCCCCAGAGCTAAGTGAATACACAGAGGTATGATTTCTCTCGAGGTGCTCCGCTGAC 654  
Qy 196 AlaGlnGlnAlaArgSerMetValAspIleValIleValIleValIleValIleValSer 215  
Db 655 TCCATCAACAGCCCAAGCATGATGATGATGATGATGATGATGATGATGATGATG 714  
Qy 216 AlaValHisThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 235  
Db 715 ACACTGCTCTGAGGGAACTATGATGATGATGATGATGATGATGATGATGATGATG 774  
Qy 236 AlaIleYr---GluGlyIleCysIleAlaHisSerYrIleYrSerAsnAlaGlyGlu 254  
Db 775 AGGAGATGCTGTGTGCTTTCATTTGCTCAGTCAAGAAATCCACCTGACCAAGACCT 834  
Qy 255 GlnSerPheAspIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 274  
Db 835 GAGGATTTGAAATAATTAATCAAGCCCTGCTA---GAAACACTTAATGCTCGAGCATG 891  
Qy 275 AlaIleYrPheCysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 294  
Db 892 ATTATGTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951  
Qy 295 LeuValGlyGluPheLeuLeuLeuGlyArgGlu 305  
Db 952 CAAAGTGGCATTTTCTCTGATTTGCTCAGAT 984



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Sequence 7, App11  
Sequence 7, App11  
Sequence 9, App11  
Sequence 9, App11

Sequence 150, App  
continued on p. 1014

Sequence	86312, A
Sequence	86313, A
Sequence	86312, A
Sequence	86313, A

Sequence 168178,

Sequence 8323, Ap

Sequence 34, Appl

Sequence 292, App

Sequence 3, April 11

Sequence 17322, A

Sequence 9874, Ap

Sequence 268503,

Sequence 268503,

# PROTEINS AND EFOR

2

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: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1110)
US-10-027-923-3

Query Match      100.0%; Score 1110; DB 14; Length 1110;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  ATGTGCTTCCTGCTGATCTCTGAGTCCTTACCTTTTGAAGAAGATGTCCTGGAGTGTCA 60
Db      1  ATGTCTCTTCCTGTTGATCTCTGTCACTTACTTACTTCTTGAAGAAGATGTCCTGGAGTGTCA 60

Oy      61  CAGTCCAGTGAAGAGAGAGGGTGTGTGGCTTCACATGCTGGGTGCATCATTTATTTGAGCTTTC 120
Db      61  CAGTCCAGTGAAGAGAGAGGGTGTGTGGCTTCACATGCTGGGTGCATCATTTATTTGAGCTTTC 120

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Qy	121	TTTTCTGTTCAACACACCTCACTGTGAGCGAAAGTTCATGAGGAAGTGTGGGGCACTC	180
Db	121	TTTTCTGTTCAACACACCTCACTGTGAGCGAAAGTTCATGAGGAAGTGTGGGGCACTC	180
Qy	181	CGTGAACGTAATGCGATTCAAGAGATGAGGCGCATGCTGCATATCCCTGAAAGATCAAT	240
Db	181	CGTGAACGTAATGCGATTCAAGAGATGAGGCGCATGCTGCATATCCCTGAAAGATCAAT	240
Qy	241	TCAGACCCCACTCTTGGCCCAACATCAACTGGGCTGTGATTAAGGATTTCCGTCTCG	300
Db	241	TCAGACCCCACTCTTGGCCCAACATCAACTGGGCTGTGATTAAGGATTTCCGTCTCG	300
Qy	301	CATTGCGCTGTGGCCCTAGACAGACAGATTGAGTTCAATAAGANTTCCCTCATTTCTTCG	360
Db	301	CATTGCGCTGTGGCCCTAGACAGACAGATTGAGTTCAATAAGANTTCCCTCATTTCTTCG	360
Qy	361	GAAAGGAAAGGGGCTTGGTAATGCTCTGTGAGATGCGCTCTCTCTTCCGTCCCAAG	420
Db	361	GAAAGGAAAGGGGCTTGGTAATGCTCTGTGAGATGCGCTCTCTCTTCCGTCCCAAG	420
Qy	421	AAGCCCATATGATGAGGCTCATTTGGGCGTGGTCCAGTTCTTTAGCCATTCAGATCCAGAT	480
Db	421	AAGCCCATATGATGAGGCTCATTTGGGCGTGGTCCAGTTCTTTAGCCATTCAGATCCAGAT	480
Qy	481	TTGCTCCAGCTTTTCAACATATCTCAGATTCTTACTCAGAAACCATCATGATGATCTGAGT	540
Db	481	TTGCTCCAGCTTTTCAACATATCTCAGATTCTTACTCAGAAACCATCATGATGATCTGAGT	540
Qy	541	GACAAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAATGATGCTCAGCAGGCAAG	600
Db	541	GACAAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAATGATGCTCAGCAGGCAAG	600
Qy	601	TCCATGTGTGACATATGATGAAGAGGATCAACCTGAGCCATATGATATACAGCCGTACACAGAA	660
Db	601	TCCATGTGTGACATATGATGAAGAGGATCAACCTGAGCCATATGATATACAGCCGTACACAGAA	660
Qy	661	GGCAACTATGAGAAAGTGGATGGAAAGCTTTCAAAAGATATGTCAGCGAAGAAAGGAGTT	720
Db	661	GGCAACTATGAGAAAGTGGATGGAAAGCTTTCAAAAGATATGTCAGCGAAGAAAGGAGTT	720
Qy	721	TGCAATCGGCCACTCTTACAAAATCTACAGTATATGACAGGGAGACAGACTTTGATTAAGTGT	780
Db	721	TGCAATCGGCCACTCTTACAAAATCTACAGTATATGACAGGGAGACAGACTTTGATTAAGTGT	780
Qy	781	CTGAAGAAAGCTCAACAGTCACTTGGCCCAAGGCGCGGAGTGTGGCCCTTACTGTGAGGGGC	840
Db	781	CTGAAGAAAGCTCAACAGTCACTTGGCCCAAGGCGCGGAGTGTGGCCCTTACTGTGAGGGGC	840
Qy	841	ATGACGGTGAAGGCTCTGCTGATGCGCCATGAGGGCGCTGGGCTTAATGTGGAGAAATTTCTG	900
Db	841	ATGACGGTGAAGGCTCTGCTGATGCGCCATGAGGGCGCTGGGCTTAATGTGGAGAAATTTCTG	900
Qy	901	CTTCTGGGACAGGAAACAGATGCGCATCTTTATGAGATCTCAAAAGACAGCATCTCTATGG	960
Db	901	CTTCTGGGACAGGAAACAGATGCGCATCTTTATGAGATCTCAAAAGACAGCATCTCTATGG	960
Qy	961	GAAAGCAAGAAATAATGCAAGTGTGCTCTTCAAGGTTTGTGAGACATATTAACAGAA	1020
Db	961	GAAAGCAAGAAATAATGCAAGTGTGCTCTTCAAGGTTTGTGAGACATATTAACAGAA	1020
Qy	1021	AGTAGTCCGTGCTGTGACATATGCGCCAGCTCTGAAATCTAGAGCTCAAGTTCAGGGGCC	1080
Db	1021	AGTAGTCCGTGCTGTGACATATGCGCCAGCTCTGAAATCTAGAGCTCAAGTTCAGGGGCC	1080
Qy	1081	ATCACTGACCTGAGGAGACAGGCTCATCTTAA	1110
Db	1081	ATCACTGACCTGAGGAGACAGGCTCATCTTAA	1110

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; Publication No. US20020142330A1
; GENERAL INFORMATION:
; APPLICANT: Brian Gatcher Bates
; APPLICANT: Kamalaka Gulukota
; APPLICANT: Yuhong Xie
; APPLICANT: Janet Elisabeth Paulsen
; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: GNN-024
; CURRENT APPLICATION NUMBER: US/10/027,923
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,589
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1823
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1110)
US-10-027-923-1

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Query Match	100.0%	Score 1110;	DB 14;	Length 1823;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 110;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	ATGGCTCTTCGTGTAATCTCTGCACTCTTATCTTTGAAAGAAATGTCCTGGGAGTGC	60
Db	4	ATGGCTCTTCGTGTAATCTCTGCACTCTTATCTTTGAAAGAAATGTCCTGGGAGTGC	63
OY			
Db	61	CAGTCCAGTGAAGAGAGGGGTGTGGCTCACTGCTGGTGCATCATTTATGGAGCTTC	120
OY			
Db	64	CAGTCCAGTGAAGAGAGGGGTGTGGCTCACTGCTGGTGCATCATTTATGGAGCTTC	123
OY			
Db	121	TTTTCTGTTCAATCAACAAGCTACTGTGGACAAGTTCATGAGAGAAATGTGGGCACTC	180
OY			
Db	124	TTTTCTGTTCAATCAACAAGCTACTGTGGACAAGTTCATGAGAGAAATGTGGGCACTC	183
OY			
Db	181	CGTGAACAGTATGGCATTCAAGAGATGGAGGCCATGCTGCATYACCTTGGAAAGATCAAT	240
OY			
Db	184	CGTGAACAGTATGGCATTCAAGAGATGGAGGCCATGCTGCATYACCTTGGAAAGATCAAT	243
OY			
Db	241	TCGAACCCCAACACTCTTGCCCAATATCACTGGGCTGTGATTAAGGGAATTCCTGCTGG	300
OY			
Db	244	TCGAACCCCAACACTCTTGCCCAATATCACTGGGCTGTGATTAAGGGAATTCCTGCTGG	303
OY			
Db	301	CATTGCGCTGTGGCCCTAGAGCAGAGCATTTAGATTCATTAAGAGATTCCTCATTTCTTCG	360
OY			
Db	304	CATTGCGCTGTGGCCCTAGAGCAGAGCATTTAGATTCATTAAGAGATTCCTCATTTCTTCG	363
OY			
Db	361	GAAGAGGAAGGGGCTTGTAATGCTCTGTGTGATGGCTCTCTCTCTTCTTCCGCTCAAG	420
OY			
Db	364	GAAGAGGAAGGGGCTTGTAATGCTCTGTGTGATGGCTCTCTCTCTTCCGCTCAAG	423
OY			
Db	421	AAGGCCAATAGAGGGGGTCAATGGGCGTGGTTCAGATTCCTTAGGCATTCAGGTCCAGAT	480
OY			
Db	424	AAGGCCAATAGAGGGGGTCAATGGGCGTGGTTCAGATTCCTTAGGCATTCAGGTCCAGAT	483
OY			
Db	481	TTGCTCCAGCTTTTCAACATACCTCAAGATTCCTACTCAAGCAACCATCATGAGATCTGAGT	540
OY			
Db	484	TTGCTCCAGCTTTTCAACATACCTCAAGATTCCTACTCAAGCAACCATCATGAGATCTGAGT	543
OY			
Db	541	GACAAAGACTCTGTTCAATAATTTTCAATGAGGGTTGTGCTTCAGATGCTCAACAAGCAAG	600
OY			
Db	544	GACAAAGACTCTGTTCAATAATTTTCAATGAGGGTTGTGCTTCAGATGCTCAACAAGCAAG	603
OY			
Db	601	TCCATGTGTGACATATGTGAAGAGGTAACAATCGACCTATGTATGATCGCGTACACAGAA	660
OY			
Db	604	TCCATGTGTGACATATGTGAAGAGGTAACAATCGACCTATGTATGATCGCGTACACAGAA	663
OY			
Db	661	GCGCACTATGTGAGAAATGGGATGGAAGCTTCAACAATATGTCAAGCAGAAAGGATTT	720

Db	664	GGCAACTATGAGAAAGTGGGTGGAAACCTTTCAAAAGTATATGTACGCCAAGGAAGCAATT	723
Qy	721	TGCATCGCCCACTCTTACAAAATCTTACAGTATATGCAAGGAGACAGAGCTTTGATTAAGCTG	780
Db	724	TGCATCGCCCACTCTTACAAAATCTTACAGTATATGCAAGGAGACAGAGCTTTGATTAAGCTG	783
Qy	781	CTGAAGAAGCTCAACAATCTTGTGCCCCAAGGCCCGGGTGTGTGGCTTACTTTCTGTAGAGGC	840
Db	784	CTGAAGAAGCTCAACAAGTCACTTGGCCCAAGGCCCGGGTGTGTGGCTTACTTTCTGTAGAGGC	843
Qy	841	ATGACGGGTGAGAGGCTGTGCTGATGGCCATGAGGGCCCTGGGCTCTTAGTGGAGAAATTTCTG	900
Db	844	ATGACGGGTGAGAGGCTGTGCTGATGGCCATGAGGGCCCTGGGCTCTTAGTGGAGAAATTTCTG	903
Qy	901	CTTCTGGGCAGGGAACAGATGCGACTTTTATTTAGATCTCAAGAAGACAGATCCTATGG	960
Db	904	CTTCTGGGCAGGGAACAGATGCGACTTTTATTTAGATCTCAAGAAGACAGATCCTATGG	963
Qy	961	GAAAGCAGAGAAAAATGCGAAGTGTCTTCTTCAGGGTTTTGGAGCATTTACACAGA	1020
Db	964	GAAAGCAGAGAAAAATGCGAAGTGTCTTCTTCAGGGTTTTGGAGCATTTACACAGA	1023
Qy	1021	AGTAGTCCCGTGTGCTGTGCACATATGCCCAAGGCTCTGAATCTAGAGCTTAGTTCAAGGCCCC	1080
Db	1024	AGTAGTCCCGTGTGCTGTGCACATATGCCCAAGGCTCTGAATCTAGAGCTTAGTTCAAGGCCCC	1083
Qy	1081	ATCACTGAGCTGAGGGACAGGCTCATCTTAA	1110
Db	1084	ATCACTGAGCTGAGGGACAGGCTCATCTTAA	1113

### RESULT 3

US-09-822-830A-61  
; Sequence 61, Application US/09822830A

Patent NO. US20020142952A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Genetics Institute, Inc.  
 ? APPLICANT: Mong, Gordon G.  
 ? APPLICANT: Clark, Hilary  
 ? APPLICANT: Rechebel, Kim  
 ? APPLICANT: Agostino, Michael J.  
 ? APPLICANT: Howes, Steven H.  
 ? APPLICANT: Resnick, Richard J.  
 ? APPLICANT: Gulukota, Kamalakara  
 ? APPLICANT: Graham, James R.  
 ? TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
 ? FILE REFERENCE: GIN 6402  
 ? CURRENT APPLICATION NUMBER: US/09/822,830A  
 ? CURRENT FILING DATE: 2001-03-29  
 ? PRIOR APPLICATION NUMBER: 60/195,604  
 ? PRIOR FILING DATE: 2000-04-06  
 ? NUMBER OF SEQ ID NOS: 631  
 ? SOFTWARE: PatentIn Ver. 2.0  
 ? SEQ ID NO 61  
 ? LENGTH: 1788  
 ? TYPE: DNA  
 ? ORGANISM: Homo sapiens  
 ? US-09-822-830A-61

Query Match	99.8%	Score 1108;	DB 10;	Length 1788;
Best Local Similarity	100.0%	Pred. NO. 0;		
Matches 1108; Conservative	0;	Mismatches	0;	Gaps 0;

QY 3 GGCCTTCCTGTTGATCTCTGACGTCTTACTTTTGGAAAGAAAGTGCCTGGGAGATGCACA 62

Db 1 GGCCTTCCTGTTGATCTCTGACGTCTTACTTTTGGAAAGAAAGTGCCTGGGAGATGCACA 60

QY 63 GTCACAGAGAGAGAGGAGGTGGTGGCTGCACATGCTGGGTACATCATATATTTGAGAGCTCTCTT 1222

Db 61 GTCACATGAGAGAGAGGTGGTGGCTGCACATGCTGGGTACATCATATATTTGAGAGCTCTCTT 1201

QY 123 TTCCTGTTATCAACACAGCTTACTGTGGACGAAAGTTTCATAGAGAGAAATGTCGTGGGAGCATGTCG 1823

Db	121	TTCTGTTTCATCCAGGCTTACTGTGGACGAAGTTCA	TGAGAGGAAGTGTGGGCAATCCG	180	
Qy	183	TGAACAGTATGGCATTGAGAGTGGAGGCCATGCTGCATAC	CTGTGAAAGATCAATTC	242	
Db	181	TGAACAGTATGGCATTGAGAGTGGAGGCCATGCTGCATAC	CTGTGAAAGATCAATTC	240	
Qy	243	AGACCCCAACCTCTGGCCCAACATCACTGGGGTGGAGA	TAAGGGATTCTGTGGCA	302	
Db	241	AGACCCCAACCTCTGGCCCAACATCACTGGGGTGGAGA	TAAGGGATTCTGTGGCA	300	
Qy	303	TTGGCTGTGGCCCTTAGAGCAGACATTTGATTCATAAGAGATT	CCCTCATTTCTTCGGA	362	
Db	301	TTGGCTGTGGCCCTTAGAGCAGACATTTGATTCATAAGAGATT	CCCTCATTTCTTCGGA	360	
Qy	363	AGAGGAAGAAGGGCTTGGTATGCTCTGTGGATGGCTCCTCCTTCTTCCGCTCCAGAA	422		
Db	361	AGAGGAAGAAGGGCTTGGTATGCTCTGTGGATGGCTCCTCCTTCTTCCGCTCCAGAA	420		
Qy	423	GCCCATGTAGAGGGGTCAATTGGGCTCGAGTTCCAGTTCTTTAGCCATTCAGGTCCAGAAATTT	482		
Db	421	GCCCATGTAGAGGGGTCAATTGGGCTCGAGTTCCAGTTCTTTAGCCATTCAGGTCCAGAAATTT	480		
Qy	483	GCTCCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGATGA	542		
Db	481	GCTCCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGATGA	540		
Qy	543	CAAGACTCTGTCCAAATTAATTCATGAAGGGTTGAGCCTTCAGATGCTCAGACGAGGAAGGTC	602		
Db	541	CAAGACTCTGTCCAAATTAATTCATGAAGGGTTGAGCCTTCAGATGCTCAGACGAGGAAGGTC	600		
Qy	603	CATGTGGACATGATGGAAGGTAACA	CTGGA	662	
Db	601	CATGTGGACATGATGGAAGGTAACA	CTGGA	660	
Qy	663	CAACTATGGAGAAAGTGGGATGGAAAGGCTTCAAGATATGTCAAGGAAAGGAAGGATTTG	722		
Db	661	CAACTATGGAGAAAGTGGGATGGAAAGGCTTCAAGATATGTCAAGGAAAGGAAGGATTTG	720		
Qy	723	CATGGCCCACTTTACAAATCTTACAGTAA	TGCAGGGGAGAGACTTTGATTAAGCTGCT	782	
Db	721	CATGGCCCACTTTACAAATCTTACAGTAA	TGCAGGGGAGAGACTTTGATTAAGCTGCT	780	
Qy	783	GAAGAGCTCACAAGTCACTTGCCCAAGGCCCGGGTGGTGGCTTACTTCTGTAGGGCAT	842		
Db	781	GAAGAGCTCACAAGTCACTTGCCCAAGGCCCGGGTGGTGGCTTACTTCTGTAGGGCAT	840		
Qy	843	GACGGTGAAGAGTCTGTGTA	TGGCCATGAAGGCCCTGGGTCTTGTAGGGAGAAATTTCTGCT	902	
Db	841	GACGGTGAAGAGTCTGTGTA	TGGCCATGAAGGCCCTGGGTCTTGTAGGGAGAAATTTCTGCT	900	
Qy	903	TCTGGGCGAGGAACGAGTSCCATCTTTATTTAGATCTCAAGAAACAGCATCTATGGGA	962		
Db	901	TCTGGGCGAGGAACGAGTSCCATCTTTATTTAGATCTCAAGAAACAGCATCTATGGGA	960		
Qy	963	AGACAGAAAGAAATGCCAAAGTGGCTCTTCAAGGGTTTGGAGACATATTTACACAGAG	1022		
Db	961	AGACAGAAAGAAATGCCAAAGTGGCTCTTCAAGGGTTTGGAGACATATTTACACAGAG	1020		
Qy	1023	TGAGTCCGTGCTGTGCACATGCCCCAGCCTTGAA	CTTGAAGCTCAATTCAGGGCCCAT	1082	
Db	1021	TGAGTCCGTGCTGTGCACATGCCCCAGCCTTGAA	CTTGAAGCTCAATTCAGGGCCCAT	1080	
Qy	1083	CACGTGACTGAGGGAGACAGGCTCAATCTPA	1110		
Db	1081	CACGTGACTGAGGGAGACAGGCTCAATCTPA	1108		

## RESULT 4

US-10-346-241-1  
; Sequence 1, Application US/10346241

; PUBLICATION NO. US20010000000  
; GENERAL INFORMATION:  
;

APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STORJOHANN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346,241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US/09/695,481  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2826  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2826)  
US-10-346-241-1

Query Match 20.0%; Score 222; DB 13; Length 2826;  
Best Local Similarity 99.1%; Pred. No. 7.3e-108;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
DB 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
QY 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGTTGTGCTT 580  
DB 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGTTGTGCTT 580  
QY 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGAGTGAAGAGTGAAGAGTGAAG 640  
DB 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGAGTGAAGAGTGAAGAGTGAAG 640  
QY 641 TATCAGCCGTGACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
DB 641 TATCAGCCGTGACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
QY 701 TGTCAAGGAAAGAGGATTTGATGCGCCACTCTTCAAAATCTACAGTAATGCAAGGG 760  
DB 701 TGTCAAGGAAAGAGGATTTGATGCGCCACTCTTCAAAATCTACAGTAATGCAAGGG 760  
QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
DB 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
QY 821 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGATGAGGCGGCTGG 880  
DB 821 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGATGAGGCGGCTGG 880  
QY 881 GTCTAG 886  
DB 881 GTCTAG 886

RESULT 5  
US-10-346-241-5  
Sequence 5, Application US/10346241  
Publication No. US20030157647A1  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STORJOHANN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.

TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/10/346,241  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US/09/695,481  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 3129  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
OTHER INFORMATION: molecule comprising portions of human mGluR5 and  
OTHER INFORMATION: the human calcium receptor.  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3129)  
US-10-346-241-5

Query Match 20.0%; Score 222; DB 13; Length 3129;  
Best Local Similarity 99.1%; Pred. No. 7.3e-108;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
DB 461 TAGCCATTGAGTTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGTTACTCAG 520  
QY 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGTTGTGCTT 580  
DB 521 CAACCATCATGATCTGATGAGCAAGACTCTGTTCAAAATTTTCATGAGGTTGTGCTT 580  
QY 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGAGTGAAGAGTGAAGAGTGAAG 640  
DB 581 CAGATCTCAGCAGGCAAGGTCATGATGAGCAATGAGAGAGTGAAGAGTGAAGAGTGAAG 640  
QY 641 TATCAGCCGTGACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
DB 641 TATCAGCCGTGACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
QY 701 TGTCAAGGAAAGAGGATTTGATGCGCCACTCTTCAAAATCTACAGTAATGCAAGGG 760  
DB 701 TGTCAAGGAAAGAGGATTTGATGCGCCACTCTTCAAAATCTACAGTAATGCAAGGG 760  
QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
DB 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGGCCCGGGTGG 820  
QY 821 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGATGAGGCGGCTGG 880  
DB 821 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGATGAGGCGGCTGG 880  
QY 881 GTCTAG 886  
DB 881 GTCTAG 886

RESULT 6  
US-10-225-567A-177  
Sequence 177, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenn C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19

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; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
; LENGTH: 4518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-177

Query Match
Best Local Similarity 99.1%; Score 222; DB 15; Length 4518;
Pred. No. 7,3e-108; Mismatches 4; Indels 0; Gaps 0;
Matches 422; Conservative 0;

QY 461 TAGCCATTGAGTCCGAATTTGCTCCAGCTTTTCAACATCTGATGCTTACTCAG 520
DB 611 TAGCCATTGAGTCCGAATTTGCTCCAGCTTTTCAACATCTGATGCTTACTCAG 670
QY 521 CAACCATCATGATCTGATGACAGACTCTGTTCAAATTTTCATGAGGGTTGCTT 580
DB 671 CAACCATCATGATCTGATGACAGACTCTGTTCAAATTTTCATGAGGGTTGCTT 730
QY 581 CAGATCTCAGCAGCAAGGCTCAGTGTGACATAGTGAAGGTAACAATGACCTATG 640
DB 731 CAGATCTCAGCAGCAGGCGCATGTGTGACATAGTGAAGGTAACAATGACCTATG 790
QY 641 TATCAGCCTTACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 700
DB 791 TATCAGCCTTACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 850
QY 701 TGTACAGGAAGAAAGGATTTGCTGCGCCACTCTTACAAATCTACATATGACAGGG 760
DB 851 TGTACAGGAAGAAAGGATTTGCTGCGCCACTCTTACAAATCTACATATGACAGGG 910
QY 761 AGCAGAGCTTTGATTAAGTCTGCTGAGAGAGCTCAAGTCACTTGCCCAAGCCGGGTG 820
DB 911 AGCAGAGCTTTGATTAAGTCTGCTGAGAGAGCTCAAGTCACTTGCCCAAGCCGGGTG 970
QY 821 TGGCTACTTCTGTGAGGGCATACGGTGAAGAGTCTGCTGATGCGCATGAGCCCTTG 880
DB 971 TGGCTACTTCTGTGAGGGCATACGGTGAAGAGTCTGCTGATGCGCATGAGCCCTTG 1030
QY 881 GTCTAG 886
DB 1031 GTCTAG 1036

RESULT 7
US-10-027-632-221104
; Sequence 221104, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221104
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-221104

Query Match
Best Local Similarity 100.0%; Score 24; DB 13; Length 611;
Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

QY 885 AGTGGAGAAATTTCTGCTTCTGGG 908
DB 49 AGTGGAGAAATTTCTGCTTCTGGG 72

RESULT 8
US-10-027-632-221105
; Sequence 221105, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221105
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-221105

Query Match
Best Local Similarity 100.0%; Score 24; DB 13; Length 611;
Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

QY 885 AGTGGAGAAATTTCTGCTTCTGGG 908
DB 49 AGTGGAGAAATTTCTGCTTCTGGG 72

RESULT 9
US-10-027-632-221104
; Sequence 221104, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 1999-08-09
```

;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 221104  
;; LENGTH: 611  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-221104

Query Match 2.2%; Score 24; DB 14; Length 611;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 885 AGTGGAGAAATTCCTCTGGG 908  
DB 49 AGTGGAGAAATTCCTCTGGG 72

RESULT 10  
US-10-027-632-221105  
;; Sequence 221105, Application US/10027632  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; POLYMORPHISMS IN THE HUMAN GENOME  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 221105  
;; LENGTH: 611  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-221105

Query Match 2.2%; Score 24; DB 14; Length 611;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 885 AGTGGAGAAATTCCTCTGGG 908  
DB 49 AGTGGAGAAATTCCTCTGGG 72

RESULT 11  
US-09-804-474A-3  
;; Sequence 3, Application US/09804474A  
;; Patent No. US20020119518A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KODET, Stefan et al

;; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
;; FILE REFERENCE: C1000891  
;; CURRENT APPLICATION NUMBER: US/09/804,474A  
;; CURRENT FILING DATE: 2001-03-13  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 126512  
;; TYPE: DNA  
;; ORGANISM: Human  
;; FEATURE:  
;; NAME/KEY: misc.feature  
;; LOCATION: (1)...(126512)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-804-474A-3

Query Match 2.0%; Score 22; DB 10; Length 126512;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 357 TTGGAAGAGAGAGAGGCTTG 378  
DB 87864 TTGGAAGAGAGAGAGGCTTG 87885

RESULT 12  
US-10-125-792-11  
;; Sequence 11, Application US/10125792  
;; Publication No. US20030051269A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Marical  
;; APPLICANT: Harris, H. William  
;; APPLICANT: Neuring, Jacqueline A.  
;; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
;; FILE REFERENCE: 2213.1006-007  
;; CURRENT APPLICATION NUMBER: US/10/125,792  
;; CURRENT FILING DATE: 2002-08-16  
;; PRIOR APPLICATION NUMBER: 10/121,441  
;; PRIOR FILING DATE: 2002-04-11  
;; PRIOR APPLICATION NUMBER: PCT/US01/31704  
;; PRIOR FILING DATE: 2001-10-11  
;; PRIOR APPLICATION NUMBER: 60/240,392  
;; PRIOR FILING DATE: 2000-10-12  
;; PRIOR APPLICATION NUMBER: 60/240,003  
;; PRIOR FILING DATE: 2000-10-12  
;; NUMBER OF SEQ ID NOS: 28  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 11  
;; LENGTH: 3824  
;; TYPE: DNA  
;; ORGANISM: Salmo salar  
US-10-125-792-11

Query Match 1.9%; Score 21; DB 15; Length 3824;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 TGCCCAACATCACACTGGGCT 277  
DB 443 TGCCCAACATCACACTGGGCT 463

RESULT 13  
US-10-125-778-11  
;; Sequence 11, Application US/10125778  
;; Publication No. US20030082574A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Marical  
;; APPLICANT: Harris, H. William  
;; APPLICANT: Neuring, Jacqueline A.

; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-005  
; CURRENT APPLICATION NUMBER: US/10/125,778  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 3824  
; TYPE: DNA  
; ORGANISM: Salmo salar  
US-10-125-778-11

Query Match 1.9%; Score 21; DB 15; Length 3824;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 257 TGCCCAACATCACACTGGGCT 277  
DB 443 TGCCCAACATCACACTGGGCT 463

RESULT 14  
US-10-125-772-11  
; Sequence 11, Application US/10125772  
; Publication No. US20030124657A1  
; GENERAL INFORMATION:  
; APPLICANT: Marical  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-006  
; CURRENT APPLICATION NUMBER: US/10/125,772  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 3824  
; TYPE: DNA  
; ORGANISM: Salmo salar  
US-10-125-772-11

Query Match 1.9%; Score 21; DB 15; Length 3824;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 257 TGCCCAACATCACACTGGGCT 277  
DB 443 TGCCCAACATCACACTGGGCT 463

RESULT 15  
US-10-125-792-7  
; Sequence 7, Application US/10125792  
; Publication No. US20030051269A1  
; GENERAL INFORMATION:

; APPLICANT: Marical  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-007  
; CURRENT APPLICATION NUMBER: US/10/125,792  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 3941  
; TYPE: DNA  
; ORGANISM: Salmo salar  
US-10-125-792-7

Query Match 1.9%; Score 21; DB 15; Length 3941;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 257 TGCCCAACATCACACTGGGCT 277  
DB 442 TGCCCAACATCACACTGGGCT 462

Search completed: December 14, 2003, 18:32:29  
Job time : 370.72 secs



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## SUMMARIES

**Description**

CDNA sequence

Human GRMX

Human GRMX

Human GRMX

Human meta

Human meta

Human meta

Human meta

## Mouse meta

Non-endoge

Hsmglur1 D

Human meta

Nucleotide

**Clone 45-A**

mcglur8 gen

Human GRM8

Chimeric h

Human meta

1000

**DNA.**

**protein;**

2

1

OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 4..1113  
PT /tag= a  
PT /product= "mglur5m"  
PT /note= "the CDS is specifically claimed in claim 1"  
FT sig\_peptide 4..63  
FT mat\_peptide 64..1110  
FT /tag= b  
XX /tag= c  
PN WO200270708-A2.  
PD 12-SEP-2002.  
PP 21-DEC-2001; 2001WO-US49817.  
PR 22-DEC-2000; 2000US-257589P.  
PA (AMHP ) WYETH.  
PI Bates BG, Xie Y, Gulukota K, Paulsen JR,  
DR WPI: 2002-750462/81.  
PS P-PSDB; ABP54921.  
XX Claim 11; Fig 1A; 99pp; English.

The present sequence is that of CDNA clone y1176 (deposited as ATCC PTA-2776) encoding a novel human metabotropic glutamate receptor subtype modulatory protein (mglur5m). The CDNA was isolated from a human brain CDNA library. Expression of mglur5m is predominant in cells and tissues of the central nervous system. The gene maps to a region of chromosome 11 associated with schizophrenia and related psychiatric disorders. The invention provides mglur5m polypeptides and nucleic acids, and methods for their detection, as well as methods for using them to identify compounds that modulate metabotropic receptor (mglur) activity. Such modulators include a mglur5m nucleic acid, a mglur5m antibody, a ribozyme, an antisense oligonucleotide, a small molecule modulator, a peptide and a peptidomimetic. They can be used in a claimed method for treating a subject having a neurological disorder, especially a psychiatric disorder selected from schizophrenia, schizoaffective disorder, bipolar affective disorder, unipolar affective disorder or adolescent conduct disorder (all claimed). mglur5m polypeptides, nucleic acids and antibodies are also useful for screening assays, and in predictive medicine, e.g., diagnostic assays (e.g., chromosome mapping and tissue typing), prognostic assays, monitoring clinical trials, and pharmacogenomics.

Db	64	CAGTCCAGTGAAGAGAGGTGGTGGCTCAACATGCTGGGTGACATCATTAATGAACTCTC	123
Oy	41	PheserValHhshIsglnProthValAapgluValHhsgluuvglyCyeglyValAval	60
Db	124	TTTTCTGTTCATCAACAGCTTACTGTGGACCAAGTTCATGAGAGAAATGTGGGGCACTC	183
Oy	61	ArgluglnTyrGlyIleGlnArValGluAmetLeuHhsthLeuGluArgIleAsn	80
Db	184	CGTGAACATATGGCATTCAGAGAGTGAAGGCCATCTGCTCAATCCCTGGAAAGATCAAT	243
Oy	81	SerAapProthLeuLeuProAsnIlethLeuGlyCyegluIleArgAapSerCysTrp	100
Db	244	TCAGACCCCACTCTTGCCCAATCACTCAGTGGCTGTGATGATAGGAAATTCCTGTGG	303
Oy	101	HhSerAlaValAlaLeuGlnInsertIleGluPheIleArgAapSerLeuIleSerSer	120
Db	304	CATTGCGCTGTGGCCCTTAGACAGAGCATTAAGTTCATMAAGAAATCCCTCATTTCTTCG	363
Oy	121	GluGluGluGluGluValCysSerValAapGlySerSerSerSerPheArgSerTyr	140
Db	364	GAAAGAGAGAGGGCTGTGTATGCTCTGTGGATGGCTCTCTCTCTTCCTGCTCCAG	423
Oy	141	LysProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn	160
Db	424	AAGCCCATAGTAGGGGTCACTTGGGCTGTGCTTCCAGTTCTTACCATTCAGGTCCAGAT	483
Oy	161	LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAapLeuSer	180
Db	484	TTGCTCCAGCTTTTCAACATACCTCAGATTCTTACTACAGAACCATATGATCTGAGT	543
Oy	181	AspIlyrThrLeuPheIlyrTyrPheMetArgValValProSerAapAlaGlnAlaArg	200
Db	544	GACAGAGATCTGTTCAAATATTTATGATAGGGGTGTGGCTTACAGATGCTCACAGAGCAAG	603
Oy	201	SerMetValAapIleValIleArgTyrAsnTrpThrTyrValSerAlaValHhsthGlu	220
Db	604	TTCCATGTGTGACATATGTAGAGAGGTACACTGAGACCTATGTATACGCCGTACACAGAA	663
Oy	221	GlyAsnTyrGlyGlnSerGlyMetGluAlaPheIlyAapMetSerAlaIlyGluGlyIle	240
Db	664	GGCAACTATGAGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCCAGCAAGAGGGGATT	723
Oy	241	CysIleAlaHhSerTyrIlyIleTyrSerAsnAlaGlyGluGlnInsertPheAapIlyLeu	260
Db	724	TGCATCGCCCACTTTACAAATCTTACAGTATACAGGGGAGCAGAGCTTTGATTAAGCTG	783
Oy	261	LeuIlyIlyLeuThrSerHhIleuProIlyAlaArgValAlaIlyPheCyegluGly	280
Db	784	CTGAAGAGCTCACAAATCACTTGGCCCAAGGCCGGGTGTGTGGCTTCTGTGAAGGCC	843
Oy	281	MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu	300
Db	844	ATGACGGGTGAGAGGTCTGTGATGGCCATGAGGGCGGCTGTAGTGGAGAAATTTCTG	903
Oy	301	LeuLeuGlyIlyArgIlyProAapAlaIlePheIleGluIleSerIlyAsnSerIleIleuTrp	320
Db	904	CTTCTGGGCAAGGAAACGATGCCATCTTATTTAGATCTCAAGAAACAGATCTCTTAGG	963
Oy	321	GluAapAArgIlyCysGlnGlyIlyArgPheLeuGlnGlyPheGlyAapIleIleuHhArg	340
Db	964	GAAAGACGAAATAAATGCAAGGTGGCTTCTTCAAGGGTTTGGAGACATATTACACAGA	1022
Oy	341	SerGluSerValLeuLeuHhIleMetProGlnProIleuAsnLeuGluLeuSerSerGlyPro	360
Db	1024	AGTATGTCCTGGTCTGTCTCAATGCCCAAGCTCTGAATCTTAGAGCTCAGTTACAGGGGCC	1082
Oy	361	IleThrGlyLeuArgAapArgLeuIle	369
Db	1084	ATCACTGGACTGAGGAGAGGCTCATC	1110

ID AAF29993 standard; DNA; 2172 BP.  
 XX AAF29993;  
 AC  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRM-X-1e DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRM-X;  
 XX Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 XX  
 PN W0200102566-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROSCIENCE BIOSCIENCES INC.  
 XX  
 PI Schwarz DA, Maki RA;  
 XX  
 DR MPI; 2001-123112/13.  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 7; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polymorphisms, polymorphisms  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 SQ Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 4,92e-203 Length: 2172  
 Score: 1870.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.73% Mismatches: 0  
 Query Match: 22 Gaps: 0  
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 QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuGluValAlaArgIleSerAla 20  
 DB 365 ATGCTCTCTGTTGTAATCTCTGCTGCTTCTTTGAAAGAAATGCTCGGAGGCA 424  
 QY 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 425 CAGTCAGTGAGAGGAGGGGTGGTGCATGCTGGTGACATCTATTGAGGCTTC 484  
 QY 41 PheSerValIleIleGlnProThrValAspGluValIleGluArgGlyValAlaVal 60  
 DB 485 TTTTCTGTTTCATCAGAGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 544  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuIleIleIleGluArgIleAsn 80  
 DB 545 CGTGAACAGTATGCAATTCAGAGAGTGGAGGCACTGCTGCAATCCCTGGAAAGATCAAT 604  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
 DB 605 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGAGATTCTGCTGG 664

QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 665 CATTGGCTGTGGCCCTTAAGCAGACATTGAGCTTCAATTAAGATTCCTCATTTCTTGG 724  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
 DB 725 GAAGAGAGAGAGGGCTGTGGTGTCTGTGTGATGAGCTCTCTCTCTCTCTCTCTCTCAAG 784  
 QY 141 LysProIleValGlyValIleGlyProGlyLysSerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 785 AAGCCCATGATGAGGGGTCTGGGCTGGTCTGCAATTCCTAAGCCATTCAGGTCAGAAAT 844  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGACCACTCATGATTCGAGT 904  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 DB 905 GACAAAGCTCTGTCAAAATATTTCATGAGGGTGTGCTTCAATCTCAGACGAGGCAAGG 964  
 QY 201 SerMetValAspIleValIleValIleValIleValIleValIleValIleValIleVal 220  
 DB 965 TCCATGCTGACATAGTGAAGAGTCAACCTGACCTATGATCAACCCGATCACAGAA 1024  
 QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyLe 240  
 DB 1025 GGCACCTATGAGAAAGTGGATGAGAGGCTTCAAGATATGTCACAGAAAGAGGATAT 1084  
 QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
 DB 1085 TGCATGCCCCACTTACAAAATCTACATTAATGACGGGAGCAGGCTTGTATTAAGCTG 1144  
 QY 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGluGly 280  
 DB 1145 CTGAAAGAGCTCAAGATGACATGCCCCAGGCGGGGTGTGCTGCTGCTGAGGGC 1204  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 1205 ATACCGGTGAGGTGTGCTGATGAGGCAAGAGGCTGGGTATGAGGAGAAATTTCTG 1264  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
 DB 1265 CTTCTGGGAGGAGAACAGATGCACTTTATTTGATCTCAAAAGACATCTATGG 1324  
 QY 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 1325 GAAGACAGAAAGAAATGCAAGGCTCGCTTCAAGGTTTGGAGACATATTACACAGA 1384  
 QY 341 SerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyPro 360  
 DB 1385 AGTGAATCCGTGCTGTGACATGCCAGCCCTGAATCTTACAGCTCAGTTACAGGCCC 1444  
 QY 361 IleThrGlyLeuArgAspArgLeuIle 369  
 DB 1445 ATCACTGAGACTAGGAGCAGGCTCATC 1471  
 RESULT 3  
 ID AAS62274 standard; cDNA; 1788 BP.  
 XX  
 AC AAS62274;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE cDNA sequence #61 encoding novel human secreted protein.  
 XX  
 KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KW immune deficiency disorder; blood disorder; inflammatory disorder;  
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
 KW immunosuppressive; antineumatic; ss.  
 OS Homo sapiens.



02-JUL-1999; 99US-0346326.

PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

PI Schwarz DA, Maki RA;

DR WPI; 2001-123112/13.

Spencer

PT Novel metabotropic glutamate receptor for prevention, treatment of  
PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, nat

PS Claim 2; Fig 3; 59pp; English.  
yy

CC The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia  
CC Metabotropic glutamate receptor polymorphisms, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.

**SQ** Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;

**Alignment Scores:**

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Score:	1830.50	Matches:	368

Percent Similarity: 86.21%  
Conservative: 1

Best Local Similarity:	85.98%	Mismatches:	0
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Query Match:	97.73%	Indels:	59
DB:	32	Calls:	1

DB:	22	Gaps:	1
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US-10-027-923-2 (1-369) x AAF29990 (1-2349)

US-10-027-923-2 (1-369) X AAF29990 (1-2349)

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Qy		MeValLeuLeuLeuLeuLeuSerValLeuLeuLeuLeuValGluAspValArgLysLeuA	20
Db			
Qy	21	GlnSerSerGluArgArgValAlaAlaHisMetLeuGluAspIleIleIleGluValLeu	40
Db	425	CAGTCCAGTAGAGAGAGGGGTGGGTGCTCAGTGTGGGTGACATCATTAATGGAGCTTC	48
Qy	41	PhSerValHisHisGlnProThrValAlaArgGluValHisGluAlaGlyGlyValAla	60
Db	485	TTTTCTGTTTCATCAACCAAGCCTACTGTGGACGAATTCATGAGAGAAATGTGGGGCAATC	54
Qy	61	ArgGluGlnThrGlyIleGluArgValGluAlaMetLeuHisIleThrLeuGluArgIleAsn	80
Db	545	CGGAAACAGATATGGCAATTCAGAGAGTGGAGGGCCAGTGTGCATACCTGTGAAAGATCAAT	60
Qy	81	SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp	100
Db	605	TCAGACCCCACTCTTGGCCAAACATCACTGGGCTGTGAGATPAGGAAATTCCTGCTGG	66
Qy	101	HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer	120
Db	665	CATTCGGCTGTGGCCCTTAGAGCAAGACATTTGAGTTCATPAGAGATTCCTCATATTTCTTGG	72
Qy	121	GluGluGluGluGluLeuValCysSerValAlaArgLysSerSerSerPheArgSerLys	140
Db	725	GAAAGAGAAAGAGGGCTTGGATGTGCTCTTGATGATGCTCTCTCTTCTCTTCCGTCCAG	78
Qy	141	LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGluValGlnAsn	160
Db	785	AAGCCCATAGTAGGGGTCAATGGGCTGGTTCAGTTCGTATGCCATTCAAGTCCAGAAAT	84
Qy	161	LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleArgSerAlaThrIleMetAspLeuSer	180
Db	845	TTTGCTCAGGCTTTTCAACATCACTCAGATGTGCTTACTCAGCAACATCATGTGACTAGT	90
Qy	181	AspLysThrIleuPheLysTrpPheMetArgValValProSerAspAlaGlnGlnAlaArg	200

Db	905	GACAAAGCTCTGTTCAAAATTTTCATGAGGGTGTGTGCTTCAAGTGTCCAGCAGGCAAG	964
Oy	201	SeTMeValIapIleValIySaGrTYrAsnTTrpThyValSerAlaValIhSthGlu	220
Db	965	TCCATGTGTGACATAGTGAAGAGGTACAACTGCACCTATGATATCAGCCGTACACAGAA	1024
Oy	220	-----	220
Db	1025	GGTTCAAAGCTATTCATATGCTCAGCTCCAGAGAGACTAGGCTGTCTTCAACTTTGG	1084
Oy	220	-----	220
Db	1085	CCTCAAGTATCTGCTCTGCTTTGGCCTTCCAAATTCGTGGATTATGCGATGAGCCACC	1144
Oy	221	-----Gly	221
Db	1145	ACAGCAGCCCGCCAGTCCGCGATCTTAGAACACTTGAAGTGTCTTGATTTTTTAGGC	1204
Oy	222	AsnTYrTlYgluSerGlyMetGluAlaPhyIleAspMetSerAlaValGluGlyIleCys	241
Db	1205	AACATATGAGAAATGTGGATGGAAGCCTTCAAAAGATATGTCAAGGAGGAAGGATTTGC	1264
Oy	242	IleAlaIhSerTYrIySleTYrSerAsnAlaGlyGluGlnSerPheAspLYleuLeu	261
Db	1265	ATGCCCACTCTTACAAATCTACAGTATGCAAGGGAGCAGACCTTGTATAGCTCTG	1324
Oy	262	LYsIySleuThrSerhIleuProLYalAArgValAlaIATyPheCYsgIuGlyMet	281
Db	1325	AAGAAGCTCAACAAGTCACTTGCCCAAGCCCGGGTGTGGCTTACTTCTGTGAGGGCATG	1384
Oy	282	ThyValIArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeuLeu	301
Db	1385	ACGGTGAAGAGTCTGCTGATGGCCATAGGCGCCTGGGTCTTAGTGGAGAAATTTCTGCTT	1444
Oy	302	IeuGlyArgGluProAspAlaIlePheIleGluIleSerLYsAsnSerIleLeuTrpGlu	321
Db	1445	CTGGGCGAGGAAACCAATGCCATCTTTATTGAGATCTCAAGAACACACATCTTATGGGAA	1504
Oy	322	AspArgArgLYsCYsgIuGlyArgPheLeuGlnGlyPheGlyAspIleLeuIhSArgSer	341
Db	1505	GACGAGAGAAATGCCAAGGTGGCTTCTTCAAGGGTTTGGAGCATATTATCACAGAGT	1564
Oy	342	GluSerValleuLeuIhSmetProGlnProLeuAsnLeuGluLeuSerSergLYProIle	361
Db	1565	GAGTCCGTGTGCTGCACATGCCCAAGCCTCTGATCTAGAGCTCAAGTCAAGGGCCCATC	1624
Oy	362	ThrGlyLeuArgAspArgLeuIle	369
Db	1625	ACTGGACTGAGGACAGGCTCATC	1648
RESULT 5			
AAAF29994			
ID	AAF29994 standard; DNA, 2149 BP.		
XX	AAF29994;		
AC	(first entry)		
XX	06-APR-2001		
DT	Human GRMX-1f DNA.		
XX	Human GRMX-1f DNA.		
XX	Human; metabotropic glutamate receptor; schizophrenia; GRMX;		
KW	Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	W0200102566-A1.		
FN	11-JAN-2001.		
PD	27-JUN-2000; 2000MO-US17798.		
XX	27-JUN-2000; 2000MO-US17798.		
XX	99US-0346326.		
PR	02-JUL-1999;		

XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA Schwarz DA, Maki RA;  
 PI WPI, 2001-123112/13.  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 9; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2,34e-194 Length: 2149  
 Score: 1794.00 Matches: 359  
 Percent Similarity: 97.30% Conservative: 1  
 Best Local Similarity: 97.03% Mismatches: 1  
 Query Match: 95.78% Indels: 9  
 Gaps: 1  
 US-10-027-923-2 (1-369) x AAF29994 (1-2149)  
 QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLeuValAlaGlySerAla 20  
 DB 365 ATGGTCTCTGTTGATCTGTCTGATCTTCTTTGAAGAAGATGCCGTGGAGTGA 424  
 QY 21 GluSerSerGluArgValAlaAlaHisMetLeuGluAspIleIleIleGlyAlaLeu 40  
 DB 425 CAGTCCAGTAGAGAGAGGTGGTGGTGCATGCTGGAGTGAATTTGAGCTCTC 484  
 QY 41 PheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60  
 DB 485 TTTTCTGTCATACCAAGCCTACTGTCGAGAGAGTTTATAGAGAGAGTGGGGCAGTC 544  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 545 CGTGAACAGTATGCAATTCAGAGAGTGGAGGCCATGCTGCATACCTCGAAAGCATCAAT 604  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 605 TCAAGACCCCACTCTTGGCCCAATCACTGGGCTGTAGATGAAGGATTCCTGCTGG 664  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 665 CATTGGCTGTGGCCCTAGAGAGAGATGAGTTGATTAAGAGATTCCTCATTTCTTCG 724  
 QY 121 GluGluGluGluGluLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
 DB 725 GAAGAGAGAAAGAGGCTGTGTGCTGTGTGATGCTCTCTCTCTCTCCGCTCAAG 784  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 785 AAGCCCACTAGAGGAGTGGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCT 844  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleSerAlaThrIleMetAspLeuSer 180  
 DB 845 TTGCTCAGCTTTTCAACATACCTCAATGCTTACTCAGACCAACATCAGATCTGAGT 904  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
 DB 905 GACAAAGACTCGTTCAATATATTTTCATGAGGTTGTGCTTCAGATGCTCAGCAGGCAAG 964

QY 201 SerMetValAspIleValLysArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 DB 965 TCCATGGTGAACATATGTAAGAGGTACCACTGACCTATATATACAGCCGTACACAGAA 1024  
 QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
 DB 1025 GGCACCTATGAGAAAGTGGATGAGAGCCTTCAAGATATGTACAGCAAGAAAGGATTT 1084  
 QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGluGlnSerPheAspLysLeu 260  
 DB 1085 TGCATGCCCACTTACCAAAATCAGTAATGACGGGAGCAAGAGCTTGTATTAAGCTG 1144  
 QY 261 LeuLysLeuThrSerHisLeuProLysAlaArgValAlaTyrPheCysGluGly 280  
 DB 1145 CTGAAGAAGCTCAACAGTCACTTGGCCCAAGCCCGGTGTGGCTTACTTGTAGAGGC 1204  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 1205 ATGACGGTGAAGAGTCTGTGATGGCCATGAGCGCCTGGGTCTAAGTGGAGAAATTTCTG 1264  
 QY 301 LeuLeuGlyValArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320  
 DB 1265 CTCTGGGACGGAGAACAGATGCCATCTTATTTAGATCTCAAAAGAACAGCATCTATGG 1324  
 QY 321 GluAspArgArgLysCysGlnGlyValArgPhe-LeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 1325 GAGAGCAAGAGAAATGCCAAAGTCCCTTCCTTC-----AG 1360  
 QY 340 GSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyPr 360  
 DB 1361 AAGTGAATCCGTCTGCTGACATGCCCCAGCCTTGAAATCTAGACTCAGTTCAGGGCC 1420  
 QY 360 oIleThrGlyLeuArgAspArgLeuIle 369  
 DB 1421 CATCACTGACCTGAGGACAGGCTCATC 1448  
 RESULT 6  
 AAF29989  
 ID AAF29989 standard; DNA; 2551 BP.  
 AC XX  
 XX AAF29989;  
 DT 06-APR-2001 (first entry)  
 DE Human GRMX-1a DNA.  
 XX Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200102566-A1.  
 XX 11-JAN-2001.  
 PD 27-JUN-2000; 2000MO-US17798.  
 PR 02-JUL-1999; 99US-0346326.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PI Schwarz DA, Maki RA;  
 DR WPI, 2001-123112/13.  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 1; 59pp; English.  
 XX



CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polypeptides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.

XX  
 SQ Sequence 2551 BP, 666 A, 566 C, 630 G, 689 T; 0 other;

# Alignment Scores:

Pred. No.:	1,21e-192	Length:	2551
Score:	1780.00	Matches:	368
Percent Similarity:	74.40%	Conservative:	1
Best Local Similarity:	74.19%	Mismatches:	0
Query Match:	95.03%	Indels:	127
DB:	22	Gaps:	1

US-10-027-923-2 (1-369) x AAF29989 (1-2551)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValArgGlySerAla 20  
 DB 365 ATGGTCCTTCTGTGATCCCTGTCAGTCTTACTTTGAAAGAGATGCTCCGTGGAGTGCA 424  
 QY 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspLeileileileGlyAlaLeu 40  
 DB 425 CAGTCCAGTGAAGAGAGGGGTGGCTCAGATCTGGGTGACATCTTATTTGAGCTCTC 484  
 QY 41 pheSerValHisIleGlnProThrValAspGluValHisGluArgGlyCysGlyAlaVal 60  
 DB 485 TTTTCTTCATCACACAGCCTACTGTGGACGAAGTTTCATGAGAGGAAGTGGGGCAGTC 544  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluValIleAsn 80  
 DB 545 CGGAAACAGATGCGCATTCAGAGAGTGGAGGCCATCTGCATACCTCGGAAAGATCAAT 604  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 605 TCGACCCCACTCTTGGCCACATCACTGGGCTGTGAGATTAAGGATTCCTGTGG 664  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 665 CATTCGGCTGTGGCCCTAGAGCAGAGCATGATGATTCAATGAATCCCTCATTTCTTG 724  
 QY 121 GluGluGluGluGluGluValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
 DB 725 GAAGAGAAAGAGGGCTGTGTGCTCTGTGGATGGCTCTCTCTCTCTCTCTCTCAAG 784  
 QY 141 LysProIleValAlaGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 785 AAGCCCATAGTAGGGGTCATTTGGGCTGTGCTTCAAGTTCTGTACCATTCAGTCCAGAA 844  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 DB 845 TTGCTCAGCTTTTCAACATCACTCAGATTGCTTACACCAACATCAATGATCTGAGT 904  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
 DB 905 GACAAAGACTCTGTCAAAATTTTCATGAGGGTGTGCTTCATATCTCAGCAGCAGAG 964  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 DB 965 TCCATGTGACATAGTAGAAGAGTACACATGAGACCTATATATACGCCGTACACAGAA 1024  
 QY 220 ----- 220  
 DB 1025 GAGCAGGCTAATTGTGAGAAAGATTGGCTACAAGTGGAGAGAAACTGATCTACTAATA 1084  
 QY 220 ----- 220  
 DB 1085 TGAATAATGGCAGTTTCTATATGATACCAATAAAGTAGATATATCTAAGATATA 1144  
 QY 220 ----- 220

DB 1145 TAAGCAAAATGCTGAATGAATAAGGCAATTGTGATGCCAAATTAATTCATGTCATTTG 1204  
 QY 220 ----- 220  
 DB 1205 CATTAAGCAGACAGAAATTTAGAGTTCAAGTATTCTCATGCTCAGCCTCAGAGAGC 1264  
 QY 220 ----- 220  
 DB 1265 TAGGCTGTCTCAACTCTTGGCTCAAGTATCTGCTGCTTGGCTTCCAAATTGCT 1324  
 QY 220 ----- 220  
 DB 1325 GGGATTATGGCATATGACCAACAGACACCCGGCCAGTCCCGATCTTAGAACACTCTTG 1384  
 QY 221 -----GlyAsnTyrGlyGlnSerGlyMetGluAlaPheLysAspMet 234  
 DB 1385 AGTGCTTCTGATTTTATGGAACATATGAGAAAGTGGATGGAGCCCTTCAAAAGATAT 1444  
 QY 234 tSerAlaLysGluGluIleCysIleAlaHisSerTyrLysIleTyrSerAspAlaGlyG 254  
 DB 1445 GTACAGCAAGAGAAAGGATTTGATGCGCCACTTTCAAAAATCTACATGTAAGCAGGG 1504  
 QY 254 uGlnSerPheAspLysLeuLeuLysLeuThrSerHisLeuProLysAlaArgValVa 274  
 DB 1505 GCAGAGCTTTGATTAAGCTCTGAAGAAGCTCACAAGTCACTTCCCAAGCCCGGTGCT 1564  
 QY 274 lAlaTyrPheCysGluGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuG 294  
 DB 1565 GGCCTACTCTGTGAGAGGATGACGGGTGAGAGGTCTGTGATGGCCATGAGGGGCTGG 1624  
 QY 294 yLeuValGlyGluPheLeuLeuGlyArgGluPProAspAlaIlePheIleGluIleSe 314  
 DB 1625 TCTAGTGGAGAAATTTCTCTCTGTGGCAGGAGAACAGATGCCATCTTATTAAGATCTC 1684  
 QY 314 rLysAsnSerIleLeuTrpGluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPh 334  
 DB 1685 AAGAAACACATCTCTATGAGGAAGACAGAAAGAAATGCCAAGTCCGTTCTTCAAGGTTT 1744  
 QY 334 eGlyAspIleLeuHisArgSerGluSerValLeuLeuHisMetProGlnProLeuAsnLe 354  
 DB 1745 TGGAGACATATTACACAGAAATGAGTCCGTGCTGTCGACATGCCACGCTCTGATCT 1804  
 QY 354 uGluLeuSerSerGlyProIleThrGlyLeuArgAspArgLeuIle 369  
 DB 1805 AAGAGCTCAAGTCAAGGCCCATCACTGAGCTGAGGAGCAGGCTCATC 1850  
 RESULT 7  
 AAF29991  
 ID AAF29991 standard; DNA; 2326 BP.  
 AC AAF29991;  
 DT 06-APR-2001 (first entry)  
 XX Human GRMX-1c DNA.  
 DE Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Human; Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 XX Homo sapiens.  
 PN WO200102566-A1.  
 PD 11-JAN-2001.  
 PF 27-JUN-2000; 2000MO-US17798.  
 PR 02-JUL-1999; 99US-0346326.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX Schwarz DA, Maki RA;  
 PI



QY 464 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 523  
 DB 611 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 670  
 QY 524 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATATTTCATGAGGGTTGTCCTT 583  
 DB 671 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATATTTCATGAGGGTTGTCCTT 730  
 QY 584 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTTATG 643  
 DB 731 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTTATG 790  
 QY 644 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGAGTGAAGGCTTTCAAAAGATA 703  
 DB 791 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGAGTGAAGGCTTTCAAAAGATA 850  
 QY 704 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACAGTAATGCAAGGG 763  
 DB 851 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACAGTAATGCAAGGG 910  
 QY 764 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCCGGGTGG 823  
 DB 911 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCCGGGTGG 970  
 QY 824 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGCTGATGAGCCATGAGGCGCTTG 883  
 DB 971 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGCTGATGAGCCATGAGGCGCTTG 1030  
 QY 884 GTCTAG 889  
 DB 1031 GTCTAG 1036

## RESULT 13

AAD04990 standard; cDNA; 4207 BP.

AAD04990;

17-JUL-2001 (first entry)

Human metabotropic glutamate receptor, mGluR5A cDNA mutant.

Human, metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 postsynaptic sensitivity; glutamate excitation; mutant; ss.

Homo sapiens.  
 Synthetic.

Key Location/Qualifiers  
 mutation replace (416, T)  
 mutation /\*tag= a  
 mutation replace (425, A)  
 mutation /\*tag= b

US6211353-B1.

03-APR-2001.

07-JUN-1996; 96US-0660148.

29-JUL-1994; 94US-0282853.

(ELIL) LILLY & CO ELI.

Burnett JP, Mayne NG, Sharp RL, Snyder YM;

WPI; 2001-289639/30.

New isolated nucleic acids for producing human metabotropic glutamate  
 receptors, which are useful for modulating the presynaptic release of

PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 PS Disclosure; Column -; 53pp; English.

CC The present sequence is a cDNA mutant encoding human metabotropic  
 CC glutamate receptor, mGluR5A. L-glutamate, the most abundant  
 CC neurotransmitter in the central nervous system (CNS), mediates excitatory  
 CC pathway in mammals. L-glutamate is referred to as excitatory amino acid  
 CC (EAA) and the receptors that respond to glutamate are EAA receptors. The  
 CC receptors are useful for modulating the presynaptic release of glutamate  
 CC and the postsynaptic sensitivity of the neuronal cell to glutamate  
 CC excitation.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the sequence referred to as SEQ ID NO.1, shown in column  
 CC 59-68 (AAD05029) of the specification.

CC Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;

Query Match 12.2%; Score 222; DB 22; Length 4207;  
 Best Local Similarity 99.1%; Pred. No. 7, 1e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 523  
 DB 920 TAGCCATTGAGGTCGAGAAATTTGCTCAGCTTTTCAACATCTAGATTGCTTACTCAG 979  
 QY 524 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATATTTCATGAGGGTTGTCCTT 583  
 DB 671 CAACCATCATGATCTGATGAGACAGACTCTGTTCAAAATATTTCATGAGGGTTGTCCTT 730  
 QY 584 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTTATG 643  
 DB 731 CAGATGCTCAGCAGGCAAGGTCATGATGAGACATGATGAAAGAGTACACTGACCTTATG 790  
 QY 644 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGAGTGAAGGCTTTCAAAAGATA 703  
 DB 791 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGAGTGAAGGCTTTCAAAAGATA 850  
 QY 704 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACAGTAATGCAAGGG 763  
 DB 851 TGTCAAGCAAGAAAGGATTTGATGCGCCCACTCTTACAAATCTACAGTAATGCAAGGG 910  
 QY 764 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCCGGGTGG 823  
 DB 911 AGCAGAGCTTTGATTAAGCTGCTGAAGAGCTCACTCAAGTCACTTGCCCAAGGCCCGGGTGG 970  
 QY 824 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGCTGATGAGCCATGAGGCGCTTG 883  
 DB 971 TGGCTTAATCTCTGTGAGGGGATGACCGGTGAGAGGTCTGCTGATGAGCCATGAGGCGCTTG 1030  
 QY 884 GTCTAG 889  
 DB 1340 GTCTAG 1345

## RESULT 14

AAD05029 standard; cDNA; 4207 BP.

AAD05029;

17-JUL-2001 (first entry)

Human metabotropic glutamate receptor, mGluR5A cDNA.

Human, metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 postsynaptic sensitivity; glutamate excitation; ss.

Homo sapiens.

Key Location/Qualifiers

DE cDNA encoding chimeric receptor containing hmglur5d portion.  
 XX Human: metabotropic glutamate receptor; mglur; splice variant;  
 KM mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
 KM anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
 KM muscic relaxant; calcium receptor; Car; mglur5d; ss.  
 XX Chimeric - Homo sapiens.  
 OS  
 PN MO200130829-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000MO-US29356.  
 XX  
 PR 25-OCT-1999; 99US-0161481.  
 XX 24-OCT-2000; 2000US-0695481.  
 PA (NPSP-) NPS PHARM INC.  
 PI Krappho K, Stormann T, Levinthal C, Hammerland L, Scorfjohann L;  
 XX WPI; 2001-308615/32.  
 DR P-PSDB; AAB47219.  
 XX  
 PT New nucleic acid encoding an isoform of human metabotropic glutamate  
 PT receptor, for identifying potential therapeutic agents for neurological  
 PT disease  
 CC  
 PS Claim 18; Page 70-75; 86pp; English.  
 XX  
 CC This sequence encodes a chimeric receptor comprising the intracellular  
 CC cytoplasmic tail of the human calcium receptor (Car) and the extra-  
 CC cellular and seven transmembrane domains of the human metabotropic  
 CC glutamate receptor (mglur) splice variant of human metabotropic  
 CC glutamate receptor 5 (mglur5), mglur5d. mglur5 are G-protein-coupled  
 CC receptors capable of activating a variety of intracellular second  
 CC messenger systems following the binding of glutamate. Recombinant  
 CC mglur5d DNA and compounds that bind to, or modulate activity of it  
 CC are useful for diagnosing or treating neurological disorders, e.g.  
 CC as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers  
 CC and muscle relaxants.  
 CC  
 SQ Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;

Query Match 12.2%; Score 222; DB 22; Length 3129;  
 Best Local Similarity 99.1%; Pred. No. 7,4e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

464 TAGCCATTAGGTCAGAGATTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 523  
 |||||  
 461 TAGCCATTAGGTCAGAGATTGCTCCAGCTTTCAACATACCTCAGATTGTTACTCAG 520  
 |||||  
 524 CAACCATCATGATCTGAGTACAGACTCTGTTCAATATTTTCATGAGGGTGTGCTT 583  
 |||||  
 521 CAACCATCATGATCTGAGTACAGACTCTGTTCAATATTTTCATGAGGGTGTGCTT 580  
 |||||  
 584 CAGATCTCAGCAGGCGAAGTCTCATGTGACATTAAGTGAAGAGTCACTGAGCTTATG 643  
 |||||  
 581 CAGATCTCAGCAGGCGAAGTCTCATGTGACATTAAGTGAAGAGTCACTGAGCTTATG 640  
 |||||  
 644 TATCAGCCGTACACAGAGAGCACTATGAGAAAGTGGATGAGAAAGCTTCAAGATTA 703  
 |||||  
 641 TATCAGCCGTACACAGAGAGCACTATGAGAAAGTGGATGAGAAAGCTTCAAGATTA 700  
 |||||  
 704 TGTACAGCAGAGAGAGGATTTGATGAGCCCACTTTACAAAATCTACAGTATGACAGGG 763  
 |||||  
 701 TGTACAGCAGAGAGAGGATTTGATGAGCCCACTTTACAAAATCTACAGTATGACAGGG 760  
 |||||  
 764 AGCAGAGCTTTGATTAAGTGTCTGAGAGAGTCAAGATCACTTGGCCAAAGCCCGGGTGG 823  
 |||||  
 761 AGCAGAGCTTTGATTAAGTGTCTGAGAGAGTCAAGATCACTTGGCCAAAGCCCGGGTGG 820  
 |||||

QY 824 TGGCTACTTCTGTGAGGCGATGACGATGAGTGTGCTGATGATGATGAGCGCTCG 883  
 |||||  
 DB 821 TGGCTACTTCTGTGAGGCGATGACGATGAGTGTGCTGATGATGATGAGCGCTCG 880  
 |||||  
 QY 884 GTCTAG 889  
 |||||  
 DB 881 GTCTAG 886  
 |||||

RESULT 12  
 ACAS6535  
 ID ACAS6535 standard; cDNA; 4078 BP.  
 XX  
 AC ACAS6535;  
 XX  
 DT 06-JUN-2003 (first entry)  
 XX  
 XX Human signalling pathway polynucleotide probe SEQ ID NO 1133.  
 DE  
 XX Human; probe; ss; array element; Parkinson's disease;  
 KM signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KM immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6500938-B1.  
 XX  
 PF 30-JAN-1998; 98US-0016434.  
 XX  
 PR 30-JAN-1998; 98US-0016434.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 PI Au-Young J, Seilhamer JU;  
 XX WPI; 2003-352189/33.  
 DR  
 XX Combination of polynucleotide probes, useful as array elements in a  
 PT microarray for monitoring the expression of a number of target  
 PT polynucleotides  
 CC  
 PS Claim 1; SEQ ID NO 1133; 65pp; English.  
 XX  
 CC The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensics and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding  
 CC for different signalling pathway populations which can be used to diagnose  
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 CC and Parkinson's disease. The present sequence represents a polynucleotide  
 CC probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.  
 CC  
 SQ Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;

Query Match 12.2%; Score 222; DB 25; Length 4078;  
 Best Local Similarity 99.1%; Pred. No. 7,1e-77;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



XX Human; metabotropic glutamate receptor; schizophrenia; GRX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX MO200102566-A1.  
 XX  
 PN 11-JAN-2001.  
 PD 27-JUN-2000; 2000MO-US17798.  
 XX  
 PF 02-JUL-1999; 99US-0346326.  
 XX  
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PA Schwarz DA, Maki RA;  
 XX  
 PI WPI, 2001-123112/13.  
 XX  
 DR Novel metabotropic glutamate receptor for prevention, treatment of  
 XX PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's; Parkinson's disease; stroke; depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 6; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 XX Sequence 2241 BP, 552 A; 516 C; 561 G; 612 T; 0 other;  
 SQ  
 Query Match 39.4%; Score 719; DB 22; Length 2241;  
 Best Local Similarity 99.9%; Pred. No. 5.1e-270;  
 Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1020 CAGAGTGAAGTCCGCTGCTGTCGACATGCCCGCTTGAATCTAAGCTCAGTTCAAG 1079  
 DB 1450 CAGAGTGAAGTCCGCTGCTGTCGACATGCCCGCTTGAATCTAAGCTCAGTTCAAG 1509  
 QY 1080 GCCCATCATGAGCTGAGGAGCAAGGCTCATCTAATCTGAGTGAATTAATCTGATTA 1139  
 DB 1510 GCCCATCATGAGCTGAGGAGCAAGGCTCATCTAATCTGAGTGAATTAATCTGATTA 1569  
 QY 1140 TAATGAAGCAACAGTCATATCTTCTGATGTGAGATTGAGAAAGCATTTGTATGGATG 1199  
 DB 1570 TAATGAAGCAACAGTCATATCTTCTGATGTGAGATTGAGAAAGCATTTGTATGGATG 1629  
 QY 1200 TGAACGTCAAAATGCGCCCATATCACTGCAACACCTCAAGTTTCTTGATGAGGTGC 1259  
 DB 1630 TGAACGTCAAAATGCGCCCATATCACTGCAACACCTCAAGTTTCTTGATGAGGTGC 1689  
 QY 1260 TGAAGTTTCACTCTGCGCAAGTATTAATCTGAGAGGTCCATGTGGGGAATCTTGAATG 1319  
 DB 1690 TGAAGTTTCACTCTGCGCAAGTATTAATCTGAGAGGTCCATGTGGGGAATCTTGAATG 1749  
 QY 1320 GGCTTTCGGTGTGTTGTAATTAAGTCTGAAAGGGAAGATTCGAATGGAATATATATG 1379  
 DB 1750 GGCTTTCGGTGTGTTGTAATTAAGTCTGAAAGGGAAGATTCGAATGGAATATATATG 1809  
 QY 1380 AAGAGGAGGACTTATAGTCTTGAGATTGTAAAGACATTCAGTGCAGTCTTTTAC 1439  
 DB 1810 AAGAGGAGGACTTATAGTCTTGAGATTGTAAAGACATTCAGTGCAGTCTTTTAC 1869  
 QY 1440 CACCTCCCAAGTTTACCTGAGATATGCCAAGACCTTACCAACATGATGATTTCTT 1499  
 DB 1870 CACCTCCCAAGTTTACCTGAGATATGCCAAGACCTTACCAACATGATGATTTCTT 1929

QY 1500 GGATTGTGAAGCTAGAACTGTGAGCTTGTGATGTAAATCAAAAGCTCCCTATATACAC 1559  
 DB 1930 GGATTGTGAAGCTAGAACTGTGAGCTTGTGATGTAAATCAAAAGCTCCCTATATACAC 1989  
 QY 1560 CATCCCTAATGTGCTCTTCTCACTCTCTCAGGCTATCTTTTGTCTGATTAATCTCTG 1619  
 DB 1990 CATCCCTAATGTGCTCTTCTCACTCTCTCAGGCTATCTTTTGTCTGATTAATCTCTG 2049  
 QY 1620 ACCAGAGCAAAATCAGAAATGTTTATCTGCTGAGGGAACCCCTATCCCAATAAGCC 1679  
 DB 2050 ACCAGAGCAAAATCAGAAATGTTTATCTGCTGAGGGAACCCCTATCCCAATAAGCC 2109  
 QY 1680 CTCTTCCTTGTGCTTATCAACAGGACAAATAGTTCTGTTTATGCTTGAATTCAT 1739  
 DB 2110 CTCTTCCTTATGCTTATCAACAGGACAAATAGTTCTGTTTATGCTTGAATTCAT 2169  
 QY 1740 TCTAATGTTATTAACCTCATTTATGTTGTTACTATTAATGTGGTAAAA 1789  
 DB 2170 TCTAATGTTATTAACCTCATTTATGTTGTTACTATTAATGTGGTAAAA 2219  
 RESULT 9  
 AAF2991  
 ID AAF2991 standard; DNA; 2326 BP.  
 XX  
 AC AAF2991;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMX-1c DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200102566-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Schwarz DA, Maki RA;  
 XX  
 DR WPI, 2001-123112/13.  
 XX  
 CC Novel metabotropic glutamate receptor for prevention, treatment of  
 CC PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's; Parkinson's disease; stroke; depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 5; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 XX Sequence 2326 BP, 581 A; 535 C; 580 G; 630 T; 0 other;  
 SQ  
 Query Match 39.4%; Score 719; DB 22; Length 2326;  
 Best Local Similarity 99.9%; Pred. No. 5.1e-270;  
 Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1020 CAGAGTGAAGTCCGCTGCTGTCGACATGCCCGCTTGAATCTAAGCTCAGTTCAAG 1079



QY 721 ATTTCATGCGCCACTCTTACAAATCTACATATGACGGGAGAGAGCTTTGATAG 780  
 DB 1082 ATTTCATGCGCCACTCTTACAAATCTACATATGACGGGAGAGAGCTTTGATAG 1141  
 QY 781 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTGTAG 840  
 DB 1142 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTGTAG 1201  
 QY 841 GGCATACCGGTGAGAGGTCTGCTGATGCGCATAGAGCGCTGGGTCTAGTGGAGAAATT 900  
 DB 1202 GGCATACCGGTGAGAGGTCTGCTGATGCGCATAGAGCGCTGGGTCTAGTGGAGAAATT 1261  
 QY 901 CTGCTTCTGGGCGGAGAACCAAGATGCCATCTTATGAGATCTCAAGAACAGATCTTA 960  
 DB 1262 CTGCTTCTGGGCGGAGAACCAAGATGCCATCTTATGAGATCTCAAGAACAGATCTTA 1321  
 QY 961 TGGGAAGACAGAAAGAAATGCCAAGTCTGCTTCTAG 999  
 DB 1322 TGGGAAGACAGAAAGAAATGCCAAGTCTGCTTCTAG 1360

## RESULT 7

AAF29995  
 ID AAF29995 standard; DNA; 2064 BP.

AAF29995;

06-APR-2001 (first entry)

Human GRMX-1g DNA.

Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.

Homo sapiens.

W0200102566-A1.

11-JAN-2001.

27-JUN-2000; 2000MO-US17798.

02-JUL-1999; 99US-0346326.

(NEUR-) NEUROCRINE BIOSCIENCES INC.

Schwarz DA, Maki RA;

WPI; 2001-123112/13.

Novel metabotropic glutamate receptor for prevention, treatment of  
 conditions associated with undesirable glutamate levels, e.g.  
 Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 schizophrenia -

Claim 2; Fig 11; 59pp; English.

The present invention relates to human metabotropic glutamate  
 receptor. An agent that decreases expression or activity of the  
 metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.

Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other;

Query Match 44.5%; Score 812; DB 22; Length 2064;

Best Local Similarity 99.8%; Pred. No. 3.7e-306;  
 Matches 912; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTGTGATCTCTAGTCTTACTTTTGAAGAAGATGCTCGGAGGT 60

DB 362 AAAATGCTCTTGTGATCTCTAGTCTTACTTTTGAAGAAGATGCTCGGAGGT 421  
 QY 61 GCACAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGGTGACATCTTATGAGCT 120  
 DB 422 GCACAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGGTGACATCTTATGAGCT 481  
 QY 121 CTCTTTCTGTTCAATCAAGAGCTACTGTGAGAGAGTTCATGAGAGAGAGTGGGCA 180  
 DB 482 CTCTTTCTGTTCAATCAAGAGCTACTGTGAGAGAGTTCATGAGAGAGAGTGGGCA 541  
 QY 181 GTCCGTGAACAGTATGAGCATTCAGAGATGAGAGCCATGATACCTTGAAGAGATC 240  
 DB 542 GTCCGTGAACAGTATGAGCATTCAGAGATGAGAGCCATGATACCTTGAAGAGATC 601  
 QY 241 AATTGACAGCCCACTCTTGGCCCAATCACTAGTGGCTGTGAGATTAAGGATTCCTGC 300  
 DB 602 AATTGACAGCCCACTCTTGGCCCAATCACTAGTGGCTGTGAGATTAAGGATTCCTGC 661  
 QY 301 TGGCATTTGGGCTGTGGCCCTTGAAGAGAGCATTAAGTTCATTAAGATTCCTCATTTCT 360  
 DB 662 TGGCATTTGGGCTGTGGCCCTTGAAGAGAGCATTAAGTTCATTAAGATTCCTCATTTCT 721  
 QY 361 TCGGAAGAGAGAGAGGCTTGTATGCTCTGTGATGAGCTCTCTCTTCCGCTCC 420  
 DB 722 TCGGAAGAGAGAGAGGCTTGTATGCTCTGTGATGAGCTCTCTCTTCCGCTCC 781  
 QY 421 AAGAGCCCATTAATAGGGGTCAATGGGCTGTGCTCAAGTCTTTAGCCATTCAGTCCAG 480  
 DB 782 AAGAGCCCATTAATAGGGGTCAATGGGCTGTGCTCAAGTCTTTAGCCATTCAGTCCAG 841  
 QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACCATCATGATCTG 540  
 DB 842 AATTGCTCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACCATCATGATCTG 901  
 QY 541 AGTGAAGAGCTCTGTTCAAAATATTTCAATGAGGTTGTGCTTCAGATGCTCAGAGCA 600  
 DB 902 AGTGAAGAGCTCTGTTCAAAATATTTCAATGAGGTTGTGCTTCAGATGCTCAGAGCA 961  
 QY 601 AGGTCCATGTTGACATTAATGAGAGAGTACATGAGCCATTAATGAGCCATTCACACA 660  
 DB 962 AGGTCCATGTTGACATTAATGAGAGAGTACATGAGCCATTAATGAGCCATTCACACA 1021  
 QY 661 GAAGGCAACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTACAGGAAGAGAGG 720  
 DB 1022 GAAGGCAACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTACAGGAAGAGAGG 1081  
 QY 721 ATTTCATGCGCCACTCTTACAAATCTACATATGACGGGAGAGAGCTTTGATAG 780  
 DB 1082 ATTTCATGCGCCACTCTTACAAATCTACATATGACGGGAGAGAGCTTTGATAG 1141  
 QY 781 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTGTAG 840  
 DB 1142 CTCTGTAAGAGCTCAAGTCACTTGTCCCAAGCCCGGGTGGCTTACTTGTAG 1201  
 QY 841 GGCATACCGGTGAGAGGTCTGCTGATGCGCATAGAGCGCTGGGTCTAGTGGAGAAATT 900  
 DB 1202 GGCATACCGGTGAGAGGTCTGCTGATGCGCATAGAGCGCTGGGTCTAGTGGAGAAATT 1261  
 QY 901 CTGCTTCTGGGCGGAGAACCAAGATGCCATCTTATGAGATCTCAAGAACAGATCTTA 960  
 DB 1262 CTGCTTCTGGGCGGAGAACCAAGATGCCATCTTATGAGATCTCAAGAACAGATCTTA 1321

## RESULT 8

AAF29992  
 ID AAF29992 standard; DNA; 2241 BP.

AAF29992;

06-APR-2001 (first entry)

Human GRMX-1d DNA.



QY 1083 CATCACTGAGCTGAGGAGAGGCTCATCTAATTCGAGTGATATTACTCTGCAATTAA 1142  
 DB 1823 CATCACTGAGCTGAGGAGAGGCTCATCTAATTCGAGTGATATTACTCTGCAATTAA 1882  
 QY 1143 TGAAGCCAAAGCATATCTTCTGATGTGAGATTTGAGAAAGCTTTGTATTTGATGTGA 1202  
 DB 1883 TGAAGCCAAAGCATATCTTCTGATGTGAGATTTGAGAAAGCTTTGTATTTGATGTGA 1942  
 QY 1203 CCGTCAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGATGAGGGTGTCA 1562  
 DB 1943 CCGTCAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGATGAGGGTGTCA 2002  
 QY 1263 GACTTCACCTCTGGCAAGTATTACTGGAAGTCCATGTGGGGGACTTTGAAATGGGC 1322  
 DB 2003 GACTTCACCTCTGGCAAGTATTACTGGAAGTCCATGTGGGGGACTTTGAAATGGGC 2062  
 QY 1323 TTTCCGTTTGTATTAAGTACTGGAAGGAGAAATCAAGTGGCAATATATATGAGA 1382  
 DB 2063 TTTCCGTTTGTATTAAGTACTGGAAGGAGAAATCAAGTGGCAATATATATGAGA 2122  
 QY 1383 GAGAGGAGCTTTAGTCTGGGATTTGTAAGAACGACATTCAGTGGAGTCTTTTACAC 1442  
 DB 2123 GAGAGGAGCTTTAGTCTGGGATTTGTAAGAACGACATTCAGTGGAGTCTTTTACAC 2182  
 QY 1443 CTCCTCCAGTTACACTGAGATATGCCAAGACCTACCAACATGTAGATTAATTCCTGA 1502  
 DB 2183 CTCCTCCAGTTACACTGAGATATGCCAAGACCTACCAACATGTAGATTAATTCCTGA 2242  
 QY 1503 TTTGTGAAGCTGAACTGTGAGCTTCTGTGATTTATCAAAAGCTCCCTTATATACACAT 1562  
 DB 2243 TTTGTGAAGCTGAACTGTGAGCTTCTGTGATTTATCAAAAGCTCCCTTATATACACAT 2302  
 QY 1563 CCTTAATGCTCTCTCTCACTCTCTCAGACCTATCTTTGCTGATTCATCTGAGC 1622  
 DB 2303 CCTTAATGCTCTCTCTCACTCTCTCAGACCTATCTTTGCTGATTCATCTGAGC 2362  
 QY 1623 AGAGCAAAATCAGAAATGTGTTATCTGCTGTGGGAACCCCTTATCCATAAGCCCTC 1682  
 DB 2363 AGAGCAAAATCAGAAATGTGTTATCTGCTGTGGGAACCCCTTATCCATAAGCCCTC 2422  
 QY 1683 TTTCTTGTGCTTATCAAAAGGCAAAATAGTCTGTTTATGCTTGAATTCATTCCT 1742  
 DB 2423 TTTCTTGTGCTTATCAAAAGGCAAAATAGTCTGTTTATGCTTGAATTCATTCCT 2482  
 QY 1743 AATGTTATTAACCTATTTATGTTACTATTAATGAGTAAAT 1789  
 DB 2483 AATGTTATTAACCTATTTATGTTACTATTAATGAGTAAAT 2529  
 RESULT 6  
 AAF29994 standard; DNA; 2149 BP.  
 XX AAF29994;  
 AC AAF29994;  
 DT 06-APR-2001 (first entry)  
 XX Human GRMx-1f DNA.  
 DE Human GRMx-1f DNA.  
 XX Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200102566-A1.  
 XX 11-JAN-2001.  
 PD 27-JUN-2000; 2000MO-US17798.  
 PF 02-JUL-1999; 99US-0346326.  
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX PA

XX Schwarzs DA, Maki RA;  
 PI WPI; 2001-123112/13.  
 DR Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX Claim 2, Fig 9, 59pp; English.  
 PS The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;  
 SO  
 Query Match 49.2%; Score 897; DB 22; Length 2149;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 997; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAAATGCTCTCTGTTGATTCCTGACGCTTATTTGAAAGAAATGCGTGGAGT 60  
 DB 362 AAAATGCTCTCTGTTGATTCCTGACGCTTATTTGAAAGAAATGCGTGGAGT 421  
 QY 61 GCACAGTCAAGTGAAGAGAGGAGTGTGCTCAATGCTGGTGAATCAATTTATGAGCT 120  
 DB 422 GCACAGTCAAGTGAAGAGAGGAGTGTGCTCAATGCTGGTGAATCAATTTATGAGCT 481  
 QY 121 CTCTTTCTGTTATCAACAGCTTACTGTGACGAAGTTCAATGAGAGAGTGTGGGCA 180  
 DB 482 CTCTTTCTGTTATCAACAGCTTACTGTGACGAAGTTCAATGAGAGAGTGTGGGCA 541  
 QY 181 GTCCGGAACAGTATGAGCAATTCAGAGAGAGGAGCCATCTGATACCTTGAAAGATC 240  
 DB 542 GTCCGGAACAGTATGAGCAATTCAGAGAGAGGAGCCATCTGATACCTTGAAAGATC 601  
 QY 241 AATTGACACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTG 300  
 DB 602 AATTGACACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTG 661  
 QY 301 TGGCATTGCGCTGTGAGCCCTTGAAGCAGACATTAAGTATTAAGATTCCTCATTTCT 360  
 DB 662 TGGCATTGCGCTGTGAGCCCTTGAAGCAGACATTAAGTATTAAGATTCCTCATTTCT 721  
 QY 361 TGGAAAGAGAAAGAGGCTTGTGATGCTTGTGAGATGCTCTCTCTTCTTCCGCTCC 420  
 DB 722 TGGAAAGAGAAAGAGGCTTGTGATGCTTGTGAGATGCTCTCTCTTCTTCCGCTCC 781  
 QY 421 AAGAAGCCCATAGTGAAGGCTCAATGGGCTGTGCTCAAGTCTTTAGCAATTCAGGCTCAG 480  
 DB 782 AAGAAGCCCATAGTGAAGGCTCAATGGGCTGTGCTCAAGTCTTTAGCAATTCAGGCTCAG 841  
 QY 481 AATTGCTCAGCTTTTCAACATCTCAGATTCCTTACTCAGAACCATCATGATCTG 540  
 DB 842 AATTGCTCAGCTTTTCAACATCTCAGATTCCTTACTCAGAACCATCATGATCTG 901  
 QY 541 AGTGACAAAGCTCTGTTCAAAATTTTCAATGAGGCTTGTGCTTCAATGCTCAGAGGCA 600  
 DB 902 AGTGACAAAGCTCTGTTCAAAATTTTCAATGAGGCTTGTGCTTCAATGCTCAGAGGCA 961  
 QY 601 AGTCCATGATGAGCACTAGTGAAGAGTCACTGAGACCTATGATCATGACCGGATCACA 660  
 DB 962 AGTCCATGATGAGCACTAGTGAAGAGTCACTGAGACCTATGATCATGACCGGATCACA 1021  
 QY 661 GAAAGCACTATGAGAAAGTGGATGGAAGGCTTCAAGATATGTCAGGAGAGAGG 720  
 DB 1022 GAAAGCACTATGAGAAAGTGGATGGAAGGCTTCAAGATATGTCAGGAGAGAGG 1081

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Db 1321 GCTGAAGAACTCAAGTCACTTGCCTCAAGCCCGGCTGCTTCTGTAGAGG 1380
QY 843 CATGACGTGAGAGGTCTGCTGATGAGCATGAGCCGCTGAGTCTAGTGGAGAAATTTCT 902
Db 1381 CATGACGTGAGAGGTCTGCTGATGAGCATGAGCCCGGCTGAGTGGAGAAATTTCT 1440
QY 903 GCTTCTGGGCAAGGAAACAGATGCTTATTTAGATCTCAAAACAGCATCTCCATG 962
Db 1441 GCTTCTGGGCAAGGAAACAGATGCTTATTTAGATCTCAAAACAGCATCTCCATG 1500
QY 963 GGAAGACAGAGAAATGCGAAGTGCCTTCTTCAAGGTTTGGAGACATATTACACAG 1022
Db 1501 GGAAGACAGAGAAATGCGAAGTGCCTTCTTCAAGGTTTGGAGACATATTACACAG 1560
QY 1023 AAGTGAATCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1082
Db 1561 AAGTGAATCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1620
QY 1083 CATCACTGGACTGAGGAGAGGCTCATCTTAATCTGATGAGATTAATCTGATTAATA 1142
Db 1621 CATCACTGGACTGAGGAGAGGCTCATCTTAATCTGATGAGATTAATCTGATTAATA 1680
QY 1143 TGAAGCCAAAGTCAATCTTCTGATGAGATTTTGAAGAGATTTGATTTGAGATGTA 1202
Db 1681 TGAAGCCAAAGTCAATCTTCTGATGAGATTTTGAAGAGATTTGATTTGAGATGTA 1740
QY 1203 CCGTCAAAATGCGCCCAATATCACTGACACCTTCAAGTTTCTTGATGAGGAGTCA 1262
Db 1741 CCGTCAAAATGCGCCCAATATCACTGACACCTTCAAGTTTCTTGATGAGGAGTCA 1800
QY 1263 GACTTTCACCTGCGGAGATTAATGAGGAGTCCAGTGGGAGACTTGGAAATGGGC 1322
Db 1801 GACTTTCACCTGCGGAGATTAATGAGGAGTCCAGTGGGAGACTTGGAAATGGGC 1860
QY 1323 TTTTCGCTGTTGTAATAGTACTGAAAGGAAAGAAATCAAAATGCGCAATATATATGAGA 1382
Db 1861 TTTTCGCTGTTGTAATAGTACTGAAAGGAAAGAAATCAAAATGCGCAATATATATGAGA 1920
QY 1383 GGAAGGACCTTTATGCTTGGGATTTGTAAGAACGACATTCAGTGCCTTTTACAC 1442
Db 1921 GGAAGGACCTTTATGCTTGGGATTTGTAAGAACGACATTCAGTGCCTTTTACAC 1980
QY 1443 CTCCCCAGTTTACACTGAGATATGTCCTCAAGCCCTTATGAGATTAATCTTCTGGA 1502
Db 1981 CTCCCCAGTTTACACTGAGATATGTCCTCAAGCCCTTATGAGATTAATCTTCTGGA 2040
QY 1503 TTTGGAAGTGAAGCTGAGACTGCTGTTGATGTTAATCAAAAGCTCCCTTATATACACAT 1562
Db 2041 TTTGGAAGTGAAGCTGAGACTGCTGTTGATGTTAATCAAAAGCTCCCTTATATACACAT 2100
QY 1563 CCTTAATGTCCTTCTCACTCTCTCAAGCCCTTATGCTGTTATCATCTGAC 1622
Db 2101 CCTTAATGTCCTTCTCACTCTCTCAAGCCCTTATGCTGTTATCATCTGAC 2160
QY 1623 AGAGACAAATCAAGAAATGTTATCTGCTGAGGAAACCCCTTATCCCAAAAGCCCTC 1682
Db 2161 AGAGACAAATCAAGAAATGTTATCTGCTGAGGAAACCCCTTATCCCAAAAGCCCTC 2220
QY 1683 TTTCTTGGCTTATCAAAACAGACAAATAGTTCGTTTATGCTTGAATTCATCT 1742
Db 2221 TTTCTTGGCTTATCAAAACAGACAAATAGTTCGTTTATGCTTGAATTCATCT 2280
QY 1743 AATGTTATTAATCAATTAATGTTATGTTATTAATTAATGTTGTAATA 1789
Db 2281 AATGTTATTAATCAATTAATGTTATGTTATTAATTAATGTTGTAATA 2327

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RESULT 5  
AAF29989  
ID AAF29989 standard; DNA; 2551 BP.  
XX  
AC AAF29989;

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XX 06-APR-2001 (first entry)
DT Human GRM-X-1a DNA.
DE Human; metabotropic glutamate receptor; schizophrenia; GRM-X;
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX Homo sapiens.
XX WO200102566-A1.
PN 11-JAN-2001.
PD 27-JUN-2000; 2000MO-US17798.
PP 02-JUL-1999; 99US-0346326.
PR (NEUR-) NEUROCRINE BIOSCIENCES INC.
PA Schwarz DA, Maki RA;
PI MPI, 2001-123112/13.
DR Novel metabotropic glutamate receptor for prevention, treatment of
XX conditions associated with undesirable glutamate levels, e.g.
XX Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
XX schizophrenia -
XX Claim 2; Fig 1; 59pp; English.
XX The present invention relates to human metabotropic glutamate
XX receptor. An agent that decreases expression or activity of the
XX metabotropic glutamate receptor is useful for treating schizophrenia.
XX Metabotropic glutamate receptor polynucleotides, polypeptides
XX are useful for treating diseases associated with undesirable
XX levels of glutamate, such as Alzheimer's disease, Parkinson's
XX disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2551 BP; 666 A; 566 C; 630 G; 689 T; 0 other;
Query Match 59.0%; Score 1076; DB 22; Length 2551;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 663 AGGCAACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAGCGAAGAGGAT 722
Db 1403 AGGCAACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAGCGAAGAGGAT 1462
QY 723 TTGCATGCGCCCACTTTACAAATCTACAGTAATGAGGGGAGACAGCTTTGATAAGCT 782
Db 1463 TTGCATGCGCCCACTTTACAAATCTACAGTAATGAGGGGAGACAGCTTTGATAAGCT 1522
QY 783 GCTGAAGAACTCAAGTCACTTGCCTCAAGGCCCGGATGAGGCTTCTGTGAGGG 842
Db 1523 GCTGAAGAACTCAAGTCACTTGCCTCAAGGCCCGGATGAGGCTTCTGTGAGGG 1582
QY 843 CATGACGTGAGAGGTCTGCTGATGAGCATGAGCCGCTGAGTCTAGTGGAGAAATTTCT 902
Db 1583 CATGACGTGAGAGGTCTGCTGATGAGCATGAGCCGCTGAGTCTAGTGGAGAAATTTCT 1642
QY 903 GCTTCTGGGCAAGGAAACAGATGCTTATTTAGATCTCAAAACAGCATCTCCATG 962
Db 1643 GCTTCTGGGCAAGGAAACAGATGCTTATTTAGATCTCAAAACAGCATCTCCATG 1702
QY 963 GGAAGACAGAGAAATGCGAAGTGCCTTCTTCAAGGTTTGGAGACATATTACACAG 1022
Db 1703 GGAAGACAGAGAAATGCGAAGTGCCTTCTTCAAGGTTTGGAGACATATTACACAG 1762
QY 1023 AAGTGAATCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1082
Db 1763 AAGTGAATCGTCTGCTGTCACATGCCCAAGCTCTGATCTGAGTCAAGTCAAGGCC 1822

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Db      842 AATTGCTCAGCTTTTCAACATATCTCAGATTGCTTACTCAGCAACCATCATGATCTG 901
Qy      541 AGTGAACAAGCTCTGTTCAATATTTGATGAGGGTGTGCTTCAGATGCTCAGCAGCA 600
Db      902 AGTGAACAAGCTCTGTTCAATATTTGATGAGGGTGTGCTTCAGATGCTCAGCAGCA 961
Qy      601 AGGTCCATGCTGATCATATGTAAGAGGTACATCTGACCTATGATATCAGCCGTACACA 660
Db      962 AGGTCCATGCTGATCATATGTAAGAGGTACATCTGACCTATGATATCAGCCGTACACA 1021
Qy      661 GAAGGCAACATATGAGAAAGTGGGATGGAAGCTTCAAGATATGTCAGGGAAGAGGG 720
Db      1022 GAAGGCAACATATGAGAAAGTGGGATGGAAGCTTCAAGATATGTCAGGGAAGAGGG 1081
Qy      721 ATTGTCATGCCCACTCTTCAAAAATCTACAGTAATGTCAGGGGAGCAGAGCTTGATAG 780
Db      1082 ATTGTCATGCCCACTCTTCAAAAATCTACAGTAATGTCAGGGGAGCAGAGCTTGATAG 1141
Qy      781 CTGCTGAAGAAGCTCACAAATCTTGCAGAGCCCGGGTGGTGGCTTCTCTGTAG 840
Db      1142 CTGCTGAAGAAGCTCACAAATCTTGCAGAGCCCGGGTGGTGGCTTCTCTGTAG 1201
Qy      841 GGCATACCGGTGAGAGGTCTGCTGATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTT 900
Db      1202 GGCATACCGGTGAGAGGTCTGCTGATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTT 1261
Qy      901 CTGCTTCTGGGCAAGGGAACAGATGCGCATCTTATTTAGATCTCAAGAAACAGATCTTA 960
Db      1262 CTGCTTCTGGGCAAGGGAACAGATGCGCATCTTATTTAGATCTCAAGAAACAGATCTTA 1321
Qy      961 TGGGAAGACAGAAAGAAATGCCAAGGTGCTTCTCAGGGTGGTGGAGACATATTAC 1020
Db      1322 TGGGAAGACAGAAAGAAATGCCAAGGTGCTTCTCAGGGTGGTGGAGACATATTAC 1381
Qy      1021 AGAAGTGAAGTCCGTGCTGCTGACATGCCCAAGCTCTGATCTAGAGCTCAGTTCAGGG 1080
Db      1382 AGAAGTGAAGTCCGTGCTGCTGACATGCCCAAGCTCTGATCTAGAGCTCAGTTCAGGG 1441
Qy      1081 CCCATCAGTGGATGAGGGGACAGGCTCATTAATCTGAGTGAATATCTGCACTTAT 1140
Db      1442 CCCATCAGTGGATGAGGGGACAGGCTCATTAATCTGAGTGAATATCTGCACTTAT 1501
Qy      1141 AATGAAGCCAAAGCATATCTTCTGATGAGATTTGAGAAAGCAATTTGATGATG 1200
Db      1502 AATGAAGCCAAAGCATATCTTCTGATGAGATTTGAGAAAGCAATTTGATGATG 1561
Qy      1201 GACCTGCAAAATGCGCCCATATCACTGCAACCTTCAAGATTTCTTGATGAGGGTCT 1260
Db      1562 GACCTGCAAAATGCGCCCATATCACTGCAACCTTCAAGATTTCTTGATGAGGGTCT 1621
Qy      1261 CAGACTTCACTCTGGCAAGATTTACTGGAAGGTCCATGTTGGGAGCTTTTGGAAATGG 1320
Db      1622 CAGACTTCACTCTGGCAAGATTTACTGGAAGGTCCATGTTGGGAGCTTTTGGAAATGG 1681
Qy      1321 GCTTTCGATGTTGTAATAGTACTGGAAGGGAAGATCAGATGGAATATATATGGA 1380
Db      1682 GCTTTCGATGTTGTAATAGTACTGGAAGGGAAGATCAGATGGAATATATATGGA 1741
Qy      1381 GAGGAGGAGCTTTTATGCTTGGATTTTAAAGCAGCATTTGAGTACTCTTTACC 1440
Db      1742 GAGGAGGAGCTTTTATGCTTGGATTTTAAAGCAGCATTTGAGTACTCTTTACC 1801
Qy      1441 AACTCCCAAGTTTCACTGCAAGTATGTCCTCAAGCCTTACAGTCAAGTCTTTTACC 1500
Db      1802 AACTCCCAAGTTTCACTGCAAGTATGTCCTCAAGCCTTACAGTCAAGTCTTTTACC 1861
Qy      1501 GATTGGAAGCTGAGACTGAGCTTCTGATGTTTAAATCAAGCTCCCTATATATAC 1560
Db      1862 GATTGGAAGCTGAGACTGAGCTTCTGATGTTTAAATCAAGCTCCCTATATATAC 1921
Qy      1561 ATCCCTAATTTGCTCTTCTCACTCTCTCAGGCTATCTTTTGTCTGATTTCACTCTGA 1620
Db      1922 ATCCCTAATTTGCTCTTCTCACTCTCTCAGGCTATCTTTTGTCTGATTTCACTCTGA 1981

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Qy      1621 CCAGAGCAAAATGAGAAATGTTTATCTGCTGAGGAACCCCTTATATCCATTAAGCCC 1680
Db      1982 CCAGAGCAAAATGAGAAATGTTTATCTGCTGAGGAACCCCTTATATCCATTAAGCCC 2041
Qy      1681 TCTTCTTGTGCTTATCAAAACAGACAATAAGTTCTGTTTATGCTTGAATTCATT 1740
Db      2042 TCTTCTTATGCTTATCAAAACAGACAATAAGTTCTGTTTATGCTTGAATTCATT 2101
Qy      1741 CTATGTTATTAATCTCATTTATTTGTTTACTTATTAATATGCTTAAA 1789
Db      2102 CTATGTTATTAATCTCATTTATTTGTTTACTTATTAATATGCTTAAA 2150

RESULT 4
AAF29990
ID AAF29990 standard; DNA; 2349 BP.
XX
AC AAF29990;
XX
XX 06-APR-2001 (first entry)
DT
DE Human GRMX-Ib DNA.
KM Human; metabotropic glutamate receptor; schizophrenia; GRMX;
XX Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
OS Homo sapiens.
XX
PN W0200102566-A1.
PD 11-JAN-2001.
PF 27-JUN-2000; 2000MO-US17798.
XX
XX 02-JUL-1999; 99US-0346326.
PR
XX
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
PA
XX Schwarz DA, Maki RA;
XX
XX WPI; 2001-123112/13.
DR
XX
XX Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
XX claim 2; Fig 3; 59pp; English.
XX
XX The present invention relates to human metabotropic glutamate
XX receptor. An agent that decreases expression or activity of the
XX metabotropic glutamate receptor is useful for treating schizophrenia.
XX Metabotropic glutamate receptor polynucleotides, polypeptides
XX are useful for treating diseases associated with undesirable
XX levels of glutamate, such as Alzheimer's disease, Parkinson's
XX disease, stroke, depression, anxiety, pain and schizophrenia.
XX
XX Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;

Query Match 59.0%; Score 1076; DB 22; Length 2349;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      663 AGCAACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCAAGAAAGGAT 722
Db      1201 AGCAACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCAAGAAAGGAT 1260
Qy      723 TTGATCGCCCACTCTTCAAAAATCTACAGTATGAGGGGAGCAGAGCTTTGATTAAGCT 782
Db      1261 TTGATCGCCCACTCTTCAAAAATCTACAGTATGAGGGGAGCAGAGCTTTGATTAAGCT 1320
Qy      783 GCTGAAGAAAGCTCACAAATCTTGCAGAGCCCGGGTGGTGGCTACTTCTGTAGAGG 842

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QY 906 TCTGGGAGGGAACCGATGCCATCTTTATTGAGATCTCAAGAACGATCCCTATGGGA 965  
 DB 901 TCTGGGAGGGAACCGATGCCATCTTTATTGAGATCTCAAGAACGATCCCTATGGGA 960  
 QY 966 AGACAGAGAAAATGCGAAGGTGCTCTTCAAGGTTTGAAGACATATTAACAGAAAG 1025  
 DB 961 AGACAGAGAAAATGCGAAGGTGCTCTTCAAGGTTTGAAGACATATTAACAGAAAG 1020  
 QY 1026 TGAATCCGTGCTGTCGACATGCCCCAGCCTGGAATCTAGAGCTCAGTCAAGGCCCAT 1085  
 DB 1021 TGAATCCGTGCTGTCGACATGCCCCAGCCTGGAATCTAGAGCTCAGTCAAGGCCCAT 1080  
 QY 1086 CACTGACCTAGAGGACAGGCTCATCTTAATCTGAGTGAATTAATCTGCAATTAATGA 1145  
 DB 1081 CACTGACCTAGAGGACAGGCTCATCTTAATCTGAGTGAATTAATCTGCAATTAATGA 1140  
 QY 1146 AGCCACAGTCATATCTTCTGATGTGAGATTGAGAAAGCATTTGATGGATGTGACCG 1205  
 DB 1141 AGCCACAGTCATATCTTCTGATGTGAGATTGAGAAAGCATTTGATGGATGTGACCG 1200  
 QY 1206 TCAAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGCAATGCGGTCTCAGAC 1265  
 DB 1201 TCAAAAATGCGCCCATATCACTGCAACACCTACAAAGTTTCTTGCAATGCGGTCTCAGAC 1260  
 QY 1266 TTTCACTCTGCGCAAGTATTACTGGGAGGTCCATGTGGGGGACTCTTGGAATTTGGGCTTT 1325  
 DB 1261 TTTCACTCTGCGCAAGTATTACTGGGAGGTCCATGTGGGGGACTCTTGGAATTTGGGCTTT 1320  
 QY 1326 CGGTGTTTGTATTAAGTACTGAAAGGGAAGAAATCAGATGCGCAATTAATATGAGAGGA 1385  
 DB 1321 CGGTGTTTGTATTAAGTACTGAAAGGGAAGAAATCAGATGCGCAATTAATATGAGAGGA 1380  
 QY 1386 GGGACTCTTATGATCTTGGGATGTGTAAGAAAGCAATTCAGTGCAGTCTTTTACCACTTC 1445  
 DB 1381 GGGACTCTTATGATCTTGGGATGTGTAAGAAAGCAATTCAGTGCAGTCTTTTACCACTTC 1440  
 QY 1446 CCCAGTTTACCTGACATGATGTCCCAAGACCTTACCAACATGATGAGATTAATCTCGAATTTG 1505  
 DB 1441 CCCAGTTTACCTGACATGATGTCCCAAGACCTTACCAACATGATGAGATTAATCTCGAATTTG 1500  
 QY 1506 TGAAGCTAGAACTGTGAGCTTGTGATGTTAATCAAGAGTCCCTTATATACACATCCC 1565  
 DB 1501 TGAAGCTAGAACTGTGAGCTTGTGATGTTAATCAAGAGTCCCTTATATACACATCCC 1560  
 QY 1566 TAAATGCTCTTCTCACTCTCTCAGAGCCTATCTTTTGTGATTAATCATCTTGACAGGA 1625  
 DB 1561 TAAATGCTCTTCTCACTCTCTCAGAGCCTATCTTTTGTGATTAATCATCTTGACAGGA 1620  
 QY 1626 GACAAATCAGAAATGTGTTTATCTGCTGTGGAACCCCTTTATCCCATAAAGCCCTCTTC 1685  
 DB 1621 GACAAATCAGAAATGTGTTTATCTGCTGTGGAACCCCTTTATCCCATAAAGCCCTCTTC 1680  
 QY 1686 CTGTGCTTATCAAAAGGATCTGTTTATGATCTGTAATGCAATTTAAT 1745  
 DB 1681 CTGTGCTTATCAAAAGGATCTGTTTATGATCTGTAATGCAATTTAAT 1740  
 QY 1746 GTTATTAATACTATTTATGTTACTATTAATTAATGTTGTAATAA 1789  
 DB 1741 GTTATTAATACTATTTATGTTACTATTAATTAATGTTGTAATAA 1784

RESULT 3  
 AAF2993  
 ID AAF2993 standard; DNA; 2172 BP.  
 XX  
 AC AAF2993;

XX 06-APR-2001 (first entry)  
 XX Human GRMx-1e DNA.  
 DE Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
 XX

KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX Homo sapiens.  
 OS  
 XX  
 PN W0200102566-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Schwarz DA, Maki RA;  
 PT WPI; 2001-123112/13.  
 DR  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's; Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 7; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polypeptides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 SQ Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;  
 Query Match 89.7%; Score 1636; DB 22; Length 2172;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1786; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 AAAAAATGCTCTTCTGTTGATCTGTGACGTTTACTTTTGAAGAAAGTCCGTGGAGT 60  
 DB 362 AAAATGCTCTTCTGTTGATCTGTGACGTTTACTTTTGAAGAAAGTCCGTGGAGT 421  
 QY 61 GCACATCCAGTGAAGAGAGGAGGTGCTCAATGCTGGGTGACATTAATTAAGAGT 120  
 DB 422 GCACATCCAGTGAAGAGAGGAGGTGCTCAATGCTGGGTGACATTAATTAAGAGT 481  
 QY 121 CTCTTTTCTGTTGATCAACGACCTTACTGTGAGAGGAATTCATGAGAGAGTGGGCA 180  
 DB 482 CTCTTTTCTGTTGATCAACGACCTTACTGTGAGAGGAATTCATGAGAGAGTGGGCA 541  
 QY 181 GTCCGTGAACGATGAGCATTCAGAGAGTGAAGCCATGCTGATACCTGGAAGAGATC 240  
 DB 542 GTCCGTGAACGATGAGCATTCAGAGAGTGAAGCCATGCTGATACCTGGAAGAGATC 601  
 QY 241 AATTGAGACCCCACTCTTGGCCCAATCAGACTGGGCTGTGAGATTAAGAGATTCCTGC 300  
 DB 602 AATTGAGACCCCACTCTTGGCCCAATCAGACTGGGCTGTGAGATTAAGAGATTCCTGC 661  
 QY 301 TGGCATTCGGCTGAGCCCTAGAGAGAGCATTAAGTTCATTAAGAGATTCCTCATTTCT 360  
 DB 662 TGGCATTCGGCTGAGCCCTAGAGAGAGCATTAAGTTCATTAAGAGATTCCTCATTTCT 721  
 QY 361 TCGAAGAGAGAGAGGCTTGTATGCTGTGAGATGCTCTCTCTCTTCCGCTCC 420  
 DB 722 TCGAAGAGAGAGAGGCTTGTATGCTGTGAGATGCTCTCTCTCTTCCGCTCC 781  
 QY 421 AAGAAGCCATTAAGAGGAGTTCAGGCGCTGTGAGATTCATTAAGAGATTCAGAGTCCAG 480  
 DB 782 AAGAAGCCATTAAGAGGAGTTCAGGCGCTGTGAGATTCATTAAGAGATTCAGAGTCCAG 841  
 QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTCCTTACTCAGCAACATCATGATCTG 540

Db 1441 ACCGCCAGTTACAGTGAATATGCCAGACCTACCAACATGATGATTTCTCG 1500  
 Qy 1501 GATTGAGCTAGACCTGAGCTGGTGAATGATTAACAAGCTCCCTATATACACC 1560  
 Db 1501 GATTGAGCTAGACCTGAGCTGGTGAATGATTAACAAGCTCCCTATATACACC 1560  
 Qy 1561 ATCCCTAATGCTCTCTCTCACTCTCTCAAGGCTATCTTTGCTGATTCATCTCGA 1620  
 Db 1561 ATCCCTAATGCTCTCTCTCACTCTCTCAAGGCTATCTTTGCTGATTCATCTCGA 1620  
 Qy 1621 CCAGAGCAAAATCGAAATGTTATCTGCTGGGAAACCCCTTTATCCATAAGCCC 1680  
 Db 1621 CCAGAGCAAAATCGAAATGTTATCTGCTGGGAAACCCCTTTATCCATAAGCCC 1680  
 Qy 1681 TCTTCTGTCCTTATCAACAGACAAATAGGCTGTTTATGTCGTAATTTGCAAT 1740  
 Db 1681 TCTTCTGTCCTTATCAACAGACAAATAGGCTGTTTATGTCGTAATTTGCAAT 1740  
 Qy 1741 CTATGTTATTTAAATCACTTATTTGTTACTATTAATGCTGTAATAAACAATAA 1800  
 Db 1741 CTATGTTATTTAAATCACTTATTTGTTACTATTAATGCTGTAATAAACAATAA 1800  
 Qy 1801 AAAAAAAAAAAAAAAAAAAAAA 1823  
 Db 1801 AAAAAAAAAAAAAAAAAAAAAA 1823

## RESULT 2

AAS62274 standard; cDNA; 1788 BP.  
 ID AAS62274

XX AAS62274;  
 XX

DT 14-FEB-2002 (first entry)  
 DE

XX cDNA sequence #61 encoding novel human secreted protein.  
 DE

KM Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KM infectious disorder; gene therapy; antimicrobial; hepatotropic;  
 KM immunosuppressive; antineumatic; ss.  
 KW

XX Homo sapiens.  
 OS

PN MO200177291-A2.  
 XX

PD 18-OCT-2001.  
 XX

PF 29-MAR-2001; 2001MO-US10485.  
 XX

PR 06-APR-2000; 2000US-195604P.  
 XX

PA (GENEY ) GENETICS INST INC.  
 XX

PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
 PI Gulukota K, Graham JR;  
 XX

XX WPI; 2002-010900/01.  
 DR

XX New polynucleotides encoding secreted proteins useful for treating e.g.  
 PT asthma, HIV and Crohn's disease -  
 PT

XX Claim 1; Page 106-107; 391pp; English.  
 PS

CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production, and the cell is also useful for identifying  
 CC compounds that modulate expression of the polynucleotide sequences  
 CC encoding the secreted proteins. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders

CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
 CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).  
 CC The polynucleotide sequences of the invention are also useful in gene  
 CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the  
 CC invention that encode for novel human secreted proteins.  
 XX

SQ Sequence 1788 BP; 454 A; 398 C; 444 G; 492 T; 0 other;

Query: Match 97.9%; Score 1784; DB 24; Length 1788;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGTCTTCTGTTATCTGTCAGTCTTACTTTGAAAGAGATGCTGGAGTGACA 65  
 Db 1 GGTCTTCTGTTATCTGTCAGTCTTACTTTGAAAGAGATGCTGGAGTGACA 60  
 Qy 66 GTCCAGTGAAGAGAGGCTGCTCAATGCTGGTGACATATTTGAGACTCTT 125  
 Db 61 GTCCAGTGAAGAGAGGCTGCTCAATGCTGGTGACATATTTGAGACTCTT 120  
 Qy 126 TTTCTTCAATCAACAGCTTACTGTCAGAGTTTCATGAGAGAGTGGGCAATCCG 185  
 Db 121 TTTCTTCAATCAACAGCTTACTGTCAGAGTTTCATGAGAGAGTGGGCAATCCG 180  
 Qy 186 TGAACAGTATGAGATTCAGAGAGTGAAGGCAATGCTGCAATCCCTGAAATGCAATTC 245  
 Db 181 TGAACAGTATGAGATTCAGAGAGTGAAGGCAATGCTGCAATCCCTGAAATGCAATTC 240  
 Qy 246 AGACCCCACTCTTCCCAATCACTGAGCTGTCAGATTAAGGATTCCTGCTGCA 305  
 Db 241 AGACCCCACTCTTCCCAATCACTGAGCTGTCAGATTAAGGATTCCTGCTGCA 300  
 Qy 306 TTGGGCTGTCGCTTGAAGAGAGATTAAGTTCAATGAGATTCCTCATTTCTTGGGA 365  
 Db 301 TTGGGCTGTCGCTTGAAGAGAGATTAAGTTCAATGAGATTCCTCATTTCTTGGGA 360  
 Qy 366 AGAGGAAGAGGCTTGTGATCTGTCAGATGCTCTCTCTTCTTCCGCTCCAGAA 425  
 Db 361 AGAGGAAGAGGCTTGTGATCTGTCAGATGCTCTCTCTTCTTCCGCTCCAGAA 420  
 Qy 426 GCCCATATGATGAGGCTGATGAGGCTGCTGCTTCAATTTAGCATTCAGGCTCAGAAATTT 485  
 Db 421 GCCCATATGATGAGGCTGATGAGGCTGCTGCTTCAATTTAGCATTCAGGCTCAGAAATTT 480  
 Qy 486 GCTCCAGCTTTTCAACATCTCAGATTCCTTCAAGCAACCATATGATTCGATGA 545  
 Db 481 GCTCCAGCTTTTCAACATCTCAGATTCCTTCAAGCAACCATATGATTCGATGA 540  
 Qy 546 CAAGACTCTGTTCAAAATTTTCAATGAGGCTGCTTCAAGTCTCAGAGCAAGGTC 605  
 Db 541 CAAGACTCTGTTCAAAATTTTCAATGAGGCTGCTTCAAGTCTCAGAGCAAGGTC 600  
 Qy 606 CATGTGACATATGATGAAGGTAACAATGACCTTATGATGACCGTACACAGAAAG 665  
 Db 601 CATGTGACATATGATGAAGGTAACAATGACCTTATGATGACCGTACACAGAAAG 660  
 Qy 666 CAATATGAGAAAGTGGAGTGAAGCTTCAAAATATGTCAGCGAAGAGAAAGATTG 725  
 Db 661 CAATATGAGAAAGTGGAGTGAAGCTTCAAAATATGTCAGCGAAGAGAAAGATTG 720  
 Qy 726 CATGCGCACTCTTCAAAATCTACAGTATGAGAGGAGCAGATTTGATTAAGTGTCT 785  
 Db 721 CATGCGCACTCTTCAAAATCTACAGTATGAGAGGAGCAGATTTGATTAAGTGTCT 780  
 Qy 786 GAAAGAGTCAACAAGCACTTGCCCAAGGCGGAGTGTGCTTACTTCTGTGAGGGCAAT 845  
 Db 781 GAAAGAGTCAACAAGCACTTGCCCAAGGCGGAGTGTGCTTACTTCTGTGAGGGCAAT 840  
 Qy 846 GACGCTGAGAGGTCTGCTGATGAGCCATGAGAGCGCTGAGTCTAGTGGAGAAATTTCTGCT 905  
 Db 841 GACGCTGAGAGGTCTGCTGATGAGCCATGAGAGCGCTGAGTCTAGTGGAGAAATTTCTGCT 900

PD 12-SEP-2002.  
 XX 21-DEC-2001; 2001MO-US49817.  
 XX 22-DEC-2000; 2000US-257589P.  
 XX (AMHP ) WYETH.  
 PA Bates BG, Xie Y, Gulukota K, Paulsen JB;  
 XX MPI; 2002-750462/81.  
 DR P-PSDB; ABP54921.  
 XX  
 PT New mGluR5M nucleic acid molecules and proteins, useful for treating  
 PT neurological or psychiatric disorders such as schizophrenia,  
 PT schizoaffective disorder, bipolar or unipolar affective disorder, or  
 PT adolescent conduct disorder -  
 XX  
 PS Claim 11; Fig 1A; 99pp; English.  
 XX  
 CC The present sequence is that of cDNA clone Y1176 (deposited as  
 CC ATCC PTA-27175) encoding a novel human metabotropic glutamate  
 CC receptor subtype modulatory protein (mGluR5M). The cDNA was  
 CC isolated from a human brain cDNA library. Expression of mGluR5M  
 CC is predominant in cells and tissues of the central nervous system.  
 CC The gene maps to a region of chromosome 11 associated with  
 CC schizophrenia and related psychiatric disorders. The invention  
 CC provides mGluR5M polypeptides and nucleic acids, and methods for  
 CC their detection, as well as methods for using them to identify  
 CC compounds that modulate metabotropic receptor (mGluR) activity.  
 CC Such modulators include a mGluR5M nucleic acid, a mGluR5M antibody,  
 CC a ribozyme, an antisense oligonucleotide, a small molecule  
 CC modulator, a peptide and a peptidomimetic. They can be used in a  
 CC claimed method for treating a subject having a neurological  
 CC disorder, especially a psychiatric disorder selected from  
 CC schizophrenia, schizoaffective disorder, bipolar affective disorder,  
 CC unipolar affective disorder or adolescent conduct disorder (all  
 CC claimed). mGluR5M polypeptides, nucleic acids and antipeptides are  
 CC also useful for screening assays, and in predictive medicine, e.g.  
 CC diagnostic assays (e.g. chromosome mapping and tissue typing),  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics.  
 CC  
 XX  
 SQ Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;  
 Query Match 100.0%; Score 1823; DB 24; Length 1823;  
 Best Local Similarly 100.0%; Pred. No. 0;  
 Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 AAATGCTCTTCTGTTGATCTGTCACTTACTTTTGAAGAAGATGTCGGAGT 60  
 QY 61 GCAAGTCCAGTGAAGAGAGGAGTGTGTCACATGCTGAGTCAATCATTTATGAGCT 120  
 DB 61 GCAAGTCCAGTGAAGAGAGGAGTGTGTCACATGCTGAGTCAATCATTTATGAGCT 120  
 QY 121 CTCTTTCTGTTCTATCAACAGCTTACTGTGACAGAAAGTTCAAGAGAGTGGGCA 180  
 DB 121 CTCTTTCTGTTCTATCAACAGCTTACTGTGACAGAAAGTTCAAGAGAGTGGGCA 180  
 QY 181 GTCCGTAAACGATGTGCAATTCAGAGAGTGGAGCCATGCTGACCTCTGGAAGATC 240  
 DB 181 GTCCGTAAACGATGTGCAATTCAGAGAGTGGAGCCATGCTGACCTCTGGAAGATC 240  
 QY 241 AATTCAAGCCCACTCTTGGCCCAACATCACTGAGCTGTGAGATTAAGGATTCCTGC 300  
 DB 241 AATTCAAGCCCACTCTTGGCCCAACATCACTGAGCTGTGAGATTAAGGATTCCTGC 300  
 QY 301 TGGCATTCGGCTGTGGCCCTTAAGACAGACTTGAATTCATTAAGATTCCTCATTTCT 360  
 DB 301 TGGCATTCGGCTGTGGCCCTTAAGACAGACTTGAATTCATTAAGATTCCTCATTTCT 360  
 QY 361 TCGAAGAGAGAGAGGCTTGATGCTGTGATGAGTCTCTCTCTTCTTCCGGCTCC 420

DB 361 TCGAAGAGAGAGAGGCTTGATGCTGTGATGAGTGGCTCTCTCTTCTTCCGGCTCC 420  
 QY 421 AAGAGCCCAATGATAGGGGTCAATGGGCTGGTTCAGATTCCTTACCATTCAGGTCCAG 480  
 DB 421 AAGAGCCCAATGATAGGGGTCAATGGGCTGGTTCAGATTCCTTACCATTCAGGTCCAG 480  
 QY 481 AATTGCTCAGCTTTTCAACATCTACATGATTCAGATTCAGTCAACATCATGATCTG 540  
 DB 481 AATTGCTCAGCTTTTCAACATCTACATGATTCAGATTCAGTCAACATCATGATCTG 540  
 QY 541 AGTGAAGACCTCTGTTCAAAATATTTCAATGAGGTTGTGCTTCAATGCTCAGAGCA 600  
 DB 541 AGTGAAGACCTCTGTTCAAAATATTTCAATGAGGTTGTGCTTCAATGCTCAGAGCA 600  
 QY 601 AGGTCCATGTTGACATTAAGAGAGTACACTGACCTTAATATTCAGCCGTACACACA 660  
 DB 601 AGGTCCATGTTGACATTAAGAGAGTACACTGACCTTAATATTCAGCCGTACACACA 660  
 QY 661 GAAGGCACTAATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGGAAGAGG 720  
 DB 661 GAAGGCACTAATGAGAAAGTGGAGTGAAGGCTTCAAAAGATATGTCAAGGAAGAGG 720  
 QY 721 ATTGTCATGCCCCACTCTTACAAATCTACATTAATGACAGGAGAGGACTTTGATTA 780  
 DB 721 ATTGTCATGCCCCACTCTTACAAATCTACATTAATGACAGGAGAGGACTTTGATTA 780  
 QY 781 CTGCTGAAGAGCTCAAGACTCTTGGCCAGGCCCCGGGTGTGCTTCTGTGAG 840  
 DB 781 CTGCTGAAGAGCTCAAGACTCTTGGCCAGGCCCCGGGTGTGCTTCTGTGAG 840  
 QY 841 GGGATACGTTGAGAGTCTGCTGATGGCCATGAGGCGCTGGGTCTAGTGGAGAAATT 900  
 DB 841 GGGATACGTTGAGAGTCTGCTGATGGCCATGAGGCGCTGGGTCTAGTGGAGAAATT 900  
 QY 901 CTGCTTCTGGGCGAGGAACCATGTCATCTTATTAAGATCTCAAGAACACATCTTA 960  
 DB 901 CTGCTTCTGGGCGAGGAACCATGTCATCTTATTAAGATCTCAAGAACACATCTTA 960  
 QY 961 TGGGAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTGGAGACATTTACAC 1020  
 DB 961 TGGGAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTGGAGACATTTACAC 1020  
 QY 1021 AGAAGTGAAGTGGTGGCTGTCACATGCCCCAGCTCTGAATCTAAGAGCTCAGTTCAGG 1080  
 DB 1021 AGAAGTGAAGTGGTGGCTGTCACATGCCCCAGCTCTGAATCTAAGAGCTCAGTTCAGG 1080  
 QY 1081 CCCATCACTGGACTGAGGAGCAGGCTCATCTAATTCAGATGATTAATCTTGCAATTAT 1140  
 DB 1081 CCCATCACTGGACTGAGGAGCAGGCTCATCTAATTCAGATGATTAATCTTGCAATTAT 1140  
 QY 1141 AATGAAGCAACAGCTATCTTCTGATGAGATTTGAAGACATTTGATTTGATGAT 1200  
 DB 1141 AATGAAGCAACAGCTATCTTCTGATGAGATTTGAAGACATTTGATTTGATGAT 1200  
 QY 1201 GACCTTCAAAATGCGCCCATATCACTGCAACCTTCAAGATTTCTTGAATGGAGTCT 1260  
 DB 1201 GACCTTCAAAATGCGCCCATATCACTGCAACCTTCAAGATTTCTTGAATGGAGTCT 1260  
 QY 1261 CAGACTTCACTCTGGAAGATTAATCTGGAAGTTCATGAGGAGCTCTTGAATTTGG 1320  
 DB 1261 CAGACTTCACTCTGGAAGATTAATCTGGAAGTTCATGAGGAGCTCTTGAATTTGG 1320  
 QY 1321 GCTTTGGTGTGTTGTAATTAAGTACATGGAAGGAGAAAGATGCAATTAATATGGA 1380  
 DB 1321 GCTTTGGTGTGTTGTAATTAAGTACATGGAAGGAGAAAGATGCAATTAATATGGA 1380  
 QY 1381 GAGAGGGAATCTTTACTCTTGGAGTTGTAAGAACATTAAGTCAAGTCTCTTACC 1440  
 DB 1381 GAGAGGGAATCTTTACTCTTGGAGTTGTAAGAACATTAAGTCAAGTCTCTTACC 1440  
 QY 1441 ACCTCCCAATTAACATGATGTCCTCAAGCTTCAACCATTAAGATTAATTCCTG 1500



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 2552756 seqs, 1349719017 residues

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1823	100.0	1823	24	ABV73899 Human glutamate re
2	1784	97.9	1788	24	AA562274 CDNA sequence #61
3	1636	89.7	2172	22	AA299993 Human GRMX-1c DNA
4	1076	59.0	2349	22	AA299990 Human GRMX-1b DNA
5	1076	59.0	2351	22	AA299989 Human GRMX-1a DNA
6	897	49.2	2149	22	AA299994 Human GRMX-1f DNA
7	812	44.5	2064	22	AA299995 Human GRMX-1g DNA
8	719	39.4	2241	22	AA299992 Human GRMX-1d DNA

9	719	39.4	2326	22	AA299991 Human GRMX-1c DNA
10	222	12.2	2826	22	AA299992 Human GRMX-1c DNA
11	222	12.2	3189	22	AA299993 Human GRMX-1c DNA
12	222	12.2	4078	25	AA299994 Human GRMX-1c DNA
13	222	12.2	4207	22	AA299995 Human GRMX-1c DNA
14	222	12.2	4207	22	AA299996 Human GRMX-1c DNA
15	222	12.2	4207	22	AA299997 Human GRMX-1c DNA
16	222	12.2	4207	22	AA299998 Human GRMX-1c DNA
17	222	12.2	4303	22	AA299999 Human GRMX-1c DNA
18	222	12.2	4303	22	AA299999 Human GRMX-1c DNA
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27	53	2.9	3918	20	AA299999 Human GRMX-1c DNA
28	33	1.8	62	22	AA299999 Human GRMX-1c DNA
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30	33	1.8	166	24	AA299999 Human GRMX-1c DNA
31	33	1.8	174	21	AA299999 Human GRMX-1c DNA
32	33	1.8	178	23	AA299999 Human GRMX-1c DNA
33	33	1.8	190	24	AA299999 Human GRMX-1c DNA
34	33	1.8	200	25	AA299999 Human GRMX-1c DNA
35	33	1.8	205	23	AA299999 Human GRMX-1c DNA
36	33	1.8	212	24	AA299999 Human GRMX-1c DNA
37	33	1.8	214	23	AA299999 Human GRMX-1c DNA
38	33	1.8	216	23	AA299999 Human GRMX-1c DNA
39	33	1.8	224	23	AA299999 Human GRMX-1c DNA
40	33	1.8	223	23	AA299999 Human GRMX-1c DNA
41	33	1.8	241	22	AA299999 Human GRMX-1c DNA
42	33	1.8	241	22	AA299999 Human GRMX-1c DNA
43	33	1.8	241	24	AA299999 Human GRMX-1c DNA
44	33	1.8	241	25	AA299999 Human GRMX-1c DNA
45	33	1.8	244	24	AA299999 Human GRMX-1c DNA

## ALIGNMENTS

RESULT 1	
ID	ABV73899 standard; cDNA, 1823 BP.
XX	ABV73899;
XX	08-JAN-2003 (first entry)
DE	Human glutamate receptor modulatory protein mglur5m cDNA.
XX	
KW	Metabotropic glutamate receptor subtype 5 modulatory protein;
KW	mglur5m; human; G-protein coupled receptor; receptor; schizophrenia;
KW	schizophrenia; bipolar affective disorder;
KW	unipolar affective disorder; adolescent conduct disorder;
KW	neurotic; neuroprotective; neuroleptic; chromosome 11;
KW	gene therapy; gene; 89.
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	4..1113
FT	/*tag= a
FT	/product= "mglur5m"
FT	/note= "The CDS is specifically claimed in Claim 1"
FT	sig_peptide
FT	4..63
FT	/*tag= b
FT	mat_peptide
FT	64..1110
FT	/*tag= c
XX	
PN	WO200270708-A2.









## COMMENT

On Jan 17, 2003 this sequence version replaced g1:27151430.  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L28531  
Center clone name: 114\_J\_20  
-----

Only the first 152.3 Kilobases of this clone are being submitted.  
The remainder overlaps accession number AC130364 [WICGR project  
L27973].

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/clone\_1lb="RPC1-11 Human Male BAC"  
complement(388..466)  
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1371..1375  
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1423..1428  
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1475..1480  
unsure /note="<30 qual SINGL region"  
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1973..1979  
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1988..1992  
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13947..14106  
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16086..16259  
repeat\_region /rpt\_family="L1MC/D"  
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complement(16778..16831)  
repeat\_region /rpt\_family="MUT2A1"  
16832..16928  
repeat\_region /rpt\_family="(TA)n"  
complement(17016..17408)

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Best Local Similarity 99.5%; Pred.No.1.2e-278;

Matches 657; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGTCCTTCTGTGATCTCTGACGCTTACTTTGAAAGAGATGTCCTGGAGTGACACA 65  
DB 50813 GGTCCTTCTGTGATCTCTGACGCTTACTTTGAAAGAGATGTCCTGGAGTGACACA 50872  
QY 66 GTCCAGTGAAGAGAGGCTGCTGCTTCACATGCTGGGTGACATCATTTATGGAAGCTCTCTT 125  
DB 50873 GTCCAGTGAAGAGAGGCTGCTGCTTCACATGCTGGGTGACATCATTTATGGAAGCTCTCTT 50932  
QY 126 TTCTGTTATCAACGACCTACGTGAGACGAAGTTATGAGAGAGAGTGGGCGAGTCGG 185  
DB 50933 TTCTGTTATCAACGACCTACGTGAGACGAAGTTATGAGAGAGAGTGGGCGAGTCGG 50992  
QY 186 TGAACAGTATGACATTCAGAGAGTGAAGCCATGCTGACATACCTGGAAGATCAATTC 245  
DB 50993 TGAACAGTATGACATTCAGAGAGTGAAGCCATGCTGACATACCTGGAAGATCAATTC 51052  
QY 246 AAGCCCAACACTCTTGGCCCAACATCACTGGGCTGTGAGATTAAGGAGATTCTGCTGGCA 305  
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                  /note="assembly_name:Contig71"

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Matches 671; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 77137 AGTGGATTTATCTGCTGATTAATGAGCCAGCATGATCTGCTGATGAGATTT 77078
QY 1179 GAGAGCATTTGATTTGATGATGAGCCGCTCAAAATGCGCCCATATCACTGCAACCTTAC 1238
DB 77077 GAGAGCATTTGATTTGATGATGAGCCGCTCAAAATGCGCCCATATCACTGCAACCTTAC 77018
QY 1239 AAGTTTCTTGGCATGGGGTCTCAGACTTTCACCTCTGCGCAAGTATTACTGGGAGGTCCA 1298
DB 77017 AAGTTTCTTGGCATGGGGTCTCAGACTTTCACCTCTGCGCAAGTATTACTGGGAGGTCCA 76958
QY 1299 TGGGGGGGACCTTTGGAATGGGGCTTGGGTTTGTATATGATGATGAGGAGGAGAA 1358
DB 76957 TGGGGGGGACCTTTGGAATGGGGCTTGGGTTTGTATATGATGATGAGGAGGAGAA 76898
QY 1359 TCAGATGAGCAATATATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1418
DB 76897 TCAGATGAGCAATATATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 76838
QY 1419 CATTCAGTGAAGTCTCTTATCCACTCTCCAGTTACCTGCAAGTATGTTCCAGAGCTTAC 1478
DB 76837 CATTCAGTGAAGTCTCTTATCCACTCTCCAGTTACCTGCAAGTATGTTCCAGAGCTTAC 76778
QY 1479 CAACCATGATGAGATTTATCCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1538
DB 76777 CAACCATGATGAGATTTATCCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 76718
QY 1539 TCAAGCTCCCTCC-TATATACACCATCCCTATATGCTCTCTCACTCTCTCAGGCTTA 1597
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QY 1598 TCTTTTCTGATTCATCTCTGACGAGAGCAATTCAGAAATGTTTATCTGCTGCGG 1657
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RESULT 14
AC136759 152269 bp DNA linear PRI 17-JAN-2003
DEFINITION Homo sapiens chromosome 11, clone RP11-114J20, complete sequence.
ACCESSION AC136759
VERSION AC136759.4 GI:27777598
KEYWORDS HNG.
SOURCE Homo sapiens (human)

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## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## AUTHORS

## TITLE

Homo sapiens chromosome 11, clone RP11-114J20

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 152269)

Bliren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barm, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

Submitted (07-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## JOURNAL

3 (bases 1 to 152269)

## REFERENCE

2 (bases 1 to 152269)

Bliren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barm, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

Submitted (17-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## JOURNAL

4 (bases 1 to 152269)

## REFERENCE

2 (bases 1 to 152269)

Bliren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barm, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

Submitted (17-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## JOURNAL

Direct Submission



Testfaye, S., Theodore, J., Topham, K., Travers, M., Vasilev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wymen, D., Young, G., Zaimoun, J.,  
 Zemek, U., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Oct 10, 2002 this sequence version replaced gi:23477886.  
 All repeats were identified using RepeatMasker:  
 Smith, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L27938  
 Center clone name: 871\_G\_20

NOTE: This is a 'working draft' sequence. It currently  
 consists of 5 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 3810: contig of 3810 bp in length  
 \* 3811 3910: gap of 100 bp  
 \* 3911 47222: contig of 43312 bp in length  
 \* 47223 47323: gap of 100 bp  
 \* 47323 54783: contig of 7461 bp in length  
 \* 54784 54883: gap of 100 bp  
 \* 54884 75151: contig of 20268 bp in length  
 \* 75152 75251: gap of 100 bp  
 \* 75252 173795: contig of 98544 bp in length.

## FEATURES

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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1179 GAGAAGATTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238  
 75799 GAGAAGATTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 75858  
 1239 AAGTTTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298  
 75859 AAGTTTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 75918  
 1299 TGTGGGAGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1358  
 75919 TGTGGGAGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 75978  
 1359 TCAGAAATGCAATATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1418  
 75979 TCAGAAATGCAATATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76038  
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 Qy 1599 CTTTGTCTGATTAATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1658  
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 Db 76399 ATGTGTAATAA 76409

RESULT 13  
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 AC073113  
 AC073113 GI:9798015  
 VERSION HTG; HTGS PHASE1; HTGS\_DRAFT.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 TITLE The sequence of Homo sapiens clone  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 203298)  
 AUTHORS Waterston, R.H.  
 DIRECT SUBMISSION  
 Submitted (08-JUN-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Aug 12, 2000 this sequence version replaced gi:8469033.

COMMENT

Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 Project Information  
 Center project name: H\_NH057D13  
 Summary Statistics  
 Sequencing vector: M13; 100%  
 Sequencing vector: plasmid; 0%  
 Chemistry: Dye-terminator Big Dye; 0% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 180558 bases at least Q40  
 Consensus quality: 188028 bases at least Q30  
 Consensus quality: 192035 bases at least Q20  
 Insert size: 16400; agarose-fp  
 Insert size: 199798; sum-of-contigs  
 Quality coverage: 4.42 in Q20 bases; sum-of-fp  
 Quality coverage: 3.69 in Q20 bases; sum-of-contigs  
 NOTE: This is a 'working draft' sequence. It currently



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27765..27850
repeat_region /rpt_family="(TA)n"
complement(27857..29995)
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Query Match 36.8%; Score 671; DB 9; Length 173032;  
 Best Local Similarity 100.0%; Fred. No. 0;  
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1119 AGTGCATATTAATCTGATATTAATGAAGCAAGATCATATCTTGATGTGAGATTT 1178  
 DB 141677 AGTGCATATTAATCTGATATTAATGAAGCAAGATCATATCTTGATGTGAGATTT 141736  
 QY 1179 GAGAGCATTTGATGTGATGATGACCGTCAAAATGCCGCCCATATCACTGCAACACTTAC 1238  
 DB 141737 GAGAGCATTTGATGTGATGATGACCGTCAAAATGCCGCCCATATCACTGCAACACTTAC 141796  
 QY 1239 AACTTTTCTGACATGGGGTCTGACACTTTCACCTCTGCGAAGTATTAATCTGCGAGGTCCA 1298  
 DB 141797 AACTTTTCTGACATGGGGTCTGACACTTTCACCTCTGCGAAGTATTAATCTGCGAGGTCCA 141856  
 QY 1299 TGTGGGGGACTCTTGGATTTGGGCTTGGTGTGTAATTAAGTATGCAAGGAGAA 1358  
 DB 141857 TGTGGGGGACTCTTGGATTTGGGCTTGGTGTGTAATTAAGTATGCAAGGAGAA 141916  
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 DB 141917 TCAGAAATGGCAATATATGAGAGAGAGGAGACTCTTACTCTTGGATTTGTTAAGACGA 141976  
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 DB 142277 GTTTATGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 142336

QY 1779 ATGTGCTAATA 1789  
 DB 142337 ATGTGCTAATA 142347

RESULT 12  
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 LOCUS  
 DEFINITION  
 Homo sapiens chromosome 11 clone RP13-871G20 map 11, 5 unordered  
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 AC130336.3 GI:23683036  
 VERSION  
 HTG; HTGS\_PHASE1; HTGS\_FULLTOP; HTGS\_CANCELLED.  
 KEYWORDS  
 Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Bacteria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 173795)  
 Birren, B., Nusbaum, C. and Lander, E.  
 Homo sapiens chromosome 11, clone RP13-871G20  
 Unpublished  
 2 (bases 1 to 173795)  
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Baran, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
 Cook, A., Cooke, P., Deatrelano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
 Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
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 Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,  
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 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
 Zemek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 173795)  
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
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 Phunhahang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,  
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
 Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
 Vei, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
 Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 173032)  
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barne, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B.,  
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 Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
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 McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,  
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 Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
 Vei, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
 Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (28-SEP-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 4 (bases 1 to 173032)  
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
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 Vei, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
 Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (10-OCT-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Oct 10, 2002 this sequence version replaced gl:23343785.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information

Center project name: L27973  
 Center clone name: 707\_M\_1  
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TITLE  
JOURNAL  
COMMENT

Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
Gardys, S., Gird, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanak, A.,  
Karatzas, A., Keller, C., Landers, T., Levine, R., Lindblad-Toh, K.,  
Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,  
McCarthy, M., Melchior, J., Meneses, L., Milova, T., Miñana, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Punhag, P., Pierre, N., Raymond, C., Ratta, R., Rise, C., Rogov, P.,  
Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P.,  
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zaimoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

Submitted (14-SBP-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Sep 14, 2002 this sequence version replaced g1:22165292.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu

Project Information  
Center Project name: L27963  
Center Clone name: 208\_A\_14  
Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 145664 bases at least Q40  
Consensus quality: 145694 bases at least Q30  
Consensus quality: 145764 bases at least Q20  
Insert size: 151000; agarose-fp  
Insert size: 146721; sum-of-coverage  
Quality coverage: 18.2 in Q20 bases; agarose-fp  
Quality coverage: 18.7 in Q20 bases; sum-of-coverage

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The order in this sequence record is  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of 'N', but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 11413: contig of 11413 bp in length  
\* 11414 11513: gap of 100 bp  
\* 11514 12216: contig of 703 bp in length  
\* 12217 12316: gap of 100 bp  
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## ORIGIN

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DEFINITION Homo sapiens chromosome 11, clone RP11-707M1, complete sequence.  
AC130364  
AC130364.5 GI:223683265  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 173032)  
AUTHORS Birren, B., Nusbaum, C. and Lander, E.  
TITLES Homo sapiens chromosome 11, clone RP11-707M1  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 173032)  
REFERENCE Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,

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Db      2050  ACCAGAGACAAATCAGAAATGTGTTATCTGCTGTGGAAACCCCTTATCCATAAGCC 2109
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RESULT 9
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LOCUS Sequence 5 from Patent WO0102566.
DEFINITION AX068370
ACCESSION AX068370
VERSION AX068370.1 GI:12578535
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Schwarz,D.A. and Makl,R.A.
TITLES Metabotropic glutamate receptors and methods of use therefor
JOURNAL Patent: WO 0102566-A 5 11-JAN-2001;
Neuroscience Biosciences, Inc. (US)
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Location/Qualifiers
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BASE COUNT 581 a 535 c 580 g 630 t
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Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1500  GGATTGTGAAGTACAGTACGATGAGCTTGTGATTTAATCAAAAGCTCCCTATATACAC 1559
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RESULT 10
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LOCUS Homo sapiens chromosome 11 clone RP11-208A14 map 11, WORKING DRAFT
DEFINITION SBOUNCE, 3 unordered pieces.
ACCESSION AC130357
VERSION AC130357.2 GI:22857687
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLES Homo sapiens chromosome 11, clone RP11-208A14
JOURNAL Unpublished
2 (bases 1 to 146921)
REFERENCE 2
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouhgalter,B.,
Camarda,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dekrelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karacas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Piere,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,R., Schnupack,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Teisfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zaimoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
JOURNAL Direct Submission
Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 146921)
REFERENCE 3
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouhgalter,B.,
Camarda,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

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VERSION AX068376.1 GI:12578539  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 11 JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
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Best Local Similarity 99.8%; Pred. No. 0;  
Matches 912; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 482 CTCTTTCTGTTGATCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 541  
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DEFINITION Sequence 6 from Patent WO0102566.  
ACCESSION AX068371  
VERSION AX068371.1 GI:12578536  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 6 JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES  
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Best Local Similarity 99.9%; Pred. No. 0;  
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DB 1690 TCAGACTTTCACCTCTGCAAGATATTAATGAGGAGGAGGAGGAGGAGGAG 1749  
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DB 1810 AAGAGAGGAGCTTTAGCTTGGAGTTGTTAAGAACGACATTCAGTGAAGCT 1869  
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Db 1883 TGAAGCAACAGATCATCTTCTGATGTGAGATTGAGAGACATTTGATTTGAGATGA 1942  
Qy 1203 CCGTCAAAATGCGCCCATATCTGACACACTACAGATTCTTCTGATGGGGTGTCA 1262  
Db 1943 CCGTCAAAATGCGCCCATATCTGACACACTACAGATTCTTCTGATGGGGTGTCA 2002  
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Db 2003 GACTTCACCTCTGGGAGATTAATGAGAGTCAATGTGGGAGACTCTTGAAATGGGG 2062  
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Qy 1503 TTGTGAAGTGAAGTGTGAGCTTCTGATGATTAATCAAGCTCCCTATATACAT 1562  
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Qy 1563 CCTTAATGCTCTTCTGACCTCTCTGAGGCTATCTTTGCTGATCATCTTGACC 1622  
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RESULT 6  
AX068374 2149 bp DNA linear PAT 25-JAN-2001  
LOCUS Sequence 9 from Patent WO0102566.  
DEFINITION AX068374  
ACCESSION AX068374.1 GI:12578538  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Schwarz, D.A. and Maki, R.A.  
Metabotropic glutamate receptors and methods of use therefor  
Patent: WO 0102566-A 9 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
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BASE COUNT 547 a 485 c 538 g 579 t  
ORIGIN

Query Match 49.2%; Score 897; DB 6; Length 2149;  
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Matches 997; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS Sequence 11 from Patent WO0102566.  
DEFINITION AX068376  
ACCESSION AX068376



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DB 2281 AATGTTATTAACCTCAATTTATGTTGTAATTAATGTTGTAATA 2327

RESULT 5  
AX068366 2551 bp DNA linear PAT 25-JAN-2001  
LOCUS AX068366  
DEFINITION Sequence 1 from Patent WO0102566.  
ACCESSION AX068366  
VERSION AX068366.1 GI:12578533  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Schwarz,D.A. and Maki,R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 1 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
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BASE COUNT 666 a 566 c 630 g 689 t

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Matches 1126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2042 TCTTCTTATGCTTATCAACAGCAATAGCTTCTGTTTATGCTTGAATTCATT 2101

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RESULT 3

AX709349 1110 bp DNA linear PAT 04-APR-2003

LOCUS Sequence 3 from Patent WO02070708.

DEFINITION AX709349

ACCESSION AX709349

VERSION AX709349.1 GI:29564891

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.

AUTHORS Glutamate receptor modulatory proteins and nucleic acids encoding

TITLE them

JOURNAL Patent: WO 02070708-A 3 12-SEP-2002;

FEATURES

source Location/Qualifiers

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TEBNYGESEMEAFKMSAKEGICIAHSYKISNAGBQSPKLLKULSHLPKRVAVAY  
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CDS

BASE COUNT 276 a 253 c 306 g 275 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

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Qy 124 TTTTCTGTTATCAACAGCTTACTGTGAGACGAGATTATGAGAGAAAGTGTGGGCAATC 183

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Qy 184 CGTGAACAGTATGCTATTCAGAGAGTGAAGCCATGCTGCATACCTCTGGAAGATCAAT 243

Db 181 CGTGAACAGTATGCTATTCAGAGAGTGAAGCCATGCTGCATACCTCTGGAAGATCAAT 240

Qy 244 TCAGACCCCACTCTTGGCCCAATCACTAGGCTGTGAGATTAAGGAGATTCTGCTGCG 303

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Db 301 CATTCGGCTGTGGCCCTTGAAGACAGACATTTAGATTCAATTAAGATTCTCATTTCTTCG 360

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Db 361 GAAGAGAGAGAGGCTTGGTATGCTGTGAGATGAGCTCCCTCTTCTCCGCTCCAG 420

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Db 481 TTGCTTCAGCTTTTCAACATACCTCAGATTTGCTTATCAGCAACCATCATGATTCGATG 540

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Db 1081 ATCACTGACTGAGGACAGGCTCATCTAA 1110

RESULT 4

AX068368 2349 bp DNA linear PAT 25-JAN-2001

LOCUS Sequence 3 from Patent WO0102566.

DEFINITION AX068368

ACCESSION AX068368

VERSION AX068368.1 GI:12578534

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Schwarz,D.A. and Maki,R.A.

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL 1

Neuroscience Biobiosciences, inc. (US)

Neuroscience Biobiosciences, inc. (US)

Patent: WO 0102566-A 3 11-JAN-2001;

Neuroscience Biobiosciences, inc. (US)

Location/Qualifiers

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/mol\_type="genomic DNA"

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ACCESSION	AX068372		PAT 25-JAN-2001
VERSION	AX068372.1	GI:12578537	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1 Schwarz, D.A. and Maki, R.A.		
TITLE	Metabotropic glutamate receptors and methods of use therefor		
JOURNAL	Patent: WO 0102566-A 7 11-JAN-2001;		
FEATURES	Neurocrine Biosciences, Inc. (US)		
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JOURNAL Patent: WO 02070708-A 1 12-SEP-2002;  
Wyeth (US)  
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Query Match 100.0%; Score 1823; DB 6; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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41: em Htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	897	44.2	2149	6	AX068374
7	812	44.5	2064	6	AX068376
8	719	39.4	2241	6	AX068371
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11	671	36.8	173032	9	AC130364
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#### ALIGNMENTS

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ACCESSION AX709347  
VERSION AX709347.1 GI:29564889  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
Glutamate receptor modulatory proteins and nucleic acids encoding  
them

DB 1040 CAGATGCTCAGCAGCAGGCGCATGTGTGACATAGTGAAGAGTCAAACTGGAACCTTATG 1099  
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RESULT 15  
 AAD05030  
 ID AAD05030 standard; mRNA; 4207 BP.  
 XX AAD05030;  
 DT 17-JUL-2001 (first entry)  
 XX

Human metabotropic glutamate receptor, mGluR5A mRNA.

XX Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 XX postsynaptic sensitivity; glutamate excitation; ss.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT 460..4002  
 FT /tag= a  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mGluR5A"  
 XX

PN US6211353-BI.

PD 03-APR-2001.

PF 07-JUN-1996; 96US-0660148.

PR 29-JUL-1994; 94US-0282853.

PA (ELIL ) LILLY & CO ELI.

PI Burnette JP, Wayne NG, Sharp RL, Snyder YM;

DR WPI, 2001-289639/30.

DR P-PSDB; AAB01156.

XX New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptors, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -

XX Claim 2; Column 43-46; 53pp; English.

XX The present sequence is a mRNA encoding human metabotropic glutamate  
 CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in  
 CC the central nervous system (CNS), mediates excitatory pathway in  
 CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
 CC the receptors that respond to glutamate are EAA receptors. The receptors  
 CC are useful for modulating the presynaptic release of glutamate and the

CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
 XX

Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;

Query Match 20.0%; Score 222; DB 22; Length 4207;

Best Local Similarity 76.3%; Pred. No. 4e-102;

Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 461 TGGCCATCTTCTGTGAGGCGCATGAGGTGTCTGTGATGCGCCATGAGCGCGCTGG 520  
 DB 920 UAGCCAUUUCAGGUCGCAAAUUGUCUCCAGCUUUCACAUUCCUAGAUUUCUACAG 979  
 QY 521 CAACCATCATGATCTGAGTGAACAAGACTCTGTTCAATATTTATGAGGGTGTGCTT 580  
 DB 980 CAACCGAUGAUUCUGAUGACAAGACUUCUUCUCAAUUAUUCAGAGGUGUUCUU 1039  
 QY 581 CAGATGCTCAGCAGCAGGCGCATGTGTGAGAGCTCAAGATGTAAGAGTCAACTGGA 640  
 DB 1040 CAGATGCTCAGCAGCAGGCGCATGTGTGAGAGCTCAAGATGTAAGAGTCAACTGGA 1099  
 QY 641 TATCAGCCCTGACACAGAAAGGCACTATGAGAAAGTGGAGAGCCTTAAAGATA 700  
 DB 1100 UAUCAAGCTGUGCAACAGAAAGGCAACUAGGAAAGUGGAGUAGAGCCUCAAAGATA 1159  
 QY 701 TGTCAAGGAAAGGAAATTTGATGCGCCACTCTTACAAATCTACATATGACGGG 760  
 DB 1160 UGUCAAGGAAAGGAAATTTGATGCGCCACTCTTACAAATCTACATATGACGGG 1219  
 QY 761 AGCAGAGCTTTGATTAAGCTGTCTGAAGAGCTCAAGATCACTTGGCCAAAGGCCGGGTGG 820  
 DB 1220 AGCAGAGCTTTGATTAAGCTGTCTGAAGAGCTCAAGATCACTTGGCCAAAGGCCGGGTGG 1279  
 QY 821 TGGCCATCTTCTGTGAGGCGCATGAGGTGTCTGTGATGCGCCATGAGCGCGCTGG 880  
 DB 1280 UGCCUCUCUUGUAGAGGCGCAUGACGUGAGAGUCUCUAGUAGGCAUAGAGCGCUCU 1339  
 QY 881 GTCTAG 886  
 DB 1340 GUCUAG 1345

Search completed: December 14, 2003, 18:46:52  
 Job time : 324.792 secs

```

FT mutation replace (425, A)
XX /tag= b
XX
XX US6211353-B1.
XX
XX 03-APR-2001.
XX
XX 07-JUN-1996; 96US-0660148.
XX
XX 29-JUL-1994; 94US-0282853.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;
XX
XX WPI; 2001-289639/30.
XX
XX New isolated nucleic acids for producing human metabotropic glutamate
XX receptors, which are useful for modulating the presynaptic release of
XX glutamate or the postsynaptic sensitivity of the neuronal cell to
XX glutamate excitation -
XX
XX Disclosure, Column -, 53pp; English.
XX
XX The present sequence is a cDNA mutant encoding human metabotropic
XX glutamate receptor, mGluR5A. L-glutamate, the most abundant
XX neurotransmitter in the central nervous system (CNS), mediates excitatory
XX pathway in mammals. L-glutamate is referred to as excitatory amino acid
XX (EAA) and the receptors that respond to glutamate are EAA receptors. The
XX receptors are useful for modulating the presynaptic release of glutamate
XX and the postsynaptic sensitivity of the neuronal cell to glutamate
XX excitation.
XX Note: The present sequence is not shown in the specification, but is
XX derived from the sequence referred as SEQ ID NO:1, shown in column
XX 59-68 (AAB05029) of the specification.
XX
XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;
XX
XX
XX Query Match 20.0%; Score 222; DB 22; Length 4207;
XX Best Local Similarity 99.1%; Pred. No. 4e-102;
XX Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATCTCAGATTGTTACTCAG 520
XX 920 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATCTCAGATTGTTACTCAG 979
XX
XX 521 CAACCATCATGATCTGAGTGCACAGACTCTGTTCAAATATTTTCATGAGGTTGTCCTT 580
XX 980 CAACCATCATGATCTGAGTGCACAGACTCTGTTCAAATATTTTCATGAGGTTGTCCTT 1039
XX
XX 581 CAGATGCTCAGCAGGAGGATTCATGATGACATAGTGAAGAGTCAACTGGAAGTCTTATG 640
XX 1040 CAGATGCTCAGCAGGAGGATTCATGATGACATAGTGAAGAGTCAACTGGAAGTCTTATG 1099
XX
XX 641 TATCAGCCCTTACACAGAGGCAATCTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700
XX 1100 TATCAGCCCTTACACAGAGGCAATCTATGAGAAAGTGGAGTGAAGCTTCAAGATA 1159
XX
XX 701 TGTGACGGAAGAGGAGATTTGATGCTCCACTCTTACAAATCTACAGTAATGACGGG 760
XX 1160 TGTGACGGAAGAGGAGATTTGATGCTCCACTCTTACAAATCTACAGTAATGACGGG 1219
XX
XX 761 AGCAGAGCTTTGATAGCTGCTGAAGAAGTCAAGTCACTTGCCCAAGGCCGGGCTG 820
XX 1220 AGCAGAGCTTTGATAGCTGCTGAAGAAGTCAAGTCACTTGCCCAAGGCCGGGCTG 1279
XX
XX 821 TGGCCCTACTTGTGTGAGGAGATGAGGTGAGAGTGTGCTGATGAGGAGGCGCTG 880
XX 1280 TGGCCCTACTTGTGTGAGGAGATGAGGTGAGAGTGTGCTGATGAGGAGGCGCTG 1339
XX
XX 881 GTCTAG 886
XX
XX 1340 GTCTAG 1345

```

```

RESULT 14
AAB05029
ID AAB05029 standard; cDNA, 4207 BP.
XX
XX AAB05029;
XX
XX 17-JUL-2001 (first entry)
XX
XX Human metabotropic glutamate receptor, mGluR5A cDNA.
XX
XX Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;
XX EAA; central nervous system; CNS; presynaptic release; neurotransmitter;
XX postsynaptic sensitivity; glutamate excitation; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 460..4002
XX /tag= a
XX /product= "Human metabotropic glutamate receptor,
XX mGluR5A"
XX
XX US6211353-B1.
XX
XX 03-APR-2001.
XX
XX 07-JUN-1996; 96US-0660148.
XX
XX 29-JUL-1994; 94US-0282853.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;
XX
XX WPI; 2001-289639/30.
XX
XX P-PSDB; AAB01156.
XX
XX New isolated nucleic acids for producing human metabotropic glutamate
XX receptors, which are useful for modulating the presynaptic release of
XX glutamate or the postsynaptic sensitivity of the neuronal cell to
XX glutamate excitation -
XX
XX Claim 2; Column 59-68; 53pp; English.
XX
XX The present sequence is a cDNA encoding human metabotropic glutamate
XX receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in
XX the central nervous system (CNS), mediates excitatory pathway in
XX mammals. L-glutamate is referred to as excitatory amino acid (EAA) and
XX the receptors that respond to glutamate are EAA receptors. The receptors
XX are useful for modulating the presynaptic release of glutamate and the
XX postsynaptic sensitivity of the neuronal cell to glutamate excitation.
XX Note: The present sequence is stated as being the same as that shown as
XX SEQ ID NO:1 (AAB05029) in column 7-18 of the specification. However the
XX sequences differ at several positions.
XX
XX Sequence 4207 BP; 1011 A; 1120 C; 1112 G; 964 T; 0 other;
XX
XX
XX Query Match 20.0%; Score 222; DB 22; Length 4207;
XX Best Local Similarity 99.1%; Pred. No. 4e-102;
XX Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATCTCAGATTGTTACTCAG 520
XX 920 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATCTCAGATTGTTACTCAG 979
XX
XX 521 CAACCATCATGATCTGAGTGCACAGACTCTGTTCAAATATTTTCATGAGGTTGTCCTT 580
XX 980 CAACCATCATGATCTGAGTGCACAGACTCTGTTCAAATATTTTCATGAGGTTGTCCTT 1039
XX
XX 581 CAGATGCTCAGCAGGAGGATTCATGATGACATAGTGAAGAGTCAACTGGAAGTCTTATG 640
XX

```







XX AAC85785;  
 AC 18-JUL-2001 (first entry)  
 DT  
 XX  
 DE cDNA encoding metabotropic glutamate receptor.  
 XX  
 KM Human; metabotropic glutamate receptor; mglur; splice variant;  
 KM mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
 KM anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
 KM muscle relaxant; ss.  
 XX  
 OS Homo sapiens.  
 PN WO200130829-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000WO-US29356.  
 XX  
 PR 25-OCT-1999; 99US-0161481.  
 XX  
 PR 24-OCT-2000; 2000US-0695481.  
 XX  
 PA (NPSP-) NPS PHARM INC.  
 XX  
 PI Krapcho K, Stormann T, Levinthal C, Hammerland L, Storjohann L;  
 XX  
 DR MPI: 2001-308615/32.  
 XX  
 DR P-PSDB; AAB47217.  
 XX  
 PT New nucleic acid encoding an isoform of human metabotropic glutamate  
 PT receptor, for identifying potential therapeutic agents for neurological  
 PT disease  
 XX  
 PS Claim 2; Page 51-56; 86pp; English.  
 XX  
 CC This sequence encodes a human metabotropic glutamate receptor (mglur).  
 CC mglur is a splice variant of human metabotropic glutamate receptor 5  
 CC (mglur5). mglur's are G-protein-coupled receptors capable of activating  
 CC (mglur5). mglur's are G-protein-coupled receptors capable of activating  
 CC a variety of intracellular second messenger systems following the  
 CC binding of glutamate. Recombinant mglur DNA and compounds that bind to,  
 CC or modulate activity of mglur are useful for diagnosing or treating  
 CC neurological disorders, e.g. as anticonvulsants, neuroprotectants,  
 CC analgesics, cognitive enhancers and muscle relaxants.  
 CC  
 XX  
 SQ Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;  
 XX  
 Query Match 20.0%; Score 222; DB 22; Length 2826;  
 Best Local Similarity 99.1%; Pred. No. 4e-102;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 461 TGGCCATTGAGTCCGAATTTGCTCCAGTTTTCACATCTGAGATTGCTTACTCAG 520  
 DB 461 TGGCCATTGAGTCCGAATTTGCTCCAGTTTTCACATCTGAGATTGCTTACTCAG 520  
 QY 521 CAACCATCATGATCTGATGACCAAGACTCTGTTCAATATTTCATGAGGGTTGCGCTT 580  
 DB 521 CAACCATCATGATCTGATGACCAAGACTCTGTTCAATATTTCATGAGGGTTGCGCTT 580  
 QY 581 CAGATGCTCAGCAGGCAAGGCTCATGATGAGACATGATGAGAGGTCAATGAGCCTATG 640  
 DB 581 CAGATGCTCAGCAGGCAAGGCTCATGATGAGACATGATGAGAGGTCAATGAGCCTATG 640  
 QY 641 TATCAGCCGTACACACAGAGGCAATATGAGAGAAAGTGGAGTGAAGCCTTCAAGATA 700  
 DB 641 TATCAGCCGTACACACAGAGGCAATATGAGAGAAAGTGGAGTGAAGCCTTCAAGATA 700  
 QY 701 TGTCAAGCAAGGAGGATTTGATGCCCACTCTTACAAATATTCATTAATGAGGGG 760  
 DB 701 TGTCAAGCAAGGAGGATTTGATGCCCACTCTTACAAATATTCATTAATGAGGGG 760  
 QY 761 AGCAGAGCTTTGATAGTGTGTAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 820  
 DB 761 AGCAGAGCTTTGATAGTGTGTAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 820

DB 761 AGCAGAGCTTTGATAGTGTGTAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 820  
 QY 821 TGGCCTACTTCTGTGAGGGCATAGCGGTGAGGCTGCTGATGGCCATGAGGGCGCTGG 880  
 DB 821 TGGCCTACTTCTGTGAGGGCATAGCGGTGAGGCTGCTGATGGCCATGAGGGCGCTGG 880  
 QY 881 GTCTAG 886  
 DB 881 GTCTAG 886  
 RESULT 11  
 AAC85787  
 ID AAC85787 standard; cDNA; 3129 BP.  
 XX  
 AC AAC85787;  
 XX  
 DT 18-JUL-2001 (first entry)  
 XX  
 DE cDNA encoding chimeric receptor containing hmglur5d portion.  
 XX  
 KM Human; metabotropic glutamate receptor; mglur; splice variant;  
 KM mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
 KM anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
 KM muscle relaxant; calcium receptor; Car; mglur5d; ss.  
 XX  
 OS Chimeric - Homo sapiens.  
 XX  
 PN WO200130829-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000WO-US29356.  
 XX  
 PR 25-OCT-1999; 99US-0161481.  
 XX  
 PR 24-OCT-2000; 2000US-0695481.  
 XX  
 PA (NPSP-) NPS PHARM INC.  
 XX  
 PI Krapcho K, Stormann T, Levinthal C, Hammerland L, Storjohann L;  
 XX  
 DR MPI: 2001-308615/32.  
 XX  
 DR P-PSDB; AAB47219.  
 XX  
 PT New nucleic acid encoding an isoform of human metabotropic glutamate  
 PT receptor, for identifying potential therapeutic agents for neurological  
 PT disease  
 XX  
 PS Claim 18; Page 70-75; 86pp; English.  
 XX  
 CC This sequence encodes a chimeric receptor comprising the intracellular  
 CC cytoplasmic tail of the human calcium receptor (Car) and the extra-  
 CC cellular and seven transmembrane domains of the human metabotropic  
 CC glutamate receptor (mglur) splice variant of human metabotropic  
 CC glutamate receptor 5 (mglur5). mglur5d. mglur's are G-protein-coupled  
 CC receptors capable of activating a variety of intracellular second  
 CC messenger systems following the binding of glutamate. Recombinant  
 CC mglur5d DNA and compounds that bind to, or modulate activity of it  
 CC are useful for diagnosing or treating neurological disorders, e.g.  
 CC as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers  
 CC and muscle relaxants.  
 CC  
 XX  
 SQ Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;  
 XX  
 Query Match 20.0%; Score 222; DB 22; Length 3129;  
 Best Local Similarity 99.1%; Pred. No. 4e-102;  
 Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 461 TGGCCATTGAGTCCGAATTTGCTCCAGTTTTCACATCTGAGATTGCTTACTCAG 520  
 DB 461 TGGCCATTGAGTCCGAATTTGCTCCAGTTTTCACATCTGAGATTGCTTACTCAG 520  
 QY 521 CAACCATCATGATCTGATGACCAAGACTCTGTTCAATATTTCATGAGGGTTGCGCTT 580  
 DB 521 CAACCATCATGATCTGATGACCAAGACTCTGTTCAATATTTCATGAGGGTTGCGCTT 580

DB 425 CAGTCCAGTGAAGAGGGGTGGCTCATCTGGGTGACATCTTTATGAGCTCTC 484  
QY 121 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAGTGGGGAGTTC 180  
DB 485 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAGTGGGGAGTTC 544  
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCCATGCTGATACCTCTGAAAAGATCAAT 240  
DB 545 CGGAACAGTATGAGCATTCAGAGAGTGGAGGCCATGCTGATACCTCTGAAAAGATCAAT 604  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
DB 605 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 664  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAATAGAGATTCCTCATTTCTTG 360  
DB 665 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAATAGAGATTCCTCATTTCTTG 724  
QY 361 GAAGAGAGAGGGCTTGGTATGCTGTGTGATGGCTCTCTCTTCTTCCGCTCCAG 420  
DB 725 GAAGAGAGAGGGCTTGGTATGCTGTGTGATGGCTCTCTCTTCTTCCGCTCCAG 784  
QY 421 AAGCCCATGTAGAGGGGCTATTTGAGCCGTTCCAGATTTAGAGCATTCAGATTCAGAA 480  
DB 785 AAGCCCATGTAGAGGGGCTATTTGAGCCGTTCCAGATTTAGAGCATTCAGATTCAGAA 844  
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACATCATGATGATGAT 540  
DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACATCATGATGATGAT 904  
QY 541 GACAAAGCTCTGTTCAAAATTTTCAATGAGGGTGTGCTTCAAGTGTCTCAGCAGGCAAG 600  
DB 905 GACAAAGCTCTGTTCAAAATTTTCAATGAGGGTGTGCTTCAAGTGTCTCAGCAGGCAAG 964  
QY 601 TCAGATGTGACATAGTGAAGAGGTACAACCTGACCTATGATCAGCCGTACACAGAA 660  
DB 965 TCAGATGTGACATAGTGAAGAGGTACAACCTGACCTATGATCAGCCGTACACAGAA 1024  
QY 661 GG 662  
DB 1025 GG 1026

RESULT 9  
AAF29989 standard; DNA; 2551 BP.  
ID AAF29989 standard; DNA; 2551 BP.  
AC AAF29989;  
XX  
DT 06-APR-2001 (first entry)  
XX  
DE Human GRMx-1a DNA.  
XX  
KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; de.  
XX  
OS Homo sapiens.  
XX  
PN WO200102566-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 27-JUN-2000; 2000WO-US17798.  
XX  
PR 02-JUL-1999; 99US-0346326.  
XX  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
PI Schwarz DA, Makl RA;  
XX  
DR WPI; 2001-123112/13.  
XX

PT Novel metabotropic glutamate receptor for prevention, treatment of  
PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
PT schizophrenia -  
XX  
PS Claim 2; Fig 1; 59pp; English.  
XX  
CC The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia.  
CC Metabotropic glutamate receptor polynucleotides, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.  
XX  
SQ Sequence 2551 BP; 666 A; 566 C; 630 G; 689 T; 0 other;  
Query Match 50.4%; Score 559; DB 22; Length 2551;  
Best Local Similarity 99.7%; Pred. No. 3.5e-273;  
Matches 659; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGCTCTTCTGTGATCTGTGATCTTACTTTTGAAGAAGATTCCTGGAGATGCA 60  
DB 365 ATGCTCTTCTGTGATCTGTGATCTTACTTTTGAAGAAGATTCCTGGAGATGCA 424  
QY 61 CAGTCCAGTGAAGAGGGGTGGCTCAATGCTGGGTGACATTAATTGAGCTCTC 120  
DB 425 CAGTCCAGTGAAGAGGGGTGGCTCAATGCTGGGTGACATTAATTGAGCTCTC 484  
QY 121 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAGTGGGGAGTTC 180  
DB 485 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAAATTATGAGAGAGTGGGGAGTTC 544  
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCCATGCTGATACCTCTGAAAAGATCAAT 240  
DB 545 CGGAACAGTATGAGCATTCAGAGAGTGGAGGCCATGCTGATACCTCTGAAAAGATCAAT 604  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
DB 605 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGGATTCCTGCTGG 664  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAATAGAGATTCCTCATTTCTTG 360  
DB 665 CATTGGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAATAGAGATTCCTCATTTCTTG 724  
QY 361 GAAGAGAGAGGGCTTGGTATGCTGTGTGATGGCTCTCTCTTCTTCCGCTCCAG 420  
DB 725 GAAGAGAGAGGGCTTGGTATGCTGTGTGATGGCTCTCTCTTCTTCCGCTCCAG 784  
QY 421 AAGCCCATGTAGAGGGGCTATTTGAGCCGTTCCAGATTTAGAGCATTCAGATTCAGAA 480  
DB 785 AAGCCCATGTAGAGGGGCTATTTGAGCCGTTCCAGATTTAGAGCATTCAGATTCAGAA 844  
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACATCATGATGATGAT 540  
DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACATCATGATGATGAT 904  
QY 541 GACAAAGCTCTGTTCAAAATTTTCAATGAGGGTGTGCTTCAAGTGTCTCAGCAGGCAAG 600  
DB 905 GACAAAGCTCTGTTCAAAATTTTCAATGAGGGTGTGCTTCAAGTGTCTCAGCAGGCAAG 964  
QY 601 TCAGATGTGACATAGTGAAGAGGTACAACCTGACCTATGATCAGCCGTACACAGAA 660  
DB 965 TCAGATGTGACATAGTGAAGAGGTACAACCTGACCTATGATCAGCCGTACACAGAA 1024  
QY 661 G 661  
DB 1025 G 1025

RESULT 10  
AAC85785 standard; cDNA; 2826 BP.  
ID AAC85785 standard; cDNA; 2826 BP.

DE Human GRMX-1c DNA.  
 XX Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX MO200102566-A1.  
 XX PN  
 XX 11-JAN-2001.  
 PD  
 XX 27-JUN-2000; 2000MO-US17798.  
 PF  
 XX 02-JUL-1999; 99US-0346326.  
 PR  
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA  
 XX Schwarz DA, Maki RA;  
 PI  
 XX WPI; 2001-123112/13.  
 DR  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS  
 XX Claim 2; Fig 5; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polymucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 SQ Sequence 2326 BP; 581 A; 535 C; 580 G; 630 T; 0 other;  
 Query Match 50.5%; Score 560; DB 22; Length 2326;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-273;  
 Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGGTCCTTCTGTGATCTGTGATCTTATCTTTGAAAGAGATGTCGGAAGTCA 60  
 DB ATGGTCCTTCTGTGATCTGTGATCTTATCTTTGAAAGAGATGTCGGAAGTCA 424  
 QY 61 CAGTCCAGTGAAGAGAGGCTGTGCTCACATGCTGGGTGACATCATTTAGAGCTCTC 120  
 DB CAGTCCAGTGAAGAGAGGCTGTGCTCACATGCTGGGTGACATCATTTAGAGCTCTC 484  
 QY 121 TTTTCGTTCAATACAGCCTTACTGTGGAAGAGTTCATGAGAGAGTGTGGGCAATC 180  
 DB TTTTCGTTCAATACAGCCTTACTGTGGAAGAGTTCATGAGAGAGTGTGGGCAATC 544  
 QY 485 TTTTCGTTCAATACAGCCTTACTGTGGAAGAGTTCATGAGAGAGTGTGGGCAATC 544  
 DB TTTTCGTTCAATACAGCCTTACTGTGGAAGAGTTCATGAGAGAGTGTGGGCAATC 240  
 QY 181 CCGAAGCAGTATGCGATTCAGAGATGAGAGGCGATGCTGACCTCGAAGAGATCAAT 240  
 DB CCGAAGCAGTATGCGATTCAGAGATGAGAGGCGATGCTGACCTCGAAGAGATCAAT 604  
 QY 545 CCGAAGCAGTATGCGATTCAGAGATGAGAGGCGATGCTGACCTCGAAGAGATCAAT 604  
 DB CCGAAGCAGTATGCGATTCAGAGATGAGAGGCGATGCTGACCTCGAAGAGATCAAT 300  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGCGCTGTGAGATTAAGAGATTCCTGCTGG 300  
 DB TCAGACCCCACTCTTGGCCCAATCACTGCGCTGTGAGATTAAGAGATTCCTGCTGG 664  
 QY 605 TCAGACCCCACTCTTGGCCCAATCACTGCGCTGTGAGATTAAGAGATTCCTGCTGG 664  
 DB TCAGACCCCACTCTTGGCCCAATCACTGCGCTGTGAGATTAAGAGATTCCTGCTGG 360  
 QY 301 CATTGGCTGTGGCCCTTAGAGAGAGATTAAGATTCCTGATTTCTTTCG 360  
 DB CATTGGCTGTGGCCCTTAGAGAGAGATTAAGATTCCTGATTTCTTTCG 724  
 QY 665 CATTGGCTGTGGCCCTTAGAGAGAGATTAAGATTCCTGATTTCTTTCG 724  
 DB CATTGGCTGTGGCCCTTAGAGAGAGATTAAGATTCCTGATTTCTTTCG 420  
 QY 361 GAAGAGAGAGAGGCTTGTGATCTGTGATGAGCTCTCTCTTCCGCTCAAG 420  
 DB GAAGAGAGAGAGGCTTGTGATCTGTGATGAGCTCTCTCTTCCGCTCAAG 784  
 QY 725 GAAGAGAGAGAGGCTTGTGATCTGTGATGAGCTCTCTCTTCCGCTCAAG 784  
 DB GAAGAGAGAGAGGCTTGTGATCTGTGATGAGCTCTCTCTTCCGCTCAAG 480  
 QY 421 AAGCCCATAGTAGAGGCTCATTTGGGCTGTTCAGATCTTTAGCCATTCAGGTCCAAAT 480  
 DB AAGCCCATAGTAGAGGCTCATTTGGGCTGTTCAGATCTTTAGCCATTCAGGTCCAAAT 844

QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACAGCAACATCATGATCTAGT 540  
 DB TTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACAGCAACATCATGATCTAGT 904  
 QY 541 GACAGAAGCTCTGTTCAAAATTTTCATGAGGGTTGTGCTTCAGATGCTCAGAGCAAG 600  
 DB GACAGAAGCTCTGTTCAAAATTTTCATGAGGGTTGTGCTTCAGATGCTCAGAGCAAG 964  
 QY 601 TCCATGATGACATATGTAAGAGAGTCAACTGGAACCTATATACGCCCTACACAGAA 660  
 DB TCCATGATGACATATGTAAGAGAGTCAACTGGAACCTATATACGCCCTACACAGAA 1024  
 QY 661 GG 662  
 DB 1025 GG 1026  
 RESULT 8  
 ID AAF29990 standard; DNA; 2349 BP.  
 AC AAF29990;  
 XX  
 DT 06-APR-2001 (first entry)  
 DE Human GRMX-1b DNA.  
 XX  
 KM Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX MO200102566-A1.  
 XX PN  
 XX 11-JAN-2001.  
 PD  
 XX 27-JUN-2000; 2000MO-US17798.  
 PF  
 XX 02-JUL-1999; 99US-0346326.  
 PR  
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA  
 XX Schwarz DA, Maki RA;  
 PI  
 XX WPI; 2001-123112/13.  
 DR  
 XX Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS  
 XX Claim 2; Fig 3; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polymucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 SQ Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;  
 Query Match 50.5%; Score 560; DB 22; Length 2349;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-273;  
 Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGGTCCTTCTGTGATCTGTGATCTTATCTTTGAAAGAGATGTCGGAAGTCA 60  
 DB ATGGTCCTTCTGTGATCTGTGATCTTATCTTTGAAAGAGATGTCGGAAGTCA 424  
 QY 61 CAGTCCAGTGAAGAGAGGCTGTGCTCACATGCTGGGTGACATCATTTAGAGCTCTC 120

```
Db 725 GAAGAGAAAGGGCTTGGTGTGCTGTGATGGCTCTCTCTTCCGCTCCAAAG 784
Qy 421 AAGCCATAGTAGGGGTCAATGGGCTGTGTCAGTCTTTAGCCATTCAAGTCCAAAT 480
Db 785 AAGCCATAGTAGGGGTCAATGGGCTGTGTCAGTCTTTAGCCATTCAAGTCCAAAT 844
Qy 481 TTGCTCAGCTTTTCAACATACCTCAAGATTGCTTACGACCAACATCATGATCTGAAGT 540
Db 845 TTGCTCAGCTTTTCAACATACCTCAAGATTGCTTACGACCAACATCATGATCTGAAGT 904
Qy 541 GACAAAGCTCTGTCAAAATATTTCAAGAGGTTGTGCTTCAGATGCTCAGACGCAAG 600
Db 905 GACAAAGCTCTGTCAAAATATTTCAAGAGGTTGTGCTTCAGATGCTCAGACGCAAG 964
Qy 601 TCCATGCTGACATAGTGAAGAGGTACAACTGACCTATGTATCAGCCGTACACAGAA 660
Db 965 TCCATGCTGACATAGTGAAGAGGTACAACTGACCTATGTATCAGCCGTACACAGAA 1024
Qy 661 GCGAAGCTATGGAAGAGTGGAGTGAAGAGCCTTCAAGATATGTCAAGGAAAGAGGATT 720
Db 1025 GCGAAGCTATGGAAGAGTGGAGTGAAGAGCCTTCAAGATATGTCAAGGAAAGAGGATT 1084
Qy 721 TGCATGCCCCACTCTTACAAATCTACAGTATGACAGGAGGAGAGCTTTGATTAAGCTG 780
Db 1085 TGCATGCCCCACTCTTACAAATCTACAGTATGACAGGAGGAGAGCTTTGATTAAGCTG 1144
Qy 781 CTGAAGAGCTCAAGAGTCACTTGGCCAGAGCCCGGGTGTGCTTACTTGTGAAGGCT 840
Db 1145 CTGAAGAGCTCAAGAGTCACTTGGCCAGAGCCCGGGTGTGCTTACTTGTGAAGGCT 1204
Qy 841 ATGACGCTGAGAGAGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 1205 ATGACGCTGAGAGAGTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1264
Qy 901 CTCTGGGCGAG 911
Db 1265 CTCTGGGCGAG 1275

RESULT 6
AAF29992
ID .AAF29992 standard; DNA; 2241 BP.
XX
AC AAF29992;
XX
DT 06-APR-2001 (first entry)
XX
DE Human GRMX-Id DNA.
XX
KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS Homo sapiens.
XX
PN W0200102566-A1.
XX
PD 11-JAN-2001.
XX
PF 27-JUN-2000; 2000MO-US17798.
XX
PR 02-JUL-1999; 99US-0346326.
XX
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Schwarz DA, Maki RA;
XX
DR WPI; 2001-123112/13.
XX
PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
```

```
PS Claim 2; Fig 6; 59pp; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC - Metabotropic glutamate receptor polynucleotides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2241 BP; 552 A; 516 C; 561 G; 612 T; 0 other;
XX
Query Match 50.5%; Score 560; DB 22; Length 2241;
Best Local Similarity 99.7%; Pred. No. 1,1e-273;
Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGATCCTTCTGTGTAATCTGTCACTCTTATCTTTGAAAGAGATGCTGGAGATGCA 60
Db 365 ATGATCCTTCTGTGTAATCTGTCACTCTTATCTTTGAAAGAGATGCTGGAGATGCA 424
Qy 61 CAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGTGAATCTATTTAGAGCTCTC 120
Db 425 CAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGTGAATCTATTTAGAGCTCTC 484
Qy 121 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAGTTCATGAGAGAGAGTGTGGGAGTC 180
Db 485 TTTTCTGTTCAATCAGCAGCTACTGTGAGAGAGTTCATGAGAGAGAGTGTGGGAGTC 544
Qy 181 CGTGAACATATGAGCATTCAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 545 CGTGAACATATGAGCATTCAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 604
Qy 241 TCAGACCCCACTCTTGGCCCAATCACTAGCTGGCTGTGAATTAAGGATTCCTGCTGG 300
Db 605 TCAGACCCCACTCTTGGCCCAATCACTAGCTGGCTGTGAATTAAGGATTCCTGCTGG 664
Qy 301 CATTGGGCTGTGGCCCTAGAGAGAGCATTTAGATCATTAAGATTCCTCATTTCTTGG 360
Db 665 CATTGGGCTGTGGCCCTAGAGAGAGCATTTAGATCATTAAGATTCCTCATTTCTTGG 724
Qy 361 GAAGAGAAAGAGGCTGTGATATGCTCTGTGATGAGCTCTCTCTTCCGCTCCAG 420
Db 725 GAAGAGAAAGAGGCTGTGATATGCTCTGTGATGAGCTCTCTCTTCCGCTCCAG 784
Qy 421 AAGCCATAGTAGGGGTCAATGGGCTGTGTCAGTCTTTAGCCATTCAAGTCCAAAT 480
Db 785 AAGCCATAGTAGGGGTCAATGGGCTGTGTCAGTCTTTAGCCATTCAAGTCCAAAT 844
Qy 481 TTGCTCAGCTTTTCAACATACCTCAAGATTGCTTACGACCAACATCATGATCTGAAGT 540
Db 845 TTGCTCAGCTTTTCAACATACCTCAAGATTGCTTACGACCAACATCATGATCTGAAGT 904
Qy 541 GACAAAGCTCTGTCAAAATATTTCAAGAGGTTGTGCTTCAGATGCTCAGACGCAAG 600
Db 905 GACAAAGCTCTGTCAAAATATTTCAAGAGGTTGTGCTTCAGATGCTCAGACGCAAG 964
Qy 601 TCCATGCTGACATAGTGAAGAGGTACAACTGACCTATGTATCAGCCGTACACAGAA 660
Db 965 TCCATGCTGACATAGTGAAGAGGTACAACTGACCTATGTATCAGCCGTACACAGAA 1024
Qy 661 GG 662
Db 1025 GG 1026

RESULT 7
AAF29991
ID .AAF29991 standard; DNA; 2326 BP.
XX
AC AAF29991;
XX
DT 06-APR-2001 (first entry)
XX
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QY 1 ATGTCCTTCTGTGATCTGTCAAGTCTTACTTTTGAAGAAGATGTCGGGAGTGA 60
DB 365 ATGTCCTTCTGTGATCTGTCAAGTCTTACTTTTGAAGAAGATGTCGGGAGTGA 424
QY 61 CAGTCCAGTGAAGAGAGGAGTGTGGCTCACTGCTGGGTGACATCATTTATTTAGCTCTC 120
DB 425 CAGTCCAGTGAAGAGAGGAGTGTGGCTCACTGCTGGGTGACATCATTTATTTAGCTCTC 484
QY 121 TTTTCTGTTCATCAACAGCTTACTGTGGAAGATTTCATAGAGGAAGTGTGGGCGATC 180
DB 485 TTTTCTGTTCATCAACAGCTTACTGTGGAAGATTTCATAGAGGAAGTGTGGGCGATC 544
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGTGCTATACCTGGAAGGATCAAT 240
DB 545 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGTGCTATACCTGGAAGGATCAAT 604
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAATTAAGGAATTCCTGTGG 300
DB 605 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAATTAAGGAATTCCTGTGG 664
QY 301 CATTCGGCTGTGGCCCTTGAAGAGAGATTAAGATTCAATAGATTCCTCATTTCTTGG 360
DB 665 CATTCGGCTGTGGCCCTTGAAGAGAGATTAAGATTCAATAGATTCCTCATTTCTTGG 724
QY 361 GAAGAGGAAGAGGGCTTGTGATGCTGTGATGCTCTCTCTTCCCTCCGCTCCAG 420
DB 725 GAAGAGGAAGAGGGCTTGTGATGCTGTGATGCTCTCTCTCTTCCCTCCGCTCCAG 784
QY 421 AAGCCCATAGTAGAGGAGTCAATGAGGCTGTGATGCTCTCTCTTCCCTCCGCTCCAG 480
DB 785 AAGCCCATAGTAGAGGAGTCAATGAGGCTGTGATGCTCTCTCTTCCCTCCGCTCCAG 844
QY 481 TTGCTCAGTCTTTCATCAATCTCAATGCTTCACTCAGCAACCATCATGATCTGAGT 540
DB 845 TTGCTCAGTCTTTCATCAATCTCAATGCTTCACTCAGCAACCATCATGATCTGAGT 904
QY 541 GAAGAAGCTCTGTTCAAAATATTCATGAGGGTGTGGCTTCAGATGCTCAGAGGCAAG 600
DB 905 GAAGAAGCTCTGTTCAAAATATTCATGAGGGTGTGGCTTCAGATGCTCAGAGGCAAG 964
QY 601 TCCATGATGAGCAATAGTGAAGAGTGAACAATGAGCTATGATCAGCCGTACACAGAA 660
DB 965 TCCATGATGAGCAATAGTGAAGAGTGAACAATGAGCTATGATCAGCCGTACACAGAA 1024
QY 661 GCGAATATGAGAGAAAGTGGAGTGAAGCTTCAAAAGATATGTCAGCGAAGAGGAGAT 720
DB 1025 GCGAATATGAGAGAAAGTGGAGTGAAGCTTCAAAAGATATGTCAGCGAAGAGGAGAT 1084
QY 721 TGCATGCGCCACTCTTACAAAATCTACAGTATGAGAGGGAGAGAGCTTGTATAGCTG 780
DB 1085 TGCATGCGCCACTCTTACAAAATCTACAGTATGAGAGGGAGAGAGCTTGTATAGCTG 1144
QY 781 CTGAAGAAGCTCAACAAGTCACTTGGCCAAAGGCCGGGTGTGGCTTAATCTGTGAGGCG 840
DB 1145 CTGAAGAAGCTCAACAAGTCACTTGGCCAAAGGCCGGGTGTGGCTTAATCTGTGAGGCG 1204
QY 841 ATGACGCTGAGAGGTGTGCTGATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 900
DB 1205 ATGACGCTGAGAGGTGTGCTGATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 1264
QY 901 CTTCGGGAGAGGAAACAGATGCACTTATTTGAAGATTCAAAAGAAAGCATCTATGG 960
DB 1265 CTTCGGGAGAGGAAACAGATGCACTTATTTGAAGATTCAAAAGAAAGCATCTATGG 1324
QY 961 GAAGAAGAGAAAGATGCAAGGTGCTCTCTCAG 996
DB 1325 GAAGAAGAGAAAGATGCAAGGTGCTCTCTCAG 1360

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RESULT 5  
AAF29995  
ID AAF29995 standard; DNA; 2064 BP.

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XX AC AAF29995;
XX DT 06-APR-2001 (first entry)
XX DE Human GRMX-Ig DNA.
XX KM Human; metabotropic glutamate receptor; schizophrenia; GRMX;
XX KM Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX OS Homo sapiens.
XX PN M0200102566-A1.
XX PD 11-JAN-2001.
XX PF 27-JUN-2000; 2000MO-US17798.
XX PR 02-JUL-1999; 99US-0346326.
XX PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX PI Schwarz DA, Maki RA;
XX DR WPI; 2001-123112/13.
XX PT Novel metabotropic glutamate receptor for prevention, treatment of
XX PT conditions associated with undesirable glutamate levels, e.g.
XX PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
XX PT schizophrenia -
XX PS Claim 2; Fig 11; 59pp; English.
XX CC The present invention relates to human metabotropic glutamate
XX CC receptor. An agent that decreases expression or activity of the
XX CC metabotropic glutamate receptor is useful for treating schizophrenia.
XX CC Metabotropic glutamate receptor polynucleotides, polypeptides
XX CC are useful for treating diseases associated with undesirable
XX CC levels of glutamate, such as Alzheimer's disease, Parkinson's
XX CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX SQ Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other;

Query Match 72.9%; Score 809; DB 22; Length 2064;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 909; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTCCTTCTGTGATCTGTCAAGTCTTACTTTTGAAGAAGATGTCGGGAGTGA 60
DB 365 ATGTCCTTCTGTGATCTGTCAAGTCTTACTTTTGAAGAAGATGTCGGGAGTGA 424
QY 61 CAGTCCAGTGAAGAGAGGAGTGTGGCTCACTGCTGGGTGACATCATTTATTTAGCTCTC 120
DB 425 CAGTCCAGTGAAGAGAGGAGTGTGGCTCACTGCTGGGTGACATCATTTATTTAGCTCTC 484
QY 121 TTTTCTGTTCATCAACAGCTTACTGTGGAAGATTTCATAGAGGAAGTGTGGGCGATC 180
DB 485 TTTTCTGTTCATCAACAGCTTACTGTGGAAGATTTCATAGAGGAAGTGTGGGCGATC 544
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGTGCTATACCTGGAAGGATCAAT 240
DB 545 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGTGCTATACCTGGAAGGATCAAT 604
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAATTAAGGAATTCCTGTGG 300
DB 605 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAATTAAGGAATTCCTGTGG 664
QY 301 CATTCGGCTGTGGCCCTTGAAGAGAGATTAAGATTCAATAGATTCCTCATTTCTTGG 360
DB 665 CATTCGGCTGTGGCCCTTGAAGAGAGATTAAGATTCAATAGATTCCTCATTTCTTGG 724
QY 361 GAAGAAGAGAGGGCTTGTGATGCTGTGATGCTCTCTCTTCCCTCCGCTCCAG 420

```

PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 7; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;

Query Match: 90.8%; Score 1008; DB 22; Length 2172;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTTGATCCCTGTCAGTCTTACTTTTGAAGAAGATGCCGTGGAGTGA 60  
 DB 365 ATGGCTCTTCTGTTGATCCCTGTCAGTCTTACTTTTGAAGAAGATGCCGTGGAGTGA 424  
 QY 61 CAGTCCAGTGAAGAGAGGAGTGTGCTCAGATGCTGGGTGACATCATTTATTTAGAGCTCTC 120  
 DB 425 CAGTCCAGTGAAGAGAGGAGTGTGCTCAGATGCTGGGTGACATCATTTATTTAGAGCTCTC 484  
 QY 121 TTTTCTGTTTCATCACCAGCTTACTGTGAGCAGAAATTTCATGAGAGAGTGTGGGCAATC 180  
 DB 485 TTTTCTGTTTCATCACCAGCTTACTGTGAGCAGAAATTTCATGAGAGAGTGTGGGCAATC 544  
 QY 181 CGTGAACAGATGTGCTTCAAGAGTGTGAGCCCATCTGTCATTCCTTGAAGAGATCAAT 240  
 DB 545 CGTGAACAGATGTGCTTCAAGAGTGTGAGCCCATCTGTCATTCCTTGAAGAGATCAAT 604  
 QY 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGAGATTCCTGCTGG 300  
 DB 605 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGAGATTCCTGCTGG 664  
 QY 301 CATTCGGCTGTGGCTTGAAGCAGAGCATTTGATTAAGATTCCTCATTTCTTTCG 360  
 DB 665 CATTCGGCTGTGGCTTGAAGCAGAGCATTTGATTAAGATTCCTCATTTCTTTCG 724  
 QY 361 GAAAGAGAAAGAGGCTTGTATGCTCTGTGAGAGCTCTCTCTTCTTCCGCTCAAG 420  
 DB 725 GAAAGAGAAAGAGGCTTGTATGCTCTGTGAGAGCTCTCTCTTCTTCCGCTCAAG 784  
 QY 421 AAGGCCATGATGAGGAGTCTTGGGCTGTGCTTCAAGCTCTTATGACATTCAGGTCAGAAAT 480  
 DB 785 AAGGCCATGATGAGGAGTCTTGGGCTGTGCTTCAAGCTCTTATGACATTCAGGTCAGAAAT 844  
 QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATGATGATGAT 540  
 DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATGATGATGATGAT 904  
 QY 541 GACAGAGCTCTGTTCAAAATATTTTATGAGGGTGTGCTTCAAGTCTCAGAGGCAAG 600  
 DB 905 GACAGAGCTCTGTTCAAAATATTTTATGAGGGTGTGCTTCAAGTCTCAGAGGCAAG 964  
 QY 601 TCATGTGTGACATGAGAGAGGTATCAACTGACCTATGATGACGCGATACACAGAA 660  
 DB 965 TCATGTGTGACATGAGAGAGGTATCAACTGACCTATGATGACGCGATACACAGAA 1024  
 QY 661 GGCACATGATGAGAGAGGTGATGAGAGCTTCAAGATATGTCAGAGGAGAGGAT 720  
 DB 1025 GGCACATGATGAGAGAGGTGATGAGAGCTTCAAGATATGTCAGAGGAGAGGAT 1084  
 QY 721 TGCATGCGCCCACTTTTCAAAATCTACATGATGACAGGAGGACAGCTTGTATGATG 780  
 DB 1085 TGCATGCGCCCACTTTTCAAAATCTACATGATGACAGGAGGACAGCTTGTATGATGATG 1144  
 QY 781 CTGAAGAAGGTCACAGATGCTTGTGCCAAGGCCCGGGTGTGAGGCTTCTGTGAGAGGC 840

DB 1145 CTGAAGAAGGTCACAGATGCTTGTGCCAAGGCCCGGGTGTGAGGCTTCTGTGAGAGGC 1204  
 QY 841 ATGACGCTGAGAGGCTGTGATGAGCAGATGAGCCCTTGAGTCTTATGAGAGATTTCTG 900  
 DB 1205 ATGACGCTGAGAGGCTGTGATGAGCAGATGAGCCCGTGTGATGAGAGATTTCTG 1264  
 QY 901 CTTCTGGGAGAGGAGACAGATGCACTTATTTAGATGTCAAAGAACAGATCTATGG 960  
 DB 1265 CTTCTGGGAGAGGAGACAGATGCACTTATTTAGATGTCAAAGAACAGATCTATGG 1324  
 QY 961 GAAGACAGAAAGAAATATCCCAAGGCTCTTCTTCAAGGTTTGGAGACATATTACACAGA 1020  
 DB 1325 GAAGACAGAAAGAAATATCCCAAGGCTCTTCTTCAAGGTTTGGAGACATATTACACAGA 1384  
 QY 1021 AGTGAATCCGTGCTGTGACATGCCCCAGCCTCTTAATCTTGAAGCTCAGTTCAAGGCC 1080  
 DB 1385 AGTGAATCCGTGCTGTGACATGCCCCAGCCTCTTAATCTTGAAGCTCAGTTCAAGGCC 1444  
 QY 1081 ATCACTGGACTGAGGAGCAGGCTCATCTTA 1110  
 DB 1445 ATCACTGGACTGAGGAGCAGGCTCATCTTA 1474

RESULT 4  
 AAF29994  
 ID AAF29994 standard; DNA; 2149 BP.  
 XX  
 AC AAF29994;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMx-1f DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN W0200102566-A1.  
 PD 11-JAN-2001.  
 PF 27-JUN-2000; 2000MO-US17798.  
 XX  
 PR 02-JUL-1999; 99US-0346326.  
 XX  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PI Schwarz DA, Maki RA;  
 XX  
 DR WPI, 2001-123112/13.  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 9; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;

Query Match: 80.5%; Score 894; DB 22; Length 2149;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 994; Conservative 0; Mismatches 2; Indels 0; Gaps 0;







Query Match	100.0%	Score 1110;	DB 24;	Length 1823;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1110; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0
Query	1	ATGGCTCTTCTGTTGATCTCTGCACTCTTAACTTTGAAAGAGATGTCCTGGAGATGCA	60	
Db	4	ATGGCTCTTCTGTTGATCTCTGCACTCTTAACTTTGAAAGAGATGTCCTGGAGATGCA	63	
Query	61	CAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGGAGCATCTTAATTGAGCTTC	120	
Db	64	CAGTCCAGTGAAGAGAGGGGTGGTCTCACTGCTGGGAGCATCTTAATTGAGCTTC	123	
Query	121	TTTTCTGTTCACTACCAAGCTTACTGTGACGAAGTTTCATGAGAGAAAGTGGGGCAGTC	180	
Db	124	TTTTCTGTTCACTACCAAGCTTACTGTGACGAAGTTTCATGAGAGAAAGTGGGGCAGTC	183	
Query	181	CGTGAACAGTATGAGCATTCAGAGATGAGAGGCCATGCTGCATACCTCGAAGAGATCAAT	240	
Db	184	CGTGAACAGTATGAGCATTCAGAGATGAGAGGCCATGCTGCATACCTCGAAGAGATCAAT	243	
Query	241	TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGAGATGAAGGAATTCGCTGG	300	
Db	244	TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGAGATGAAGGAATTCGCTGG	303	
Query	301	CATTGGCTGTGGCCCTGAGAGAGCATTTGATTCATTAAGAGATTCCTCATTTCTTGG	360	
Db	304	CATTGGCTGTGGCCCTGAGAGAGCATTTGATTCATTAAGAGATTCCTCATTTCTTGG	363	
Query	361	GAAAGAGAAAGAGGCTTGATGCTCTGTGATGAGTGGCTCTCTCTTCTTCCGCTCAAG	420	

Db	364	GAAGAGGAAGAAGGAGCTTGATGCTCTGTGGATGGCTCTCTCTCTCCGCTCCAAAG	423
Qy	421	AAGCCCATAGAGGGCTCATTTGGGCTCTGGTTCCAGTCTTTAAGCATTCAGSTCCAAAT	480
Db	424	AAGCCCATATAGAGGGCTCATTTGGGCTCTGGTTCCAGTCTTTAAGCATTCAGSTCCAAAT	483
Qy	481	TTGCTCAGGCTTTTCAACATACCTCAGATTGCTTAACAGCAACATCATGATCTGAGT	540
Db	484	TTGCTCAGGCTTTTCAACATACCTCAGATTGCTTAACAGCAACATCATGATCTGAGT	543
Qy	541	GACAAAGCTCTGTTCAAAATATTCATAGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG	600
Db	544	GACAAAGCTCTGTTCAAAATATTCATAGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG	603
Qy	601	TCCATGGTGGACATATGTGAAGAGGTACACTGGAACCTATGTATACGCCCTACACAGAA	660
Db	604	TCCATGGTGGACATATGTGAAGAGGTACAACCTGGAACCTATGTATACGCCCTACACAGAA	663
Qy	661	GGCAACTATGAGAGAAATGGGATGGAAGCCCTTCAAGATATGTGAGGCAAGAGGATTT	720
Db	664	GGCAACTATGAGAGAAATGGGATGGAAGCCCTTCAAGATATGTGAGGCAAGAGGATTT	723
Qy	721	TGCATCGCCCACTCTTACAAATCTACATATGACAGGAGCAGAGCTTTGATTAAGCTG	780
Db	724	TGCATCGCCCACTCTTACAAATCTACATATGACAGGAGCAGAGCTTTGATTAAGCTG	783
Qy	781	CTGAAAGAGCTCACAGATCACTTGCCCAAGGCCCGGGTGTGAGCTTACTTGTGAGGGC	840
Db	784	CTGAAAGAGCTCACAGATCACTTGCCCAAGGCCCGGGTGTGAGCTTACTTGTGAGGGC	843
Qy	841	ATGACGGTGAAGGTCCTGCTGATGAGCCATAGAGGGCCCTGGGTCTATGTGGAGAAATTCGTG	900
Db	844	ATGACGGTGAAGGTCCTGCTGATGAGCCATAGAGGGCCCTGGGTCTATGTGGAGAAATTCGTG	903
Qy	901	CTTCTGGGCAAGGAGCAACAGATGCCATCTTATATGAGATCTTCAAGAAACAGCATCTTAAG	960
Db	904	CTTCTGGGCAAGGAGCAACAGATGCCATCTTATATGAGATCTTCAAGAAACAGCATCTTAAG	963
Qy	961	GAAGACAGAAAGAAATGCCAAGGTGCTTCTTCAAGGGTTTGGAGACATATTCACACAGA	1020
Db	964	GAAGACAGAAAGAAATGCCAAGGTGCTTCTTCAAGGGTTTGGAGACATATTCACACAGA	1023
Qy	1021	AGTGAATCCGTCGTCTGTGCACATGCCCCAGGCTCTGAAATCTAAGATCTCAGTTCAAGGCC	1080
Db	1024	AGTGAATCCGTCGTCTGTGCACATGCCCCAGGCTCTGAAATCTAAGATCTCAGTTCAAGGCC	1083
Qy	1081	ATCAGCTGGACTGAGGAGCAGGCTCATCTTAA	1110
Db	1084	ATCAGCTGGACTGAGGAGCAGGCTCATCTTAA	1113

RESULT 2

AA562274 standard; cDNA, 1788 BP.

AA562274;

14-FEB-2002 (first entry)

cdNA sequence #61 encoding novel human secreted protein.

Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antitubercular; hepatotropic; immunosuppressive; antirheumatic; ss.

Homo sapiens.

MO200177291-A2.

18-OCT-2001.





QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGTGAACAGATGGCATTCAGAGAGTGAAGCCATGTCATACCTCGAAGAAAGATCAAT 639  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 700 TCAGACCCCACTCTGGCCCAACATCACTGGGCTGTGAGATTAAGGAGCTCCTGCTGG 759  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 760 CATTGGCTGTGGCCCTGAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 819  
 QY 121 GluGluGluGluGluValCysSerValAspGlySerSerSerSerPheArgSerIle 140  
 DB 820 GAAGAGGAAGAAGGCTTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 879  
 QY 141 LysProIleValIleValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 880 AAGCCCATAGTAAAGGCGTCATTGGGCTGCTCCAGATTCCTAGCCATTCAGATTCAGAAAT 939  
 QY 161 LeuLeuGluLeuPheAsnIleProGlnIleAlaIleThrSerIleAlaThrIleMetAspLeuSer 180  
 DB 940 TTGCTCCAGCTTTTCAACATACCTCAGATTCCTTACTCAGACCAACAGCATGATCTGAGT 999  
 QY 181 AspLysThrLeuPheLeuPheLysTyrPheMetArgValValProSerAspAlaGlnIleAlaArg 200  
 DB 1000 GACAAAGCTCTGTCAAAATTTTCATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1059  
 QY 201 SerMetValAspIleValIleValIleValIleValIleValIleValIleValIleValIle 220  
 DB 1060 GCCATGGTGGACATAGAGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 1119  
 QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLeuAspMetSerAlaIleGluGlyIle 240  
 DB 1120 GGCACCTATGGAAGAAAGTGGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 1179  
 QY 241 CysAlaAlaHisSerTyrIleValIleValIleValIleValIleValIleValIleValIleVal 260  
 DB 1180 TGATGCGCCCACTCTTCAAAATTTTCATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1239  
 QY 261 LeuLeuValLeuLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGluGly 280  
 DB 1240 CTGAAGAGCTCAAGATTCATCCCAAGCCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1299  
 QY 281 MetThrValIleGlyIleLeuMetAlaMetArgIleGluGlyIleValIleGluPheLeu 300  
 DB 1300 ATGACGCTGAGAGCTGT 1359  
 QY 301 LeuLeuGlyValArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrp 320  
 DB 1360 CTTCTGGGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
 QY 321 GluAspArgArgIleCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 1381 GCTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1410  
 QY 340 GSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 DB 1411 CAGCGAGAGAGCTGT 1468  
 RESULT 15  
 AAD05030 standard; mRNA; 4207 BP.  
 ID AAD05030;  
 AC AAD05030;  
 XX  
 XX 17-JUL-2001 (first entry)  
 XX Human metabotropic glutamate receptor, mGluR5A mRNA.  
 DE Human metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KM Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KW Human; central nervous system; CNS; presynaptic release; neurotransmitter;

KW postsynaptic sensitivity; glutamate excitation; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 PH CDS 460..4002  
 FT /\*tag= a  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mGluR5A"  
 XX  
 XX US6211353-B1.  
 PN  
 XX  
 XX 03-APR-2001.  
 PD  
 XX  
 XX 07-JUN-1996; 96US-0660148.  
 PF  
 XX  
 XX 29-JUL-1994; 94US-0282853.  
 PR  
 XX  
 XX (BLIL ) LILLY & CO ELI.  
 PA  
 XX  
 XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;  
 PI  
 XX  
 XX WPI, 2001-289639/30.  
 DR  
 XX P-PSDB; AAB01156.  
 XX  
 XX  
 PT New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptors, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 PS  
 XX  
 XX Claim 2; Column 43-46; 53pp; English.  
 CC  
 XX The present sequence is a mRNA encoding human metabotropic glutamate  
 CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in  
 CC the central nervous system (CNS), mediates excitatory pathway in  
 CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
 CC the receptors that respond to glutamate are EAA receptors. The receptors  
 CC are useful for modulating the presynaptic release of glutamate and the  
 CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
 XX  
 XX  
 SQ Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;  
 Alignment Scores:  
 Pred. No.: 1.5e-158 Length: 4207  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.228 Conservative: 8  
 Best Local Similarity: 85.008 Mismatches: 22  
 Query Match: 79.264 Indels: 24  
 DB: 22 Gaps: 2  
 US-10-027-923-2 (1-369) x AAD05030 (1-4207)  
 QY 1 MetValLeuLeuLeuIleLeuSerValLeuLeuLeuLeuGluAspValIleArgIleSerAla 20  
 DB 460 AUGGUCUCUCUGUGAUCUCUGACAGUCUCUUAUUAAGAAAGAUUCUGGUGGAGUUGCA 519  
 QY 21 GlnSerSerGluArgArgValValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 520 CAGUCCAGUGAGAGAGGAGGUGUGUGUCUACAUUGCCGAGUACUUAUUGGAGUCUCC 579  
 QY 41 PheSerValHisHisGlnProThrValAspGluValHisGluIleArgLysCysGlyAlaVal 60  
 DB 580 UUUUCUGUUCACUACACAGCCUACUGUGACAAAGUUCAGAGAGAGAGAGUGUGGCGGUC 639  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGUGAAGCAUAGUGCAUUCAGAGAGAGGCGCAUGCCUACUACCCUGGAGAGAGUACA 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 700 UCAGACCCCACTCTGGCCCAACATCACTGGGCTGTGAGATTAAGGAGCTCCTGCTGG 759  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120



US-10-027-923-2 (1-369) x ACA56535 (1-4078)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValArgGlySerAla 20  
 DB 151 ATGGTCTCTGTTGATCTGTCAGTCTTTCATTTGAAAGAAAGATGCTCGGAGAGTGA 210  
 QY 21 GlnSerSerGluArgArgValAlaAlaHISmetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 211 CAGTCCAGTGAAGAGAGGGGTGGTGGCTCAATGCCGGGTGACATCATTTATGAGGCTCTC 270  
 QY 41 PheSerValHISHisGlnProThrValAspGluValHISGluArgGlyCysGlyAlaVal 60  
 DB 271 TTTTCTGTTTCATCAGCAGCTTCTGTGACAAAGTTTCATAGAGAAAGTGTGGGGGGTTC 330  
 QY 61 ArgGluGlnThrGlyIleGlnArgValGluAlaMetLeuHISThrLeuGluArgGlyIleAsn 80  
 DB 331 CGTGAACAGATGACATTCAGAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 390  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 391 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGTAAAGGAGCTCTGCTGG 450  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGlnPheIleArgAspSerLeuIleSerSer 120  
 DB 451 CATTCGGCTGTGGCCCTAGAGCAGACATTCAGTTCAATAGAGATTCCTCATTTCTTCA 510  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerIys 140  
 DB 511 GAAAGAGAGAGAGAGGCTGTGACCTGTGTGATGAGTCCCTCTCTCTCTCTCTCCAG 570  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 571 AAGCCCATGTAAGGGGTGATGGGCTGGCTCCAGTTCTGTACCATTCAGTCCAGAAAT 630  
 QY 161 LeuLeuGlnLeuPheLeuHISProGlnIleAlaIleTyrSerAlaThrIleMetAspLeuSer 180  
 DB 631 TTGCTCAGCTTTTCAACATCACTCAGATTCCTTACTCAGCAACAGCATGATCTGAGT 690  
 QY 181 AspLeuThrLeuPheLeuTyrPheMetArgValValProSerAspAlaGlnGlnAlaArg 200  
 DB 691 GAAAGAACTCTGTCAAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCGAGAAAG 750  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHISThrGlu 220  
 DB 751 GCATGTGTGACATTAAGTGAAGAGGTACATGACCTATATTAACCCGTCGACACAGAA 810  
 QY 221 GlyAsnTrpGlyGluSerGlyMetGluAlaPheLeuAspMetSerAlaIleGluGlyIle 240  
 DB 811 GGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAAGGAAAGAGGAGATT 870  
 QY 241 CysIleAlaHISerTyrIleTyrSerAsnAlaGlyGluGlnSerPheAspLeu 260  
 DB 871 TGCATGCCCACTTACAAATCTACATGATGAGGGAGAGAGAGCTTTGATAGCTG 930  
 QY 261 LeuIleValLeuThrSerHISLeuProIleValAlaArgValAlaIleTyrPheCysGluGly 280  
 DB 931 CTGAAGAAAGCTCAAGAGTCACTTGCCCAAGGCCCGGGTGTGGCTCTCTGTGAGGGC 990  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 991 ATGACGGTGAAGAGTCTGCTGATGGCCATGAGCGCTGGGTCTAGGGGAGAAATTTCTG 1050  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerTyrAsnSerIleLeuTrp 320  
 DB 1051 CTTCTGGGAGAGTATGAGC-----TGG 1071  
 QY 321 GluAspArgArgGlyCysGlnIleArgPheLeuGlnIlePheGlyAspIleLeuHISArg 340  
 DB 1072 GCTGACAGGTATATGATGACAG-----ATGATAT 1101  
 QY 340 gSerGluSerValLeuLeuHISMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 DB 1102 CAGCGAAGAGCTGTGTGTGATCACAATCAAGCTCAATCTCCGATGTCAAGTGT 1159

# RESULT 13

AAD04990 ID AAD04990 standard; cDNA; 4207 BP.

AC AAD04990;

DT 17-JUL-2001 (first entry)

DE Human metabotropic glutamate receptor; mGluR5A cDNA mutant.

KW Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid; EAA; central nervous system; CNS; presynaptic release; neurotransmitter; postsynaptic sensitivity; glutamate excitation; mutant; ss.

OS Homo sapiens.

OS Synthetic.

FT Key Location/Qualifiers

FT mutation replace (416, T) /\*tag= a

FT mutation replace (425, A) /\*tag= b

PN US6211353-B1.

PD 03-APR-2001.

PP 07-JUN-1996; 96US-0660148.

PP 29-JUL-1994; 94US-0282853.

PA (BLU ) DINDY-6-66-BLZ.

PI Burnett JP, Wayne NG, Sharp RL, Snyder YM;

DR WPI; 2001-289639/30.

PT New isolated nucleic acids for producing human metabotropic glutamate receptors, which are useful for modulating the presynaptic release of

PT glutamate or the postsynaptic sensitivity of the neuronal cell to

PS disclosure; Column -; 53pp; English.

CC The present sequence is a cDNA mutant encoding human metabotropic

CC glutamate receptor, mGluR5A. L-glutamate, the most abundant

CC neurotransmitter in the central nervous system (CNS), mediates excitatory

CC pathway in mammals. L-glutamate is referred to as excitatory amino acid

CC (EAA) and the receptors that respond to glutamate are EAA receptors. The

CC receptors are useful for modulating the presynaptic release of glutamate

CC and the postsynaptic sensitivity of the neuronal cell to glutamate

CC excitation.

CC Note: The present sequence is not shown in the specification, but is

CC derived from the sequence referred as SEQ ID NO.1, shown in column

CC 59-68 (AAD05029) of the specification.

XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;

SQ Alignment Scores:

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuGluAspValArgGlySerAla 20

DB 460 ATGGTCTCTGTTGATCTGTCAGTCTTTCATTTGAAAGAAAGATGCTCGGAGAGTGA 519

Query Match: 79.26% Indels: 24  
 DB: 22 Gaps: 2  
 US-10-027-923-2 (1-369) x AAC85787 (1-3129)

QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLeuValArgGlySerAla 20  
 DB 1 ATGGTCTTCTGTGATCCGTCAAGTCTTCTTTGAAAGAAATGTCCTGGAGTGA 60  
 QY 21 GlnSerSerGluArgValValAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 61 CAGTCCAGTGAAGAGGGGTGGTGGCTCACATGCCGGGTACATCATTTATGAGCTTC 120  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisIleGluArgGlyValAla 60  
 DB 121 TTTTCTGTTCATACCAAGCTTCTGTGACAAAGTTATAGAGAGAGTGGGGGTG 180  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 181 CGTGAACAGTATGGCATTCAGAGAGTGAAGGCCATGTGTGATCCCTGGAAAGATCAAT 240  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGTGTGAGATTAAGGAGCTCTGGTGG 300  
 QY 101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerIleSerSer 120  
 DB 301 CATTCGGCTGTGGCCCTAGAGAGCATTGAGTTCAATTAAGATTCCTCATTTCTTCA 360  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIle 140  
 DB 361 GAAGAGAAAGAGCTTGTGTAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValAsn 160  
 DB 421 AACCCCATGATAGGGGTGATGGGCTGGCTCCAGTTCTGTAGCATTCAGTCCAGAAAT 480  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerIleAspIleMetAspLeuSer 180  
 DB 481 TTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACACACACAGCATGATGTGAGT 540  
 QY 181 AspLeuThrLeuPheLeuTyrPheMetArgValValProSerAspAlaGlnAlaArg 200  
 DB 541 GACAAAGCTGTGTTCAAATTTTCATGAGGTTGTGCTTCAGATGCTCAGAGGCAAG 600  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 DB 601 GCCATGTGTGACATAGTGAAGAGGTACACTGACCTATGTATCAGCCGTGCACACAGAA 660  
 QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLeuAspMetSerAlaValGluGlyIle 240  
 DB 661 GGCAACTATGAGAAAGTGGATGGAAGCCCTTCAAAATATGTACAGGAAGAAAGGATTT 720  
 QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGlnSerPheAspIleValLeu 260  
 DB 721 TGCATGCCCACTTTCACAAATTTACATGATGACAGGAGAGAGCTTGTATAGCTG 780  
 QY 261 LeuIleValLeuThrSerHisLeuProGlyAlaArgValAlaTyrPheCysGlyGly 280  
 DB 781 CTCAAGAGAGCTCAAGTCACTTGGCCCAAGGCCGGGTGGTGGCTCTCTGTGAGGGC 840  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuValGlyGluPheLeu 300  
 DB 841 ATGACGGTGAAGGTGTGTGATGTGATGAGGCGCTGGGTCTTACGGGAGAAATTTCTG 900  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleValSerIleLeuTrp 320  
 DB 901 CTTCTGGGAGTATGGC-----TGG 921  
 QY 321 GluAspArgArgIleCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 922 GCTGACAGGTATGATGTGACAG-----ATGATAT 951

QY 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 DB 952 CACGCAAGAGCTGT 1009

RESULT 12  
 ID ACAS6535 standard; cDNA; 4078 BP.  
 ACAS6535;  
 06-JUN-2003 (first entry)  
 Human signalling pathway polynucleotide probe SEQ ID NO 1133.  
 Human; probe; ss; array element; Parkinson's disease;  
 signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 Homo sapiens.  
 US6500938-B1.  
 31-DEC-2002.  
 30-JAN-1998; 98US-0016434.  
 30-JUN-1998; 98US-0016434.  
 (INCYTE GENOMICS INC.  
 An-Young J, Sellhammer JJ;  
 WPI; 2003-352189/33.  
 Combination of polynucleotide probes, useful as array elements in a  
 microarray for monitoring the expression of a number of target  
 polynucleotides -  
 Claim 1, SEQ ID NO 1133; 65pp; English.  
 The invention relates to a combination which comprises a number of  
 polynucleotide probes comprising a sequence selected from one of the 1490  
 sequences mentioned in the specification. The combination is useful as an  
 array element in a microarray for monitoring the expression of a number  
 of target polynucleotides. The microarray is particularly useful in the  
 diagnosis and treatment of cancer and immunopathology and neuropathology.  
 The microarray is useful in diagnostics and treatment regimens, drug  
 discovery and development, toxicological and carcinogenicity studies,  
 forensics and pharmacogenomics. The microarray is also useful for  
 monitoring progression of diseases and for developing sophisticated  
 profiles for the effects of currently available therapeutic drugs. The  
 combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 and genomic fragments and in research and diagnostic applications. The  
 array can detect changes in expression in a large number of genes coding  
 for different signalling pathway populations which can be used to diagnose  
 various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 and Parkinson's disease. The present sequence represents a polynucleotide  
 probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?docId=6500938B1.  
 XX  
 SQ Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;

Alignment Scores:  
 Pred. No.: 1,43e-158 Length: 4078  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 Gaps: 2



CC or modulate activity of mGluR are useful for diagnosing or treating  
CC neurological disorders, e.g. as anticonvulsants, neuroprotectants,  
CC analgesics, cognitive enhancers and muscle relaxants.  
xx

**SQ** Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;

### Alignment Scores:

Pred. No.:	8.2e-159	Length:	2826
Score:	1484.50	Matches:	306
Percent Similarity:	87.22%	Conservative:	8
Best Local Similarity:	85.00%	Mismatches:	22
Query Match:	79.26%	Indels:	24
DB:	22	Gaps:	2

US-10-027-923-2 (1-369) x AAC85785 (1-2826)

Qy	1	MeValLeuLeuLeuLeuLeuSerValLeuLeuLeuValArgG1SerLa	20
Db	1	ATGGTCTTCTGTGATCCTGCTCAAGCTTACTTTTGAAGAAGATGTCCTGGAGATGCA	60
Qy	21	GlInSeSerG1uArgArValAlaAh1smetLeuG1yAspLe1e1eG1yAlaLeu	40
Db	61	CAGTCCAGTGAAGAGAGGGGTGGGTGCCTCAATGCCGGGTGACATATTATTTAGAGCTTC	120
Qy	41	PhSeSerValAh1sh1eG1nProThrValLaapG1uValH1eG1uArgG1yCyG1yAlaVal	60
Db	121	TTTTCTGTTTATACCAAGCCTACTGTGCAAAAGTTCAAGAGGAAGATGTGGGGCGGTC	180
Qy	61	ArgG1uG1nTyrG1y1LeG1nArgValG1uAla1smetLeuH1eThLeuG1uArg1Leasn	80
Db	181	CGTGAACAGTATGGATCTTACAGAGAGTGGAGGCCATGTCTGCATACCTCTGAAAGATCAAT	240
Qy	81	Se7AspProThrLeuLeuProAsn1eThrLeuG1yCyG1u1LaArgAspSerCySTp	100
Db	241	TCAGACCCCAACACTTCTTGCCCAACATCAACATCGGGCTGTGAATTAAGGACTCTCTGGCG	300
Qy	101	HiSeSerAlaValAlaLeuG1uG1nSer1LeG1uPhe1LeArgAspSerLeu1SeSer	120
Db	301	CATTCCGGCTGTGGCCTTAGACAGACATTTGAGTTCAATAGAGATTCCTCATTTCTTCA	360
Qy	121	Gl1uG1uG1uG1uG1yLeuValCySerValaAspG1ySerSerSerPheArgSerLyS	140
Db	361	GAAGAGGAAGAAGGCTTGTGACGTGTGTGGATGGCTCCTCTCTTCCCTCCGCTCCAAG	420
Qy	141	LysPro1LeValAG1yAla1LeG1yProG1ySerSerSerSerLeuAla1LeG1nValG1asn	160
Db	421	AMGCCCCATGTAAGGGCTATGGGGCTGGCTCAAGTCTGTAAGCCATTCAGAGTCCAGAT	480
Qy	161	LeuLeuG1nLeuPheAsn1LeProG1n1LeAla1TyrSerAla1th1LeMeCAspLeuSer	180
Db	481	TTGCTCAGCTTTTCAACATACCTCAGATTGTTACTCAGAACCAAGCATGGATCTGAGT	540
Qy	181	AspLySThrLeuPheLyS1TyrPheMetArgValValProSerAspAlaG1nG1nAlaArg	200
Db	541	GACAAACACTGTCTCAAAATATTTCATGAAGGTGTGGCTTCAGAGCTCAACAGCAAG	600
Qy	201	SeMeCValAsp1LeValLySArG1yAsn1PThrTyrValaSerAlaValAh1eThnG1u	220
Db	601	GCCATGGTGAACATAGTGAAGAGCTACACTGACCTATGTAACGCCGTGCACACAGAA	660
Qy	221	GlYAsnTyrG1yG1uSeSerG1yMetG1uAlaPheLySAspMetSerAlaLyG1uG1y1Le	240
Db	661	GGCAACCTATGAGAAATGGAGATGGAAGCCTTCAAAAGATATGTACGCAAGAGAGGAGATT	720
Qy	241	Cys1LeAlaAh1SeSerTyrLyS1LeTyrSerAsnAlaG1yG1uG1nSerPheAspLyLeu	260
Db	721	TGATGGCCCACTTTACAAAATCTACAGTAATGCAAGGAGACAGAGCTTTGATTAACCTG	780
Qy	261	LeuLyG1yLeuThSer1Se1LeuProLySAlaArGValAla1TyrPheCyG1uG1y	280
Db	781	CTGAADAACCTCAACAGTCACTTGGCCCAAGGCCCGGGTGTGGCTGTTCTGTGAAGGC	840
Qy	281	MetThrValArgG1yLeuLeuMetAlaMetArgLeuG1yLeuValG1yG1uPheLeu	300

```

Db      841 ATGACGGGTGAGAGCTTCTGCTGATGGCCATGAGGCGCTGGGGTCTTAGCGGGAGAAATTTCG 3
Oy      301 LeuGluGlyArgGluProAspAlaIlePheIleGluIleSerIysAsnSerIleLeuTyr 3
Db      901 CTTCTGGGCGAGTGAATGCG-----TGG 9
Oy      321 GluAspArgArgIysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisar 3
Db      922 GCTACACAGGATATGATGTGACAG-----ATGCATAT 9
Oy      340 GSeGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359
Db      952 CAGCGAAGAGCTGTTGGTGGCATTCAATCAATCAAGCTCCAAATCTCCCATGTCAAGTGGT 100
RESULT 11
AAC85787
ID AAC85787 standard; cDNA; 3129 BP.
XX
XX AAC85787;
XX
XX 18-JUN-2001 (first entry)
DE cDNA encoding chimeric receptor containing hmglur5d portion.
XX
XX Human; metabotropic glutamate receptor; mglur; splice variant;
XX mglur3; G-protein-coupled receptor; glutamate; neurological disorder;
XX anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;
XX muscle relaxant; calcium receptor; CaR; mglur5d; ss.
XX
XX OS Chimeric - Homo sapiens.
XX
XX WO200130829-A1.
XX
XX 03-MAY-2001.
XX
XX 25-OCT-2000; 2000MO-US29356.
XX
XX 25-OCT-1999; 99US-0161481.
XX
XX 24-OCT-2000; 2000US-0695481.
XX
XX (NPS)- NPS PHARM INC.
XX
XX Krapcho K, Stormann T, Levinthal C, Hammerland L, Storjohann L,
XX
XX WPI; 2001-308615/32.
XX
XX P-PSDB; AAB47219.
XX
XX New nucleic acid encoding an isoform of human metabotropic glutamate
XX receptor, for identifying potential therapeutic agents for neurological
XX disease
XX
XX Claim 18; Page 70-75; 86pp; English.
XX
XX This sequence encodes a chimeric receptor comprising the intracellular
XX cytoplasmic tail of the human calcium receptor (CaR) and the extra-
XX cellular and seven transmembrane domains of the human metabotropic
XX glutamate receptor (mglur) splice variant of human metabotropic
XX glutamate receptor 5 (mglur5), mglur5d. mglur's are G-protein-coupled
XX receptors capable of activating a variety of intracellular second
XX messenger systems following the binding of glutamate. Recombinant
XX mglur5d DNA and compounds that bind to, or modulate activity of it
XX are useful for diagnosing or treating neurological disorders, e.g.,
XX as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers
XX and muscle relaxants.
XX
XX Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;
XX
Alignment Scores:
Pred. No.: 9,57e-159 Length: 3129
Score: 1484,50 Matches: 306
Percent Similarity: 87,22% Conservative: 8
Best Local Similarity: 85,00% Mismatches: 22

```





DE Human GRMx-ID DNA.  
XX Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
XX Homo sapiens;  
XX MO200102566-A1.  
XX 11-JAN-2001.  
XX 27-JUN-2000; 2000MO-US17798.  
XX 02-JUL-1999; 99US-0346326.  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX Schwarz DA, Maki RA;  
XX MPI; 2001-123112/13.  
XX Novel metabotropic glutamate receptor for prevention, treatment of  
PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
PT schizophrenia -  
XX Claim 2; Fig 6; 59pp; English.  
XX The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia.  
CC Metabotropic glutamate receptor polynucleotides, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.  
XX Sequence 2241 BP; 552 A; 516 C; 561 G; 612 T; 0 other;  
SQ  
Query Match 76.2%; Score 1389.6; DB 22; Length 2241;  
Best Local Similarity 85.4%; Pred. No. 0;  
Matches 1697; Conservative 1; Mismatches 5; Indels 285; Gaps 2;  
QY 1 AAAATGTCCTTCTGTTGATCTGTCAGTCTTACTTTGAAAGAAATGCCGGAGT 60  
DB 362 AAAATGTCCTTCTGTTGATCTGTCAGTCTTACTTTGAAAGAAATGCCGGAGT 421  
QY 61 GCACAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 120  
DB 422 GCACAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 481  
QY 121 CTCTTTCTGTTGATCTGTCAGTCTTACTTTGAAAGAAATGCCGGAGT 180  
DB 482 CTCTTTCTGTTGATCTGTCAGTCTTACTTTGAAAGAAATGCCGGAGT 541  
QY 181 GTCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 240  
DB 542 GTCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 601  
QY 241 AATTGACAGCCACACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 300  
DB 602 AATTGACAGCCACACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 661  
QY 301 TGGCATTCGGCTGTGGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGT 360  
DB 662 TGGCATTCGGCTGTGGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGT 721  
QY 361 TCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 420  
DB 722 TCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 781  
QY 421 AAGAGCCCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 480  
DB 782 AAGAGCCCATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 841

QY 481 AATTGCTCCAGCTTTTCAACATACCTGATGTTGCTTACTCAGCAACCATCATGATCTG 540  
DB 842 AATTGCTCCAGCTTTTCAACATACCTGATGTTGCTTACTCAGCAACCATCATGATCTG 901  
QY 541 AGTGAACAAGACTCTGTTCAAAATATTTTCATGAGAGGTTGTCCTTCAGATCTCAGCAGCA 600  
DB 902 AGTGAACAAGACTCTGTTCAAAATATTTTCATGAGAGGTTGTCCTTCAGATCTCAGCAGCA 961  
QY 601 AGTTCATGTTGACATGATGAAGAGTCAACTGGAACCTATGATATCAGCCGATACACCA 660  
DB 962 AGTTCATGTTGACATGATGAAGAGTCAACTGGAACCTATGATATCAGCCGATACACCA 1021  
QY 661 GA----- 662  
DB 1022 GAAGTTCAAGCTATTCTATGCTTCAGCTCCAGAGAGACTAGGCTGCTTCAACTCT 1081  
QY 663 ----- 662  
DB 1082 TGGCTCAAGTATGCTGCTGTTGGCCTTCCAAATTTGCTGGGATTTATGGGATGAGCC 1141  
QY 663 -----A 663  
DB 1142 ACCACAGCACCCGCGCAGTGCAGCATCTTAGAACCTTGTAGAGTCTTGTGATTTTAA 1201  
QY 664 GCGAATATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAGGAGAGAGAGATTT 723  
DB 1202 GCGAATATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAGGAGAGAGAGATTT 1261  
QY 724 TGCATGCCCACTCTTACAAAATCTACAGTAAATGACAGGAGAGAGAGAGAGT 783  
DB 1262 TGCATGCCCACTCTTACAAAATCTACAGTAAATGACAGGAGAGAGAGAGT 1321  
QY 784 CTGAAGAAGTCAAGATGACTTGGCCCAAGGCGCGGAGTGTGCTTCTGTGAGGCG 843  
DB 1322 CTGAAGAAGTCAAGATGACTTGGCCCAAGGCGCGGAGTGTGCTTCTGTGAGGCG 1381  
QY 844 ATGAGGTGAGAGAGTGTGCTGATGAGGCTGATGAGGCGCTGGGTCTAGGGAGAAATTTCTG 903  
DB 1382 ATGAGGTGAGAGAGTGTGCTGATGAGGCTGATGAGGCGCTGGGTCTAGGGAGAAATTTCTG 1441  
QY 904 CTTCTGGGAGGAGAACAGATGCTATTTATGAGATCTCAAGATCTCAAGATCTATG 963  
DB 1442 CTTCTGGG----- 1449  
QY 964 GAAAGCAAGAAATATCCAAAGTCCCTTCCTTCAAGGTTTGGAGACATATTAACACGA 1023  
DB 1450 -----CAGA 1453  
QY 1024 AGTGAATCCGTGCTGTCGACATGCCCAGGCTCTGAATCTAGAGCTCAGTCAAGGCCC 1083  
DB 1454 AGTGAATCCGTGCTGTCGACATGCCCAGGCTCTGAATCTAGAGCTCAGTCAAGGCCC 1513  
QY 1084 ATCACTGSACTGAGGAGACAGGCTCATCTAATTTCTGAGTGAATTAATCTGCTGAATTAAT 1143  
DB 1514 ATCACTGSACTGAGGAGACAGGCTCATCTAATTTCTGAGTGAATTAATCTGCTGAATTAAT 1573  
QY 1144 GAAGCAACAGTCATATCTTGTATGAGATTTGAGAGCAATTTGTATTTGATGTGAC 1203  
DB 1574 GAAGCAACAGTCATATCTTGTATGAGATTTGAGAGCAATTTGTATTTGATGTGAC 1633  
QY 1204 CGTCAAAATGCGCCCATATATCATCTGCAACACCTTCAAGTTTCTTGGATGGGGTCTCAG 1263  
DB 1634 CGTCAAAATGCGCCCATATATCATCTGCAACACCTTCAAGTTTCTTGGATGGGGTCTCAG 1693  
QY 1264 ACTTCACTCTGCGAAGTATTAATCTGAGAGTCCATGTTGGGAGACTTGTGAATTTGGGCT 1323  
DB 1694 ACTTCACTCTGCGAAGTATTAATCTGAGAGTCCATGTTGGGAGACTTGTGAATTTGGGCT 1753  
QY 1324 TTCGGTGTGTAATTAAGTATCTGAAAGGAGAGATCAAGATGAGCAATATATATGAGAG 1383  
DB 1754 TTCGGTGTGTAATTAAGTATCTGAAAGGAGAGATCAAGATGAGCAATATATATGAGAG 1813

OY	181	GTCCGCGTGAACAGTATATGGCATTTGAGAGAGTGGAGGGCCATGCTGTCATATACCTGTGAAGAAGATC	240
Db	542	GTCCGTGTAACAGTATATGGCATTTGAGAGAGTGGAGGGCCATGCTGTCATATACCTGTGAAGAAGATC	601
OY	241	AATTGACAGCCCACTCTTGTGCCAATCACTGAGCTGGCTGTGAGATTAAGGGATTCTGCG	300
Db	602	AATTGACAGCCCACTCTTGTGCCAATCACTGAGCTGGCTGTGAGATTAAGGGATTCTGCG	661
OY	301	TGGCATTTGGGCTGTGGCCCTTAAGCAAGCATTTGAGTTGATTAAGAGATTCCCTCATTTCT	360
Db	662	TGGCATTTGGGCTGTGGCCCTTAAGCAAGCATTTGAGTTGATTAAGAGATTCCCTCATTTCT	721
OY	361	TCGGAAAGAGAAAGAGGGCTGTGATATGCTGTGAGATAGGTCCTCTCTTCTTCCGCTCC	420
Db	722	TCGGAAAGAGAAAGAGGGCTGTGATATGCTGTGAGATAGGTCCTCTCTTCTTCCGCTCC	781
OY	421	AAGAAGCCCATATGATAGGGGTCAATTGGGCGTGGTCCAGTTCTTTAGSCATTAGGGTCAG	480
Db	782	AAGAAGCCCATATGATAGGGGTCAATTGGGCGTGGTCCAGTTCTTTAGSCATTAGGGTCAG	841
OY	481	AATTGTCTCAGCTTTTCAACATACCTCAGATGCTTACTGACAAACATCAATGATCTTG	540
Db	842	AATTGTCTCAGCTTTTCAACATACCTCAGATGCTTACTGACAAACATCAATGATCTTG	901
OY	541	AGTGAAGAAGCTCTGTTCAAAATTTCTATGAGGGTGTGGCTTCAAGATGCTCAGACAGCA	600
Db	902	AGTGAAGAAGCTCTGTTCAAAATTTCTATGAGGGTGTGGCTTCAAGATGCTCAGACAGCA	961
OY	601	AGGTCATATGTGAGCATATGTGAAGAGGTACATGCACTGATATGTATCAGCCGTACACACA	660
Db	962	AGGTCATATGTGAGCATATGTGAAGAGGTACATGCACTGATATGTATCAGCCGTACACACA	1021
OY	661	GA-----	662
Db	1022	GAAAGACAGCTAATTGTGAGGAAGATTGGCTACAAAGTGGACAGAAACTGATCTTACTAC	1081
OY	663	-----	662
Db	1082	AAATGAAAATGCGCAGTTTCTATATGTATACCCATAAATGATGATATATCTTAAGAT	1141
OY	663	-----	662
Db	1142	ATATATGACGAATATGCTGATGAAATGAAGGCAATGTGATGCCAAATATCAATCATATCAAT	1201
OY	663	-----	662
Db	1202	TGTCTAATGACAGACAGAAATTTTGAGGTTCAAGCTATTTCTATGCTCAGGCTCCAGAG	1261
OY	663	-----	662
Db	1262	AGCTAGGCTGTGCTTCAACTCTTGGCTCAAGTGAATGCTGTGGCTTTGGCCTTCCAAAT	1321
OY	663	-----	662
Db	1322	GCTGGGATTTATGGGCAATGACCAACACAGCACCCGGCCAGTGCAGATCTTAAACATCTC	1381
OY	663	-----	701
Db	1382	TTGAGGTGCTTCTGATTTTAAAGGCACTATGAGAAATGGGATGAGAGCCTTCAAGAA	1441
OY	702	TATGTCAAGCAGAAAGGAATTTTGATGCGCCACTTTACAAATCTTACAGTAAATGACAG	761
Db	1442	TATGTCAAGCAGAAAGGAATTTTGATGCGCCACTTTACAAATCTTACAGTAAATGACAG	1501
OY	762	GGAGCAGAGCTTTGATTAAGCTGTGTAAGAGAGCTCAAGTCACTTGTCCCAAGGCCGGGT	821
Db	1502	GGAGCAGAGCTTTGATTAAGCTGTGTAAGAGAGCTCAAGTCACTTGTCCCAAGGCCGGGT	1561
OY	822	GGTGGCCCTACTTCTGTGAGGGCAGACGGGTGAGAGGTGTGCTGATATGGCATGAGAGCGCT	881
Db	1562	GGTGGCCCTACTTCTGTGAGGGCAGACGGGTGAGAGGTGTGCTGATATGGCATGAGAGCGCT	1621

QY	882	GGGCTGAGTGGAGAAATTTCTGCTTCGGGACAGGAACCAATGCAATCTTTATTGAAAT	941
Db	1632	GGGCTGAGTGGAGAAATTTCTGCTTCGGGACAGGAACCAATGCAATCTTTATTGAAAT	1689
QY	942	CTCAAGAACGACATCCATTAGGAAAGACAGAGAAAATGCCAAGGTGCTTCTTACAGG	1001
Db	1682	CTCAAGAACGACATCCATTAGGAAAGACAGAGAAAATGCCAAGGTGCTTCTTACAGG	1741
QY	1002	TTTTGGAGACATATTACAGAAATGAGTCCGTCTGTGACATGCCCCAGCCTCTGAA	1066
Db	1742	TTTTGGAGACATATTACAGAAATGAGTCCGTCTGTGACATGCCCCAGCCTCTGAA	1801
QY	1062	TCTAGAGCTCAGTTCAAGGACCATCACTGACCTAGGGAACAGGCTCATCTTAATCTGAGT	1121
Db	1802	TCTAGAGCTCAGTTCAAGGACCATCACTGACCTAGGGAACAGGCTCATCTTAATCTGAGT	1861
QY	1122	GGATATTACTCTGCAATTATAATGAAGCCAAACGTCAATCTTCTGATGTGAGATTGAG	1181
Db	1862	GGATATTACTCTGCAATTATAATGAAGCCAAACGTCAATCTTCTGATGTGAGATTGAG	1921
QY	1182	AAGCATTTGATTTGGAATGTGACCTCAAAATGGCCCCCATATCACTGCAACCTTACAG	1241
Db	1922	AAGCATTTGATTTGGAATGTGACCTCAAAATGGCCCCCATATCACTGCAACCTTACAG	1981
QY	1242	TTTTCTTGCAATGGGGGTCTGAGACTTTCACCTCTGGCAAGTATTACTGGGAGGTCCATGT	1301
Db	1982	TTTTCTTGCAATGGGGGTCTGAGACTTTCACCTCTGGCAAGTATTACTGGGAGGTCCATGT	2041
QY	1302	GGGGGACTCTTGGAATTTGGGCTTTCGGTGTTTGTAAATAGTACTGAAAGGGAATCA	1361
Db	2042	GGGGGACTCTTGGAATTTGGGCTTTCGGTGTTTGTAAATAGTACTGAAAGGGAATCA	2101
QY	1362	GAATGGCAATATATATGGAAGAGAGGGAATCTTTAAGTCTTGGATTTGTTAAGACGACAT	1421
Db	2102	GAATGGCAATATATATGGAAGAGAGGGAATCTTTAAGTCTTGGATTTGTTAAGACGACAT	2161
QY	1422	TCAGTGAAGTCTCTTTACACACTCCGAGTTTACACTGCAATGTGCCAAGACTTACAA	1481
Db	2162	TCAGTGAAGTCTCTTTACACACTCCGAGTTTACACTGCAATGTGCCAAGACTTACAA	2221
QY	1482	CCATGTAGGATTTATCTCGAGATTTGTGAAGCTAGAACTGTGAGCTTCGTTAGTTAAATCA	1541
Db	2222	CCATGTAGGATTTATCTCGAGATTTGTGAAGCTAGAACTGTGAGCTTCGTTAGTTAAATCA	2281
QY	1542	AAGTCCCCCTATATACCAATCCCTTAATTTGCTCTTCTCACTCTCTCAAGCCTATCTT	1601
Db	2282	AAGTCCCCCTATATACCAATCCCTTAATTTGCTCTTCTCACTCTCTCAAGCCTATCTT	2341
QY	1602	TTGCTGATTCATCTCTGACACAGAGCAAAATCAGAAATGTGTTATCTGCTGTGGAAAC	1661
Db	2342	TTGCTGATTCATCTCTGACACAGAGCAAAATCAGAAATGTGTTATCTGCTGTGGAAAC	2401
QY	1662	CCTTATCCCATTAAGCCCTCTTCTCTGTGCTTATCAACAGAGCAAAATAGGTTCTGTT	1721
Db	2402	CCTTATCCCATTAAGCCCTCTTCTCTGTGCTTATCAACAGAGCAAAATAGGTTCTGTT	2461
QY	1722	TTATGTCTTGAATTGCAATCTTAATGTTATTAATCTCAATTTATTTGTTACTATTAATG	1781
Db	2462	TTATGTCTTGAATTGCAATCTTAATGTTATTAATCTCAATTTATTTGTTACTATTAATG	2521
QY	1782	TTGTTAAAMCAAAAAAAAAAAAAAAAAAAAAA 1811	
Db	2522	TTGTTAAAMCACTTAAAAAAAAAAAAAAAAAAAA 2551	

RESULT	9
AAFP29992	
ID	AAFP299992 standard; DNA; 2241 BP
XX	
XX	
AC	AAFP29992;
XX	
DT	06-APR-2001 (first entry)
XX	

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QY 663 -----A 663
Db 1142 ACCACAGCACCCGCGCAGTCCGCGATCTTGAACAACCTTGAAGTCTTCTGATTTTA 1201
QY 664 GGGCACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAAGCAAGAGGATTT 723
Db 1202 GGGCACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAAGCAAGAGGATTT 1261
QY 724 TGCATGCCCCACTTTACAAAATCTACAGTAATGCGAGGGAGCGAGCTTTGATTAAGCTG 783
Db 1262 TGCATGCCCCACTTTACAAAATCTACAGTAATGCGAGGGAGCGAGCTTTGATTAAGCTG 1321
QY 784 CTGAAGAAGCTCAAGTCACTTGCCCAAGGCCGCGGTGCTGAGCTACTTCTGAGGGC 843
Db 1322 CTGAAGAAGCTCAAGTCACTTGCCCAAGGCCGCGGTGCTGAGCTACTTCTGAGGGC 1381
QY 844 ATGACGGTGAAGAGTCTGCTGATGCGCATGAGCGCGCTGGGTCTAAGTGGAGAAATTTCTG 903
Db 1382 ATGACGGTGAAGAGTCTGCTGATGCGCATGAGCGCGCTGGGTCTAAGTGGAGAAATTTCTG 1441
QY 904 CTTCTGGGCGGGAAACCAAGTGCATTTTATGAGATCTCAAAAGACAGCATCTTATGG 963
Db 1442 CTTCTGGGCGGGAAACCAAGTGCATTTTATGAGATCTCAAAAGACAGCATCTTATGG 1501
QY 964 GAAGACAGAAAGAAATGCGCAAGGTGCTCTCAAGGTTTGGAGACATATTACACAGA 1023
Db 1502 GAAGACAGAAAGAAATGCGCAAGGTGCTCTCT-----CAGA 1538
QY 1024 AGTGAATCCGTGCTGTCACATGCCCGCCAGCTCTGAATCTAAGCTCAAGGCGCC 1083
Db 1539 AGTGAATCCGTGCTGTCACATGCCCGCCAGCTCTGAATCTAAGCTCAAGGCGCC 1598
QY 1084 ATCACTGAGTGAAGGACAGGCTCATTAATCTGAGTGAATATTAATCTGCACTTAAAT 1143
Db 1599 ATCACTGAGTGAAGGACAGGCTCATTAATCTGAGTGAATATTAATCTGCACTTAAAT 1658
QY 1144 GAAGCCAAAGTATATCTCTGATGAGATTTGAGAGCAATTTGATTTGAGATGAG 1203
Db 1659 GAAGCCAAAGTATATCTCTGATGAGATTTGAGAGCAATTTGATTTGAGATGAG 1718
QY 1204 CGTCAAAATGCGCCCATATCACTGCAACAAGTCTTTCGATGGGGTCTCAG 1263
Db 1719 CGTCAAAATGCGCCCATATCACTGCAACAAGTCTTTCGATGGGGTCTCAG 1778
QY 1264 ACTTTCACCTCTGGCAAGTATTAATGAGAGTCCATGTTGGGGACTTTTGAATTTGGGCT 1323
Db 1779 ACTTTCACCTCTGGCAAGTATTAATGAGAGTCCATGTTGGGGACTTTTGAATTTGGGCT 1838
QY 1324 TTGGGTGTTTGTATATAGTACTGGAAGGAGAAAGATCAGATGAGCAATATATATGAGAG 1383
Db 1839 TTGGGTGTTTGTATATAGTACTGGAAGGAGAAAGATCAGATGAGCAATATATATGAGAG 1898
QY 1384 GAGGGAATCTTTAGTCTTGGGATTTGTAAGACGACATTCAGTCACTCTCTTACCAACC 1443
Db 1899 GAGGGAATCTTTAGTCTTGGGATTTGTAAGACGACATTCAGTCACTCTTACCAACC 1958
QY 1444 TCCCCAGTTACATGCGAGTATGTCCTCAAGACTACCAACCATGAGATTAATCTCGAT 1503
Db 1959 TCCCCAGTTACATGCGAGTATGTCCTCAAGACTACCAACCATGAGATTAATCTCGAT 2018
QY 1504 TGTGAAGCTGAGACTGAGCTTGTGATGTTATCAAAAGCTCCCTATATACACATC 1563
Db 2019 TGTGAAGCTGAGACTGAGCTTGTGATGTTATCAAAAGCTCCCTATATACACATC 2078
QY 1564 CTTAATTTGCTCTTCACTCTCTCAGGCTATCTTTTGTCTGATTAATCTCTGACCA 1623
Db 2079 CTTAATTTGCTCTTCACTCTCTCAGGCTATCTTTTGTCTGATTAATCTCTGACCA 2138
QY 1624 GAGACAAATAGAAATGTGTTATCTGCTGGGAAACCCCTTATCCCAATAAAGCCCTCT 1683
Db 2139 GAGACAAATAGAAATGTGTTATCTGCTGGGAAACCCCTTATCCCAATAAAGCCCTCT 2198
QY 1684 TCCTTGTGCTTATCAAAAGAGACAAATAGGTTCTGTTTATGCTTGAATTGATCTTA 1743

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Db 2199 TCCATATGCTTATACAAACAGGACAAATAGTCTGTTTATGCTTGAATGCAATCTTA 2258
QY 1744 ATGTTATTTAAACTCACTTTATTTGTGTTACTATTAAATGTGTAATAACCAAAAAA 1803
Db 2259 ATGTTATTTAAACTCACTTTATTTGTGTTACTATTAAATGTGTAATAACCAAAAAA 2318
QY 1804 AAAAAAA 1811
Db 2319 AAAAAAA 2326

RESULT 8
AAF29989
ID AAF29989 standard; DNA; 2551 BP.
XX
AC AAF29989;
XX
DT 06-APR-2001 (first entry)
XX
DE Human GRMx-1a DNA.
XX
KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;
KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX
OS Homo sapiens.
XX
PN WO200102566-A1.
XX
PD 11-JAN-2001.
XX
PF 27-JUN-2000; 2000MO-US17798.
XX
PR 02-JUL-1999; 99US-0346326.
XX
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Schwarz DA, Maki RA;
XX
DR WPI, 2001-123112/13.
XX
PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX
PS Claim 2; Fig 1; 59pp; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC Metabotropic glutamate receptor polynucleotides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2551 BP; 666 A; 566 C; 630 G; 689 T; 0 other;

Query Match 77.5%; Score 1413.6; DB 22; Length 2551;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 1805; Conservative 1; Mismatches 5; Indels 379; Gaps 1;
QY 1 AAAAAATGCTCTTGTGTTATCTCTGATGTTTAAAGAAATGCTCGTGGAGT 60
Db 362 AAAAAATGCTCTTGTGTTATCTCTGATGTTTAAAGAAATGCTCGTGGAGT 421
QY 61 GCAAGTCCAGTGAAGAGAGGAGGAGTGTGCTCACATGCTGGGTGACATTAATGAGCT 120
Db 422 GCAAGTCCAGTGAAGAGAGGAGGAGTGTGCTCACATGCTGGGTGACATTAATGAGCT 481
QY 121 CTTCTTTTGTTCATCAGCAAGCTTACTGTGAGCAAGATTTCATGAGAGAGAGTGGGCA 180
Db 482 CTTCTTTTGTTCATCAGCAAGCTTACTGTGAGCAAGATTTCATGAGAGAGAGTGGGCA 541

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Db      1454 GACCGTCAAAATCGCCCCCATATCATGCAACACTCAAGTTTCTTGATGGGGTCT 1513
Qy      1261 CAACTTTCACCTCTGCGCAATATCTGGAGAGTCCATGTGGGGACTCTTGAATGG 1320
Db      1514 GACACTTTCACCTCTGCGCAATATCTGGAGAGTCCATGTGGGGACTCTTGAATGG 1573
Qy      1321 GCTTTCGATTTGTAATAGTACTGGAAGGAAGAAATAGATGGAATATATATGA 1380
Db      1574 GCTTTCGATTTGTAATAGTACTGGAAGGAAGAAATAGATGGAATATATATGA 1533
Qy      1381 GAGAGAGGACTCTTATAGTCTTGGAGTTTGAAGACATTCAGTCACTCTTACC 1440
Db      1634 GAGAGAGGACTCTTATAGTCTTGGAGTTTGAAGACATTCAGTCACTCTTACC 1693
Qy      1441 ACCTCCCACTTACATGCGATGATGTCCTCAAGACCTACCAACATGATGATTTCTG 1500
Db      1694 ACCTCCCACTTACATGCGATGATGTCCTCAAGACCTACCAACATGATGATTTCTG 1753
Qy      1501 GATTGAGCTGAACTGAGCTTGTGATGTTAATGAAGCTCCCTATATACACC 1560
Db      1754 GATTGAGCTGAACTGAGCTTGTGATGTTAATGAAGCTCCCTATATACACC 1813
Qy      1561 ATCCCTAATGCTCTCTTCACTCTCTCAGGCTATCTTTGCTGATTCATCTGA 1620
Db      1814 ATCCCTAATGCTCTCTTCACTCTCTCAGGCTATCTTTGCTGATTCATCTGA 1873
Qy      1621 CCAGAGCAAAATGAAATGTGTTATCTGCTGTGGAAACCCCTTATCCATAAGCCC 1680
Db      1874 CCAGAGCAAAATGAAATGTGTTATCTGCTGTGGAAACCCCTTATCCATAAGCCC 1933
Qy      1681 TCTTCTGTCCTTATCAACAGAGCAAAATAGGTTCTGTTTATGCTGAAATGCAAT 1740
Db      1934 TCTTCTGTCCTTATCAACAGAGCAAAATAGGTTCTGTTTATGCTGAAATGCAAT 1993
Qy      1741 CTAATGTTAATAACTCATTTATGTGTACTAATTAATGTGTAAACACAAAAAA 1800
Db      1994 CTAATGTTAATAACTCATTTATGTGTACTAATTAATGTGTAAACACAAAAAA 2053
Qy      1801 AAAAAAAAAA 1811
Db      2054 AAAAAAAAAA 2064

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## RESULT 7

AAF29991 standard; DNA; 2326 BP.

AAF29991;

06-APR-2001 (first entry)

Human GRMX-1c DNA.

Human; metabotropic glutamate receptor; schizophrenia; GRMX;

Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.

Homo sapiens.

W0200102566-A1.

11-JAN-2001.

27-JUN-2000; 2000MO-US17798.

02-JUL-1999; 99US-0346326.

(NEUR-) NEUROCRINE BIOSCIENCES INC.

Schwarz DA, Maki RA;

WPI; 2001-123112/13.

XX

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PT Novel metabotropic glutamate receptor for prevention, treatment of
PT conditions associated with undesirable glutamate levels, e.g.
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT schizophrenia -
XX Claim 2; Fig 5; 59p; English.
XX
CC The present invention relates to human metabotropic glutamate
CC receptor. An agent that decreases expression or activity of the
CC metabotropic glutamate receptor is useful for treating schizophrenia.
CC Metabotropic glutamate receptor polypeptides, polypeptides
CC are useful for treating diseases associated with undesirable
CC levels of glutamate, such as Alzheimer's disease, Parkinson's
CC disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ Sequence 2326 BP; 581 A; 535 C; 580 G; 630 T; 0 other;

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Query Match 85.6%; Score 1559.6; DB 22; Length 2326;

Best Local Similarity 89.6%; Pred. No. 0;

Matches 1782; Conservative 1; Mismatches 5; Indels 200; Gaps 2;

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Qy      1 AAATGCTCTTCTGTTGATCTGTGATCTTACTTTTGAAGAATGTCCTGGAGT 60
Db      362 AAATGCTCTTCTGTTGATCTGTGATCTTACTTTGAAAGAAATGTCCTGGAGT 421
Qy      61 GCACAGTCCAGTGAAGAGAGGGGTGTCATGCTGGGTGATCATTTATGAGCT 120
Db      422 GCACAGTCCAGTGAAGAGAGGGGTGTCATGCTGGGTGATCATTTATGAGCT 481
Qy      121 CTCCTTCTGTTTCATCAGCAGCTTACTGTGACGAAGTTTATGAGAGAGTGTGGGCA 180
Db      482 CTCCTTCTGTTTCATCAGCAGCTTACTGTGACGAAGTTTATGAGAGAGTGTGGGCA 541
Qy      181 GTCCGTGAACAGTATGAGCATTCAGAGATGAGAGCCATGCTGCATCCCTGGAAGATC 240
Db      542 GTCCGTGAACAGTATGAGCATTCAGAGATGAGAGCCATGCTGCATCCCTGGAAGATC 601
Qy      241 AATTGACACCCCACTCTTGGCCCAATCACAATGAGGCTGATGAGATTAAGGATTCCTGC 300
Db      602 AATTGACACCCCACTCTTGGCCCAATCACAATGAGGCTGATGAGATTAAGGATTCCTGC 661
Qy      301 TGGCATTCGGCTGTGCGCTAGAGCAGACATTTAGATTAAGATTCCTCATTTCT 360
Db      662 TGGCATTCGGCTGTGCGCTAGAGCAGACATTTAGATTAAGATTCCTCATTTCT 721
Qy      361 TCGAAGAGAGAGAGGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCC 420
Db      722 TCGAAGAGAGAGAGGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCC 781
Qy      421 AAGAAGCCCATGATGAGGCTCAATGGGCTGTGATTCATTTAGCAATTCAGATTCAG 480
Db      782 AAGAAGCCCATGATGAGGCTCAATGGGCTGTGATTCATTTAGCAATTCAGATTCAG 841
Qy      481 AATTGCTCAGCTTCTTCAACATCACTCAGATTTGCTTACTCAGCAACATCATGATCTG 540
Db      842 AATTGCTCAGCTTCTTCAACATCACTCAGATTTGCTTACTCAGCAACATCATGATCTG 901
Qy      541 AGTGACAAGACTCTGTTCAAATATTTTCATGAGGTTTGTCTTCAGATCTCAGAGCA 600
Db      902 AGTGACAAGACTCTGTTCAAATATTTTCATGAGGTTTGTCTTCAGATCTCAGAGCA 961
Qy      601 AGGTCCATGTGACATAGTGAAGAGGTACATGAGCACTATGATATACCCGTACACCA 660
Db      962 AGGTCCATGTGACATAGTGAAGAGGTACATGAGCACTATGATATACCCGTACACCA 1021
Qy      661 GA----- 662
Db      1022 GAAGGTTCAAGCTATTTCTATGCTCAGCTCCAGAGAGCTAGAGGCTTTCAACTCT 1081
Qy      663 ----- 662
Db      1082 TGGCTCAAGTATGCTGCTTGGCTTCCAAATGCTGGGATTTATGGCATGAGCC 1141

```



Db 2162 GAGACAAATCAGAAATGCTTTATCTGCTGTGGAAACCCCTTATCCCATTAAGCCCTCT 2221  
Qy 1684 TCCCTGTGCTTATCAACAGAGCAAAATAGTTCTGTATTATGCTTGAATGCAATTCCTA 1743  
Db 2222 TCCCTATGCTTATCAACAGAGCAAAATAGTTCTGTATTATGCTTGAATGCAATTCCTA 2281  
Qy 1744 ATGTTATTAACCTCTTTATTTGTCTATCTATTAATGTGTAAACCAAAACAAAAA 1803  
Db 2282 ATGTTATTAACCTCTTTATTTGTCTATCTATTAATGTGTAAACCAAAACAAAAA 2341  
Qy 1804 AAAAAAA 1811  
Db 2342 AAAAAAA 2349

RESULT 6  
AAF29995  
ID AAF29995 strand; DNA; 2064 BP.  
XX AAF29995;  
AC AAF29995;  
DT 06-APR-2001 (first entry)  
XX  
DE Human GRMx-1g DNA.  
XX  
KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
XX Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
XX  
OS Homo sapiens.  
XX  
PN M0200102566-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 27-JUN-2000; 2000MO-US17798.  
XX  
PR 02-JUL-1999; 99US-0346326.  
XX  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
PI Schwarz DA, Maki RA;  
XX  
DR WPI; 2001-123112/13.  
XX  
PT Novel metabotropic glutamate receptor for prevention, treatment of  
XX PT conditions associated with undesirable glutamate levels, e.g.  
XX PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
XX PT schizophrenia -  
XX  
PS Claim 2; Fig 11; 59pp; English.  
XX  
CC The present invention relates to human metabotropic glutamate  
XX CC receptor. An agent that decreases expression or activity of the  
XX CC metabotropic glutamate receptor is useful for treating schizophrenia.  
XX CC Metabotropic glutamate receptor polynucleotides, polypeptides  
XX CC are useful for treating diseases associated with undesirable  
XX CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
XX CC disease, stroke, depression, anxiety, pain and schizophrenia.  
XX  
SQ Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other;

Query Match 86.5%; Score 1576.6; DB 22; Length 2064;  
Best Local Similarity 93.7%; Pred. No. 0;  
Matches 1697; Conservative 1; Mismatches 5; Indels 108; Gaps 1;

Qy 1 AAAAAATGCTTCTGTTGATCTCTGCACTTACTTTTGAAGAAGATGCCGAGGAGT 60  
Db 362 AAAAAATGCTTCTGTTGATCTCTGCACTTACTTTTGAAGAAGATGCCGAGGAGT 421  
Qy 61 GCACAGTCCAGTGAAGAGGAGGTGTGCTCACAATGCTGAGTGAATCATTTATTTGAGCT 120  
Db 422 GCACAGTCCAGTGAAGAGGAGGTGTGCTCACAATGCTGAGTGAATCATTTATTTGAGCT 481

Qy 121 CTCTTTCTGTTCAATCAACAGCTCTAGTGAAGAAAGTTCAATGAGAGAGTGTGGGCA 180  
Db 482 CTCTTTCTGTTCAATCAACAGCTCTAGTGAAGAAAGTTCAATGAGAGAGTGTGGGCA 541  
Qy 181 GTCCGTGAACAGTATGAGATTCAGAGAGTGAAGGCAATGCTGATACCTGTGAAAGATC 240  
Db 542 GTCCGTGAACAGTATGAGATTCAGAGAGTGAAGGCAATGCTGATACCTGTGAAAGATC 601  
Qy 241 AATTGACACCCCACTCTTGGCCCAATCAATCACTGGGCTGTGAATTAAGGATTCCTGC 300  
Db 602 AATTGACACCCCACTCTTGGCCCAATCAATCACTGGGCTGTGAATTAAGGATTCCTGC 661  
Qy 301 TGGCAATGGGCTGTGGCCCTAGAGCAGAGCATTTGATCATTAAGATTCCTCATTTCT 360  
Db 662 TGGCAATGGGCTGTGGCCCTAGAGCAGAGCATTTGATCATTAAGATTCCTCATTTCT 721  
Qy 361 TCGAAGAGAGAGAGGCTTGTGATGCTGTGATGCTGTGATGCTGTCTCTCTTCCGCTCC 420  
Db 722 TCGAAGAGAGAGAGGCTTGTGATGCTGTGATGCTGTGATGCTGTCTCTCTTCCGCTCC 781  
Qy 421 AAGAGCCCATATGATGAGGCTCATTTGGGCTGTGATGCTGTGATGCTGTGATGCTGTG 480  
Db 782 AAGAGCCCATATGATGAGGCTCATTTGGGCTGTGATGCTGTGATGCTGTGATGCTGTG 841  
Qy 481 AATTGCTCCAGCTTTCAACATPACTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 540  
Db 842 AATTGCTCCAGCTTTCAACATPACTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 901  
Qy 541 AGTGAACAAGCTCTGTTCAAAATATTTCAATGAGGCTTGTGCTTCAAGATCTGACAGGCA 600  
Db 902 AGTGAACAAGCTCTGTTCAAAATATTTCAATGAGGCTTGTGCTTCAAGATCTGACAGGCA 961  
Qy 601 AGGTCATGATGAGCATTAATGAGAGGCTCAACTGAGCTTAATGATACCCGATACACA 660  
Db 962 AGGTCATGATGAGCATTAATGAGAGGCTCAACTGAGCTTAATGATACCCGATACACA 1021  
Qy 661 GAAGGCACTATGAGAGAGGAGTGAAGGCTTCAAAAGATATGTCAGAGAGAGAGG 720  
Db 1022 GAAGGCACTATGAGAGAGGAGTGAAGGCTTCAAAAGATATGTCAGAGAGAGAGG 1081  
Qy 721 ATTGATGCGCCCACTCTTACAAATCTACATGATGACAGGAGAGAGCTTTGATTAAG 780  
Db 1082 ATTGATGCGCCCACTCTTACAAATCTACATGATGACAGGAGAGAGCTTTGATTAAG 1141  
Qy 781 CTGCTGAAGAAGTCAACAGTCACTTGGCCCAAGGCGCGGTGTGCTTCTGTGAG 840  
Db 1142 CTGCTGAAGAAGTCAACAGTCACTTGGCCCAAGGCGCGGTGTGCTTCTGTGAG 1201  
Qy 841 GGCATGACGCTGAGAGTGTGCTGATGAGGCGGCTGTGATGAGGAGATTT 900  
Db 1202 GGCATGACGCTGAGAGTGTGCTGATGAGGCGGCTGTGATGAGGAGATTT 1261  
Qy 901 CTGCTTGTGGGCAAGGAGACAGATGCACTTTATTGAATCTCAAGAGACATCTTA 960  
Db 1262 CTGCTTGTGG----- 1272  
Qy 961 TGGAGAGACAGAGAGAGAGTCCAGAGTGTCTTCAAGGCTTTGGAGACATTTACAC 1020  
Db 1273 -----C 1273  
Qy 1021 AGAAGTGAAGTCCGTGCTGTCATGATGCCCACTCTGAATCTAGAGTCAAGTTCAGGG 1080  
Db 1274 AGAAGTGAAGTCCGTGCTGTCATGATGCCCACTCTGAATCTAGAGTCAAGTTCAGGG 1333  
Qy 1081 CCCATCACTGAGTGAAGGAGCAGGCTCATTTAATTTGAGTGAATTAATCTGCAATTA 1140  
Db 1334 CCCATCACTGAGTGAAGGAGCAGGCTCATTTAATTTGAGTGAATTAATCTGCAATTA 1393  
Qy 1141 AATGAAGCAACAGTCAATCTTCTGATGAGATTTGAAGAGATTTGATTTGATGAT 1200  
Db 1394 AATGAAGCAACAGTCAATCTTCTGATGAGATTTGAAGAGATTTGATTTGATGAT 1453  
Qy 1201 GACCGTGAAGAGGCGCCCATATCACTGCAACACTCAAGTTTCTTGTGATGGGATGCT 1260

XX MPI; 2001-123112/13.  
DR Novel metabotropic glutamate receptor for prevention, treatment of  
XX PT conditions associated with undesirable glutamate levels, e.g.  
PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
PT schizophrenia -  
XX Claim 2; Fig 3; 59pp; English.  
XX  
XX The present invention relates to human metabotropic glutamate  
CC receptor. An agent that decreases expression or activity of the  
CC metabotropic glutamate receptor is useful for treating schizophrenia.  
CC Metabotropic glutamate receptor polymucleotides, polypeptides  
CC are useful for treating diseases associated with undesirable  
CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
CC disease, stroke, depression, anxiety, pain and schizophrenia.  
XX  
XX Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;  
SQ  
Query Match 88.6%; Score 1615.6; DB 22; Length 2349;  
Best local Similarity 90.8%; Pred. No. 0;  
Matches 1805; Conservative 1; Mismatches 5; Indels 177; Gaps 1;  
QY 1 AAAATGCTCTTCTGTGATCTGTGATCTTATCTTTGAAGAGATGCCGTGGAGT 60  
DB AAAATGCTCTTCTGTGATCTGTGATCTTATCTTTGAAGAGATGCCGTGGAGT 421  
QY GCACATGTCAGTGAAG 120  
DB GCACATGTCAGTGAAG 422  
QY CTTCTTTCTGTTTCATACCAAGCCCTACCTGTTGAGAGAGAGAGAGAGAGAGAG 180  
DB CTTCTTTCTGTTTCATACCAAGCCCTACCTGTTGAGAGAGAGAGAGAGAGAGAG 482  
QY GTCCCGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
DB GTCCCGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 542  
QY AATTTCAGACCCCACTCTTGGCCCAATCACTGAGAGAGAGAGAGAGAGAGAGATC 300  
DB AATTTCAGACCCCACTCTTGGCCCAATCACTGAGAGAGAGAGAGAGAGAGAGATC 602  
QY TGGCATTGGGCTGTGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 360  
DB TGGCATTGGGCTGTGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 662  
QY TCGGAAG 420  
DB TCGGAAG 722  
QY AAG 480  
DB AAG 782  
QY AATTGCTCAGCTTTTCAACATCTCAGATTCCTTACCTGAGAGAGAGAGAGAGATC 540  
DB AATTGCTCAGCTTTTCAACATCTCAGATTCCTTACCTGAGAGAGAGAGAGATC 842  
QY AGTGAAG 600  
DB AGTGAAG 902  
QY AGTGAAG 660  
DB AGTGAAG 962  
QY AGTGAAG 1021  
DB AGTGAAG 1022  
QY GA----- 662  
DB GAAGGTTCAAGCTATTCATGCTCAGCTCAGAGAGAGAGAGAGAGAGAGATCCT 1081  
QY ----- 662

DB TGGCTCAAGTATCTGCTGCTTGGCTTCCAAATGCTGGAGATTAAGCATGAGCC 1141  
QY ----- A 663  
DB ACCACAGACCCCGCAGTGGCCGATCTTAAGACCTTTGAGGTCCTTCTGATTTTGA 1201  
QY GGCACTATGAT 723  
DB GGCACTATGAT 1202  
QY TGCATGCTCCTTTTCAAAATCTACAGTAATGAGAGAGAGAGAGAGAGAT 783  
DB TGCATGCTCCTTTTCAAAATCTACAGTAATGAGAGAGAGAGAGAGAGAT 1262  
QY CTGAAGAT 843  
DB CTGAAGAT 1322  
QY ATGACGATGAT 903  
DB ATGACGATGAT 1382  
QY CTTCTGGGAT 963  
DB CTTCTGGGAT 1442  
QY GAAAGAT 1023  
DB GAAAGAT 1502  
QY AGTGAAGAT 1083  
DB AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1562  
QY ATCACTGAT 1143  
DB ATCACTGAT 1622  
QY GAAAGAT 1203  
DB GAAAGAT 1682  
QY GGTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1263  
DB GGTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1742  
QY ACTTTCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1323  
DB ACTTTCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1742  
QY ACTTTCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1383  
DB ACTTTCAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1802  
QY TTCGATGTTTGAATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAT 1443  
DB TTCGATGTTTGAATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAT 1862  
QY TTCGATGTTTGAATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAT 1493  
DB TTCGATGTTTGAATTAAGTCTGAGAGAGAGAGAGAGAGAGAGAT 1921  
QY GAGGAGCTTATGCTTGAATTAAGTCTGAGAGAGAGAGAGAGAGAT 1553  
DB GAGGAGCTTATGCTTGAATTAAGTCTGAGAGAGAGAGAGAGAGAT 1981  
QY TCCCAAGTTCACATGAGATTCCTCAAGAGAGAGAGAGAGAGAT 1503  
DB TCCCAAGTTCACATGAGATTCCTCAAGAGAGAGAGAGAGAGAT 2041  
QY TGTGAAGCTGAAGCTGAGATTCCTCAAGAGAGAGAGAGAGAT 1563  
DB TGTGAAGCTGAAGCTGAGATTCCTCAAGAGAGAGAGAGAGAT 2042  
QY CTTATTTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1623  
DB CTTATTTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2102  
QY GAT 1683  
DB GAT 1683



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Db      421 GCCCAGTAGAGGGTCATTTGGGCTCGGTTCCAGTTCTTTAGCCATTCAGTCCAGAAATT 480
Qy      486 GCTCCAGCTTTTCAACATACCTGAGATTGCTTACTACGACCAACATCAATGATCTGAGGA 545
Db      481 GCTCCAGCTTTTCAACATACCTGAGATTGCTTACTACGACCAACATCAATGATCTGAGGA 540
Qy      546 CAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAAGATCTCAGCAGGCAAGTTC 605
Db      541 CAAGACTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAAGATCTCAGCAGGCAAGTTC 600
Qy      606 CATGCTGACATATGTAAGAGGTACCACTGACCTATGATACAGCCGTACACAGAAAG 665
Db      601 CATGCTGACATATGTAAGAGGTACCACTGACCTATGATACAGCCGTACACAGAAAG 660
Qy      666 CAATATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGGAGGATTTG 725
Db      661 CAATATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGGAGGATTTG 720
Qy      726 CATGCCCACTCTTACAAAATCTACAGTAATGCAAGGAGCAGAGCTTTGATTAAGTCT 785
Db      721 CATGCCCACTCTTACAAAATCTACAGTAATGCAAGGAGCAGAGCTTTGATTAAGTCT 780
Qy      786 GAAGAACTCAACATGACTTCTCCCAAGGCCGGGTGTGGCTTACTTGTGAGGCGAT 845
Db      781 GAAGAACTCAACATGACTTCTCCCAAGGCCGGGTGTGGCTTACTTGTGAGGCGAT 840
Qy      846 GACGGTGAAGGTGTGCTGATGAGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTGCT 905
Db      841 GACGGTGAAGGTGTGCTGATGAGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTGCT 900
Qy      906 TCTGGGCAAGGAAACAGATGCCATCTTATTTGAGATCTCAAGAAACAGATCTTATGGA 965
Db      901 TCTGGGCAAGGAAACAGATGCCATCTTATTTGAGATCTCAAGAAACAGATCTTATGGA 960
Qy      966 AGACAGAAAGAAATGCCAAGTGTCTTCCAGGGTTTGGAGACATTTATTCACAGAG 1025
Db      961 AGACAGAAAGAAATGCCAAGTGTCTTCCAGGGTTTGGAGACATTTATTCACAGAG 1020
Qy      1026 TGAATCCGTCGTGTCACATGCCCCAGCCCTGGAATCTAGAGTCAAGTCAAGGCCCAT 1085
Db      1021 TGAATCCGTCGTGTCACATGCCCCAGCCCTGGAATCTAGAGTCAAGTCAAGGCCCAT 1080
Qy      1086 CACTGCACTGAGGAGCAGGCTCATCTTAATCTGAGTGAATATTTACTCTGCAATTAATGA 1145
Db      1081 CACTGCACTGAGGAGCAGGCTCATCTTAATCTGAGTGAATATTTACTCTGCAATTAATGA 1140
Qy      1146 AGCCAAACATCATATCTTCTGATGTGAGATTGGAAGCAATTTGATGATGTGACCG 1205
Db      1141 AGCCAAACATCATATCTTCTGATGTGAGATTGGAAGCAATTTGATGATGTGACCG 1200
Qy      1206 TCAAAATGGGCCCATATCACTGCAACACTTACAAAGTTTCTTCCAGTGGGTCTCAGAC 1265
Db      1201 TCAAAATGGGCCCATATCACTGCAACACTTACAAAGTTTCTTCCAGTGGGTCTCAGAC 1260
Qy      1266 TTTCACTCTGCGAAGATTAATCTGAGAGTCCATGTTGGGGAATCTTTGAAATGGGCTTT 1325
Db      1261 TTTCACTCTGCGAAGATTAATCTGAGAGTCCATGTTGGGGAATCTTTGAAATGGGCTTT 1320
Qy      1326 CGGTGTTTGAATPAAGTCTGGAAGGGAAGAAATCAGAAATGGAATATATATGAGAGGA 1385
Db      1321 CGGTGTTTGAATPAAGTCTGGAAGGGAAGAAATCAGAAATGGAATATATATGAGAGGA 1380
Qy      1386 GGAATCTTTAATGCTTGGGATTTGTTAAGAACGACATTCAGTGCAGTCTTTTACCACTTC 1445
Db      1381 GGAATCTTTAATGCTTGGGATTTGTTAAGAACGACATTCAGTGCAGTCTTTTACCACTTC 1440
Qy      1446 CCCAGTTTACCTGACATGATCTCCCAAGACCTTACCAACATGATGAGATTTATTCGGAATG 1505
Db      1441 CCCAGTTTACCTGACATGATCTCCCAAGACCTTACCAACATGATGAGATTTATTCGGAATG 1500
Qy      1506 TGAAGCTAGAAGCTGTGAGCTTGTGATGTTAATCAAAAGTCTCCCTATATACACATCC 1565
Db      1501 TGAAGCTAGAAGCTGTGAGCTTGTGATGTTAATCAAAAGTCTCCCTATATACACATCC 1560

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Qy      1566 TAAATGCTCTTCTCAACCTCTCTCAGGCTATCTTTGCTGATTCATCTGACAGA 1625
Db      1561 TAAATGCTCTTCTCAACCTCTCTCAGGCTATCTTTGCTGATTCATCTGACAGA 1620
Qy      1626 GACAAATCAGAAATGTTATATCTGCTGTGGGAAACCCCTTATCCATAAGCCCTCTTC 1685
Db      1621 GACAAATCAGAAATGTTATATCTGCTGTGGGAAACCCCTTATCCATAAGCCCTCTTC 1680
Qy      1686 CTGTGCTTATCAACAGGACAAATAGCTTCTTATGCTGAAATGCAATTCAT 1745
Db      1681 CTGTGCTTATCAACAGGACAAATAGCTTCTTATGCTGAAATGCAATTCAT 1740
Qy      1746 GTTATTAACCTGATTAATGTTACTATTAATGATGTAAMC 1793
Db      1741 GTTATTAACCTGATTAATGTTACTATTAATGATGTAAMC 1788

RESULT 4
AAFP2994
ID   AAFP2994 standard; DNA; 2149 BP.
XX
AC   AAFP2994;
XX
DT   06-APR-2001 (first entry)
XX
DE   Human GRMX-1f DNA.
XX
KW   Human; metabotropic glutamate receptor; schizophrenia; GRMX;
KM   Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; de.
OS   Homo sapiens.
PN   M0200102566-A1.
XX
PD   11-JAN-2001.
XX
PE   27-JUN-2000; 2000MO-US17798.
XX
PR   02-JUL-1999; 99US-0346326.
XX
PA   (NEUR-) NEUROCRINE BIOSCIENCES INC.
PI   Schwarz DA, Maki RA;
XX
DR   WPI; 2001-123112/13.
XX
PT   Novel metabotropic glutamate receptor for prevention, treatment of
PT   conditions associated with undesirable glutamate levels, e.g.
PT   Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and
PT   schizophrenia.
XX
PS   Claim 2; Fig 9; 59pp; English.
XX
CC   The present invention relates to human metabotropic glutamate
CC   receptor. An agent that decreases expression or activity of the
CC   metabotropic glutamate receptor is useful for treating schizophrenia.
CC   Metabotropic glutamate receptor polynucleotides, polypeptides
CC   are useful for treating diseases associated with undesirable
CC   levels of glutamate, such as Alzheimer's disease, Parkinson's
CC   disease, stroke, depression, anxiety, pain and schizophrenia.
XX
SQ   Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;
Query Match          95.8%; Score 1746.6; DB 22; Length 2149;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1782; Conservative 1; Mismatches 5; Indels 23; Gaps 1;
Qy      1 AAAAAATGCTCTTCTGATGATCTGATGATCTTAAAGAAAGATGCTCGTGGAGT 60
Db      362 AAAAAATGCTCTTCTGATGATCTGATGATCTTAAAGAAAGATGCTCGTGGAGT 421
Qy      61 GACAGTCCAGTGAAGAGGAGGTGTGCTCAGATGCTGGTGAATCATTTATGAGGCT 120

```

Db 1382 AGAAGTGAAGTCCGTGCTGCTGCACATGCCCAAGCTCTGATCTAGAGCTCAAGTCAAGG 1441  
 Qy 1081 CCCATCACTGAGTGAAGGAGCAGGCTCATTAATCTGAGTGATTAATCTTGCAATTAT 1140  
 Db 1442 CCCATCACTGAGTGAAGGAGCAGGCTCATTAATCTGAGTGATTAATCTTGCAATTAT 1501  
 Qy 1141 AATGAAGCCCAAGTCAATCTCTGATGAGTGAATTTGAGCAATTTGATTTGATGAT 1200  
 Db 1502 AATGAAGCCCAAGTCAATCTCTGATGAGTGAATTTGAGCAATTTGATTTGATGAT 1561  
 Qy 1201 GACCGTCAAAATGCGCCCATATCACTGACAACCTCAAGTTTCTTGATGAGGCT 1260  
 Db 1562 GACCGTCAAAATGCGCCCATATCACTGACAACCTCAAGTTTCTTGATGAGGCT 1621  
 Qy 1261 CAGACTTTCACCTCTGAGCAATTAATCTGAGAGTTCATGAGGAGCTCTTGAAATGG 1320  
 Db 1622 CAGACTTTCACCTCTGAGCAATTAATCTGAGAGTTCATGAGGAGCTCTTGAAATGG 1681  
 Qy 1321 GCTTTGGGTGTTGTATAGTACTGAAAGGAAAGAAATGGAATGGAATATATATGA 1380  
 Db 1682 GCTTTGGGTGTTGTATAGTACTGAAAGGAAAGAAATGGAATGGAATATATATGA 1741  
 Qy 1381 GAGGAGGAGTCTTTAGTCTTGAGATTTGAAGACAGATTCAGTCAAGTCTTTACC 1440  
 Db 1742 GAGGAGGAGTCTTTAGTCTTGAGATTTGAAGACAGATTCAGTCAAGTCTTTACC 1801  
 Qy 1441 ACCTCCCAAGTACACTGAGATATGTCACAAAGCTTACCAACCATGATGATTAATCTG 1500  
 Db 1802 ACCTCCCAAGTACACTGAGATATGTCACAAAGCTTACCAACCATGATGATTAATCTG 1861  
 Qy 1501 GATTGGAAGTGAAGTGAAGTGTGAGCTTGTGATGATTAATGAAGCTCCCTATATACAC 1560  
 Db 1862 GATTGGAAGTGAAGTGAAGTGTGAGCTTGTGATGATTAATGAAGCTCCCTATATACAC 1921  
 Qy 1561 ATCCCTAATAGTCTCTTCACTCTGAGGCTTCTGAGGCTTCTTTGCTGATTAATCTG 1620  
 Db 1922 ATCCCTAATAGTCTCTTCACTCTGAGGCTTCTGAGGCTTCTTTGCTGATTAATCTG 1981  
 Qy 1621 CCAGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680  
 Db 1982 CCAGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2041  
 Qy 1681 TCTTCTTGCTGCTTATCAAAACAGAGCAAAATAGTCTGTTTATGCTTGAATGCAAT 1740  
 Db 2042 TCTTCTTGCTGCTTATCAAAACAGAGCAAAATAGTCTGTTTATGCTTGAATGCAAT 2101  
 Qy 1741 CTATGTTATTAACACTCATTTATGTTACTTAAATGAGTAAACACAAAAAAA 1800  
 Db 2102 CTATGTTATTAACACTCATTTATGTTACTTAAATGAGTAAACACAAAAAAA 2161  
 Qy 1801 AAAAAAAAAA 1811  
 Db 2162 AAAAAAAAAA 2172  
 Db  
 RESULT 3  
 ID AAS62274 standard; cDNA; 1788 BP.  
 XX AAS62274;  
 AC  
 XX  
 DT 14-FEB-2002 (first entry)  
 DE cDNA sequence #61 encoding novel human secreted protein.  
 XX  
 DE  
 XX  
 KM Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KM infectious disorder; blood disorder; inflammatory disorder;  
 KM immunosuppressive; gene therapy; antimicrobial; hepatotropic;  
 XX  
 OS Homo sapiens.  
 XX

PN WO200177291-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 29-MAR-2001; 2001WO-US10485.  
 XX  
 PR 06-APR-2000; 2000US-195604P.  
 XX  
 XX (GEMT) GENETICS INST INC.  
 PA  
 PI Wong GG, Clark HF, Fecthel K, Agostino MJ, Howes SH, Resnick RJ,  
 PI Gulukota K, Graham JR;  
 XX  
 DR WPI; 2002-010900/01.  
 XX  
 PT New polynucleotides encoding secreted proteins useful for treating e.g.  
 PT asthma, HIV and Crohn's disease -  
 XX  
 PS Claim 1; Page 106-107; 391pp; English.  
 XX  
 CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production, and the cell is also useful for identifying  
 CC compounds that modulate expression of the polynucleotide sequences  
 CC encoding the secreted proteins. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
 CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).  
 CC The polynucleotide sequences of the invention are also useful in gene  
 CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the  
 CC invention that encode for novel human secreted proteins.  
 XX  
 SQ Sequence 1788 BP; 454 A; 398 C; 444 G; 492 T; 0 other;  
 Query Match 98.1%; Score 1787.6; DB 24; Length 1788;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1787; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 GGTCTTCTGTTGATCTCTGCACTCTTACTTTGAAAGAAAGTCCGTGGAGTCA 65  
 Db 1 GGTCTTCTGTTGATCTCTGCACTCTTACTTTGAAAGAAAGTCCGTGGAGTCA 60  
 Qy 66 GTCCAGTGAAGGAGGAGTGGTGGCTCACATGCTGGTGAACATTAATTGAGACTCTT 125  
 Db 61 GTCCAGTGAAGGAGGAGTGGTGGCTCACATGCTGGTGAACATTAATTGAGACTCTT 120  
 Qy 126 TTCTGTTCACTACAGCTACTGTGAGCAAGTTCTGAGAGAGAGTGGGCACTCCG 185  
 Db 121 TTCTGTTCACTACAGCTACTGTGAGCAAGTTCTGAGAGAGAGTGGGCACTCCG 180  
 Qy 186 TGAACAGTATGAGTCAAGAGAGTGAAGGCTCATGCTGCAATCCCTGGAAAGATTC 245  
 Db 181 TGAACAGTATGAGTCAAGAGAGTGAAGGCTCATGCTGCAATCCCTGGAAAGATTC 240  
 Qy 246 AGACCCCACTCTTCCCAACATCACTGAGCTGAGATTAAGGATTCCTGCTGCA 305  
 Db 241 AGACCCCACTCTTCCCAACATCACTGAGCTGAGATTAAGGATTCCTGCTGCA 300  
 Qy 306 TTGAGCTGAGCCCTTGAAGAGAGATTAAGTCAATAGAGATTCCTCAATTTCTT 365  
 Db 301 TTGAGCTGAGCCCTTGAAGAGAGATTAAGTCAATAGAGATTCCTCAATTTCTT 360  
 Qy 366 AGAGGAAGAGGCTTGTATGCTCTGTGATGAGTCTCTCTTCTTCCGCTCCAAGA 425  
 Db 361 AGAGGAAGAGGCTTGTATGCTCTGTGATGAGTCTCTCTTCTTCCGCTCCAAGA 420  
 Qy 426 GCCCATAGTAGGGGTCAATGAGGCTGAGTCCAGTCTTTAGCAATCAGGTCAGAAAT 485

Db	1441	ACCTCCCAAGTTACACGTGACGTAAGTGTCCCAAGACCTAACCAACGATGTAGATTATTTCTGT	1500
Qy	1501	GATTGTGAAGCTAGACACTGTGAAGCTTCTTGAATGTTAATCAAAGCTCCCTTATATACAC	1560
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Qy	1801	AAAAAAAAAAAAAAAAAAAAAAAA 1823	
Db	1801	AAAAAAAAAAAAAAAAAAAAAAAA 1823	

RESULT 2  
 AAF29993  
 ID AAF29993 standard; DNA; 2172 BP.  
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 AC AAF29993;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMx-1e DNA.  
 XX  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMx;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200102566-A1.  
 XX  
 PN 11-JAN-2001.  
 XX  
 PD 27-JUN-2000; 2000WO-US17798.  
 XX  
 PF 02-JUL-1999; 99US-0346326.  
 XX  
 PR (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 XX  
 PA Schwarz DA, Makl RA;  
 XX  
 PI WPI; 2001-123112/13.  
 XX  
 DR Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 XX  
 PS Claim 2; Fig 7; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 CC  
 CC Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;  
 CC

Query Match	98.9%;	Score 1802.6;	DB 22;	Length 2172;
Best Local Similarity	99.7%;	Pred. No. 0;		
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DB	362	AAATGCTCTTCTGTTGATCTGTCACTCTTACTTTATGGAAGAAGATGTCCTGGAGT	421	
OY	61	GCACAGTCCAGTGAAGAGAGGGGTGGCTCACTGCTGGTGACATCATTTATGAGCT	120	
DB	422	GCACAGTCCAGTGAAGAGAGGGGTGGCTCACTGCTGGTGACATCATTTATGAGCT	481	
OY	121	CTCTTTCTGTTCATCAACAGCCCACTGTTGAGCAAGTTCAATGAGAGAAAGTGGGACA	180	
DB	482	CTCTTTCTGTTCATCAACAGCCCACTGTTGAGCAAGTTCAATGAGAGAAAGTGGGACA	541	
OY	181	GTCCGTGAACAGTATGACATTCAGAGAGTGAAGGCCATGCTGCATACCTCTGAAGATC	240	
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OY	241	AATTCAAGCCCACTCTTGGCCCAATCAACTGGGCTGTGATGAAGGATTCCTGC	300	
DB	602	AATTCAAGCCCACTCTTGGCCCAATCAACTGGGCTGTGATGAAGGATTCCTGC	661	
OY	301	TGGCAATTGCGTGCGGCCCTAGAGCAGAGCAAGCAATTGAGTTCAATAAGATTCCTCATTTCT	360	
DB	662	TGGCAATTGCGTGCGGCCCTAGAGCAGAGCAAGCAATTGAGTTCAATAAGATTCCTCATTTCT	721	
OY	361	TCGGAAGAGGAAGAGGCTTGGTATGCTCTGTGATGGCTCTCTCTTCCCTCCGCTCC	420	
DB	722	TCGGAAGAGGAAGAGGCTTGGTATGCTCTGTGATGGCTCTCTCTTCCCTCCGCTCC	781	
OY	421	AAGAGCCCATAGTAGGGGTCAATTGGGCTGGTCCAGTTCTTTAGCCATTCAGGTCCAG	480	
DB	782	AAGAGCCCATAGTAGGGGTCAATTGGGCTGGTCCAGTTCTTTAGCCATTCAGGTCCAG	841	
OY	481	AATTGTCTCAAGCTTTCAACATACCTCAATATGGCTACTCAGAACCATATGGGATCTG	540	
DB	842	AATTGTCTCAAGCTTTCAACATACCTCAATATGGCTACTCAGAACCATATGGGATCTG	901	
OY	541	AGTGAACAAGACTCTGTTCAAATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGACACA	600	
DB	902	AGTGAACAAGACTCTGTTCAAATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGACACA	961	
OY	601	AGGTCCATGCTGACATAGTGAAGAGGTCAACTGACCTATGTATCAGCCGTACACACA	660	
DB	962	AGGTCCATGCTGACATAGTGAAGAGGTCAACTGACCTATGTATCAGCCGTACACACA	1021	
OY	661	GAAGGCACTATGGAAGAAATGGGATGGAAGCCTTCAAAATATGTCAAGGAAGGAAGGG	720	
DB	1022	GAAGGCACTATGGAAGAAATGGGATGGAAGCCTTCAAAATATGTCAAGGAAGGAAGGG	1081	
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DB	1082	ATTTCATGCGCCACTCTTACAAAATATGACAGTATGACAGGAGCAGACTTTGATTAAG	1141	
OY	781	CTGCTGAAGAGCTCACTGATCTTGCACCAAGGCCCGGCTGGTGGCTTACTCTGTGAG	840	
DB	1142	CTGCTGAAGAGCTCACTGATCTTGCACCAAGGCCCGGCTGGTGGCTTACTCTGTGAG	1201	
OY	841	GGCATGACGGTGAAGAGTCTGCTGATATGGCCATGAAGGCGCTGGGTCTAAGTGGAGAAATTT	900	
DB	1202	GGCATGACGGTGAAGAGTCTGCTGATATGGCCATGAAGGCGCTGGGTCTAAGTGGAGAAATTT	1261	
OY	901	CTGCTTCGCGGACGGGAAACAGATGCCATCTTTATGAGATCTCAAGAACAGCATCTCA	960	
DB	1262	CTGCTTCGCGGACGGGAAACAGATGCCATCTTTATGAGATCTCAAGAACAGCATCTCA	1321	
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DB	1322	TGGGAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGTTTTTGGAGCATATTAAC	1381	
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PD 12-SEP-2002.  
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 PF 21-DEC-2001; 2001MO-US49817.  
 XX  
 PR 22-DEC-2000; 2000US-257589P.  
 XX  
 PA (AMHP) WYETH.  
 XX  
 PI Bates BG, Xie Y, Gulukota K, Paulsen JR;  
 XX  
 DR MPI; 2002-750462/81.  
 XX P-PSDB; ABP54921.  
 PT New mglur5m nucleic acid molecules and proteins, useful for treating  
 PT neurological or psychiatric disorders such as schizophrenia,  
 PT schizoaffective disorder, bipolar or unipolar affective disorder, or  
 PT adolescent conduct disorder -  
 XX  
 PS Claim 11, Fig 1A; 99p; English.  
 CC The present sequence is that of cDNA clone y1176 (deposited as  
 CC ATCC PTA-27175) encoding a novel human metabotropic glutamate  
 CC receptor subtype modulatory protein (mglur5m). The cDNA was  
 CC isolated from a human brain cDNA library. Expression of mglur5m  
 CC is predominant in cells and tissues of the central nervous system.  
 CC The gene maps to a region of chromosome 11 associated with  
 CC schizophrenia and related psychiatric disorders. The invention  
 CC provides mglur5m polypeptides and nucleic acids, and methods for  
 CC their detection, as well as methods for using them to identify  
 CC compounds that modulate metabotropic receptor (mglur) activity.  
 CC Such modulators include a mglur5m nucleic acid, a mglur5m antibody,  
 CC a ribozyme, an antisense oligonucleotide, a small molecule  
 CC modulator, a peptide and a peptidomimetic. They can be used in a  
 CC claimed method for treating a subject having a neurological  
 CC disorder, especially a psychiatric disorder selected from  
 CC schizophrenia, schizoaffective disorder, bipolar affective disorder,  
 CC unipolar affective disorder or adolescent conduct disorder (all  
 CC claimed). mglur5m polypeptides, nucleic acids and antibodies are  
 CC also useful for screening assays, and in predictive medicine, e.g.  
 CC diagnostic assays (e.g. chromosome mapping and tissue typing),  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics.  
 CC  
 CC  
 CC Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;  
 SO  
 Query Match 100.0%; Score 1822.6; DB 24; Length 1823;  
 Best Local Similarly 100.0%; Pred. No. 0;  
 Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 361 TCGAAGAGAGAGAGGCTTGGATGCTCTGTGAGAGGCTCCTCTTCTCCGCTCC 420  
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 QY 481 AATTGCTCAGCTTTTCAACATCTGAGATTTGCTTACAGCAACCATATGATATCG 540  
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 QY 541 AGTGAACAAGCTCTGTCAAAATATTTATGAGGGTGTGCTTCAGATGTCAGAGGCA 600  
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 QY 601 AGGTCCATGATGAGCACTAGTGAAGAGGTCAACTGAGCCTATGATATCAGCCGTACACA 660  
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 QY 661 GAAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGGAAGGAAGG 720  
 DB 661 GAAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGGAAGGAAGG 720  
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 DB 721 ATTGTCATGCCCCACTCTTACAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAG 780  
 QY 781 CTGCTGAAGAGTCAAGATCACTTCCCAAGGCCCGGAGTGTGCTTACTCTGTAG 840  
 DB 781 CTGCTGAAGAGTCAAGATCACTTCCCAAGGCCCGGAGTGTGCTTACTCTGTAG 840  
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 DB 841 GGCATACGGTGAAGAGTCTGCTGATGAGCAATGAGGCGCTGGGTATAGTGGAGAAATT 900  
 QY 901 CTGCTTCTGGGCGAGGAAACAGATGACATCTTATATGAGATCTCAAGAACAGACATCTTA 960  
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 DB 961 TGGGAAGACAGAAAGAAATGCAAGGTGCTTCTCAAGGTTTGGAGACATATTACAC 1020  
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 DB 1021 AGAAGTATCGCTGTGCTGCAATGCCCGGCTCTGAATCTAGAGTCACTTCAAGG 1080  
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 DB 1141 AATGAAGCAACAGTATATCTTCTGATGTGAGATTTGAGAAAGCAATTTGATTTGAGATGT 1200  
 QY 1201 GACCTGCAAAATGCGCCCATATCATCTGCAACACCTTCAAGTTTCTTGGATGAGGCTGT 1260  
 DB 1201 GACCTGCAAAATGCGCCCATATCATCTGCAACACCTTCAAGTTTCTTGGATGAGGCTGT 1260  
 QY 1261 CAGACTTTCACCTCTGGAAGATTTACTGGAAGGCTCATATGAGGAGCTCTTGGAAATTTGG 1320  
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OM nucleic - nucleic search, using sw model

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(Without alignments)  
9369.765 Million cell updates/sec

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1802.6	98.9	2172	22	AAE29993 Human GRM4-1e DNA
3	1787.6	98.1	1788	24	AAE29993 Human GRM4-1e DNA
4	1746.6	95.8	2149	22	AAE29994 Human GRM4-1e DNA
5	1615.6	88.6	2349	22	AAE29990 Human GRM4-1b DNA
6	1576.6	86.5	2064	22	AAE29995 Human GRM4-1c DNA
7	1559.6	85.6	2336	22	AAE29991 Human GRM4-1c DNA
8	1413.6	77.5	2551	22	AAE29989 Human GRM4-1a DNA

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15	891.4	48.9	4303	22	AAE29991
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26	715.6	39.3	2163	23	AAE29987
27	715.6	39.3	2163	23	AAE29989
28	458.2	25.1	2634	23	AAE29984
29	458.2	25.1	3395	24	AAE29985
30	458.2	25.1	3321	16	AAE29986
31	458.2	25.1	3382	14	AAE29987
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#### ALIGNMENTS

RESULT 1	ABV73899	standard; cDNA, 1823 BP.
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AC	ABV73899	
XX	08-JAN-2003	(first entry)
DT	08-JAN-2003	
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DE	Human glutamate receptor modulatory protein mglur5m cDNA.	
XX		
KW	Metabotropic glutamate receptor subtype 5 modulatory protein;	
KW	mglur5m; human; G-protein coupled receptor; receptor; schizophrenia;	
KW	schizophrenia; bipolar affective disorder; adolescent conduct disorder;	
KW	unipolar affective disorder; neuroleptic; neuroleptic; chromosome 11;	
KW	neuroleptic; neuroleptic; neuroleptic; chromosome 11;	
KW	gene therapy; gene; ss.	
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OS	Homo sapiens.	
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QY 361 TCGGAGAGAGAGAGGCGTTGGTATGCTCTGTGAGATGAGCTCTCTCTCTCTCTCTCTCC 420
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Db 628 AATTGCTCCAGCTTTTCAACATACCTCAAGTTGCTTACTCAGCAACCATCATGATCTG 687
QY 541 AGTGACAAGACTCTGTTCAATAATTTTCATGAGGGTTGTGCTTTCAGATGCTCAGCAGCA 600
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QY 841 GGCATGACGGGTGAGAGGTGTGCTGATGAGCCATGAGGGGCTGGGCTTATGAGGAGATTT 900
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RESULT 14
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DEFINITION Sequence 6 from patent US 6211353.
ACCESSION  ARI45367
VERSION     ARI45367.1  GI:15107234
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 4303)
AUTHORS    Burnett,J.Paul, Jr., Mayne,N.Gall., Sharp,R.Leon. and
            Snyder,X.Marie.
            Isolated nucleic acid encoding a human mgluR5
            Patent: US 6211353-A 6 03-APR-2001;
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BASE COUNT  1043 a 1139 c 1144 g 977 t
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Best Local Similarity 98.3%; Pred. No. 2.6e-226;
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy      121 CTCTTTCTGTTGATCAACAGCCTACTGTGACAGCAAGTTGATGAGAGAGTGGGCA 180
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Qy      181 GTCCGTGAACAGTATGGCATTCAGAGAGTGAAGCCATGCTGCATACCTCGAAGATC 240
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Qy      481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATGATCTG 540
Db      937 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGAACCATCATGATCTG 996
Qy      541 AGTGAACAAGACTCTGTCCAAATATTTCAATGAGGGTGTGCTTCAATGCTCAGACGCA 600
Db      997 AGTGAACAAGACTCTGTCCAAATATTTCAATGAGGGTGTGCTTCAATGCTCAGACGCA 1056
Qy      601 AGTGAACAAGACTCTGTCCAAATATTTCAATGAGGGTGTGCTTCAATGCTCAGACGCA 660

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Db      1057 AGGGCCATGTGGACATATGTAAAGGTATCAATGGACCTATGATCACCGGACACACA 1116
Qy      661 GAAGGCACATATGAGAAAGTGGATGAAAGCTTTAAAGATATGTCAAGCAAGAGAGG 720
Db      1117 GAAGGCACATATGAGAAAGTGGATGAAAGCTTTAAAGATATGTCAAGCAAGAGAGG 1176
Qy      721 AATTGATGGCCCACTTACAAATCTACAGTAATGACGGGAGAGAGCTTGTATAG 780
Db      1177 AATTGATGGCCCACTTACAAATCTACAGTAATGACGGGAGAGAGCTTGTATAG 1236
Qy      781 CTGCTGAAGAGCTCAACAGTCACTTGCCCAAGCCCGGTGTGCTTCTGTGAG 840
Db      1237 CTGCTGAAGAGCTCAACAGTCACTTGCCCAAGCCCGGTGTGCTTCTGTGAG 1296
Qy      841 GGCATACCGTGAAGAGCTTCTGCTGATGGCCATGAGAGCCGCTGGTCTAGTGGAGAAATTT 900
Db      1297 GGCATACCGTGAAGAGCTTCTGCTGATGGCCATGAGAGCCGCTGGTCTAGTGGAGAAATTT 1356
Qy      901 CTGCTTCTGGGACAGGA 917
Db      1357 CTGCTTCTGGGACAGTA 1373

RESULT 15
AX548892
LOCUS      AX548892          4518 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 177 from Patent W002061087.
ACCESSION  AX548892
VERSION     AX548892.1  GI:25813755
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1
AUTHORS    Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE      Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
            Patent: WO 02061087-A 177 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
            Location/Qualifiers
                source          1..4518
                               /organism="Homo sapiens"
                               /mol_type="genomic DNA"
                               /db_xref="taxon:9606"
BASE COUNT  1114 a 1170 c 1145 g 1089 t
ORIGIN
Query Match      48.9%; Score 891.4; DB 6; Length 4518;
Best Local Similarity 98.3%; Pred. No. 2.6e-226;
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy      1 AAAATGCTCTTCTGTTGATCTGTCACTTACTTTTGAAGAAGATGCTGGAGT 60
Db      148 AAAATGCTCTTCTGTTGATCTGTCACTTACTTTTGAAGAAGATGCTGGAGT 207
Qy      61 GCACAGTCCAGTGAAGAGAGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 120
Db      208 GCACAGTCCAGTGAAGAGAGGTGGTGCACATGCTGGGTGACATCATTTATTTGAGCT 267
Qy      121 CTCTTTCTGTTGATCAACAGCCTACTGTGACAGAACTTATGAGAGAGTGGGCA 180
Db      268 CTCTTTCTGTTGATCAACAGCCTACTGTGACAGAACTTATGAGAGAGTGGGCG 327
Qy      181 GTCCGTGAACAGTATGGCATTCAGAGAGTGAAGCCATGCTGACATACCTCGAAGATC 240
Db      328 GTCCGTGAACAGTATGGCATTCAGAGAGTGAAGCCATGCTGACATACCTCGAAGATC 387
Qy      241 AATTGAGACCCACACTTGGCCCAATCACTGGGCTGTGATTAAGGAATTCCTGC 300
Db      388 AATTGAGACCCACACTTGGCCCAATCACTGGGCTGTGATTAAGGAATTCCTGC 447

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Db 457 AAAATGCTCTTCTGTGATCTGTGACGTCTTAATTGAAAGAGATGCCGGAGT 516  
Qy 61 GCACAGTCCAGTGAAGAGAGGAGTGGTCAATGCTGGGTGACATCATTTATGAGCT 120  
Db 517 GCACAGTCCAGTGAAGAGAGGAGTGGTCAATGCTGGGTGACATCATTTATGAGCT 576  
Qy 121 CTCTTTTCTGTTCAATCAAGCTTCTGTGACGAAAGTTCATGAGAAAGTGGGCA 180  
Db 577 CTCTTTTCTGTTCAATCAAGCTTCTGTGACGAAAGTTCATGAGAAAGTGGGCG 636  
Qy 181 GTCCGGAACAGTATGGCATTTGAGAGTGGAGCCATGCTGATACCTCTGAAAGATC 240  
Db 637 GTCCGGAACAGTATGGCATTTGAGAGTGGAGCCATGCTGATACCTCTGAAAGATC 696  
Qy 241 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 300  
Db 697 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 756  
Qy 301 TGGCATTCGGCTGTGGCCCTTGAAGAGCATTTGATTAAGAGATTCCTCATTTCT 360  
Db 757 TGGCATTCGGCTGTGGCCCTTGAAGAGCATTTGATTAAGAGATTCCTCATTTCT 816  
Qy 361 TCGGAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGCTCTCTCTTCCGCTCC 420  
Db 817 TCGGAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGCTCTCTCTTCCGCTCC 876  
Qy 421 AAGAACCCCAATAGTAGGGGTCAATTGGGCTGTGGCCATTTAGCATTAAGTCCAG 480  
Db 877 AAGAACCCCAATAGTAGGGGTCAATTGGGCTGTGGCCATTTAGCATTAAGTCCAG 936  
Qy 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTAACAGCAACATCATGATCTG 540  
Db 937 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTAACAGCAACATCATGATCTG 996  
Qy 541 AGTGAACAAGACTTGTTCAAATATTTCAATGAGGCTTGTGCTTCAATGCTCAGAGCA 600  
Db 997 AGTGAACAAGACTTGTTCAAATATTTCAATGAGGCTTGTGCTTCAATGCTCAGAGCA 1056  
Qy 601 AGGTCCATGATGACATAGTAAGAGATCAACTGAGCCATGATCAGCCGACACCA 660  
Db 1057 AGGTCCATGATGACATAGTAAGAGATCAACTGAGCCATGATCAGCCGACACCA 1116  
Qy 661 GAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGGAGAGAGG 720  
Db 1117 GAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGGAGAGAGG 1176  
Qy 721 ATTGATGAGCCCACTTTACAAATCTTACAGTAATGTCAGGAGAGAGCTTGAATAG 780  
Db 1177 ATTGATGAGCCCACTTTACAAATCTTACAGTAATGTCAGGAGAGAGCTTGAATAG 1236  
Qy 781 CTGCTGAAGAGCTCAAGAGTCACTTGGCCAAAGCCCGGGTGGTGGCTTCTGTAG 840  
Db 1237 CTGCTGAAGAGCTCAAGAGTCACTTGGCCAAAGCCCGGGTGGTGGCTTCTGTAG 1296  
Qy 841 GGCATGACGATGAGAGAGTCTGCTGATGAGCAGCCTGGGCTTATGAGGAGATTT 900  
Db 1297 GGCATGACGATGAGAGAGTCTGCTGATGAGCAGCCTGGGCTTATGAGGAGATTT 1356  
Qy 901 CTGCTTCTGGGAGAGGA 917  
Db 1357 CTGCTTCTGGGAGAGGA 1373

RESULT 13  
ARI45366 ARI45366 4303 bp DNA 1linear PAT 08-AUG-2001  
DEFINITION Sequence 4 from Patent US 6211353.  
ACCESSION ARI45366  
VERSION ARI45366.1 GI:15107233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

Unclassified.

REFERENCE 1 (bases 1 to 4303)  
AUTHORS Burnett,J.Paul., Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder Y.Marie.  
TITLE Isolated nucleic acid encoding a human mclurs  
JOURNAL Patent: US 6211353-A 4 03-APR-2001;  
FEATURES  
source Location/Qualifiers  
1. 4303  
BASE COUNT 1044 a 1138 c 1144 g 977 t  
ORIGIN  
Query Match 48.9%; Score 891.4; DB 6; Length 4303;  
Best Local Similarity 98.3%; Pred. No. 2.6e-226;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
Qy 1 AAAATGCTCTTCTGTGATCTGTGACGTCTTAATTGAAAGAGATGCCGGAGT 60  
Db 457 AAAATGCTCTTCTGTGATCTGTGACGTCTTAATTGAAAGAGATGCCGGAGT 516  
Qy 61 GCACAGTCCAGTGAAGAGAGGAGTGGTCAATGCTGGGTGACATCATTTATGAGCT 120  
Db 517 GCACAGTCCAGTGAAGAGAGGAGTGGTCAATGCTGGGTGACATCATTTATGAGCT 576  
Qy 121 CTCTTTTCTGTTCAATCAAGCTTCTGTGACGAAAGTTCATGAGAAAGTGGGCA 180  
Db 577 CTCTTTTCTGTTCAATCAAGCTTCTGTGACGAAAGTTCATGAGAAAGTGGGCG 636  
Qy 181 GTCCGGAACAGTATGGCATTTGAGAGTGGAGCCATGCTGATACCTCTGAAAGATC 240  
Db 637 GTCCGGAACAGTATGGCATTTGAGAGTGGAGCCATGCTGATACCTCTGAAAGATC 696  
Qy 241 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 300  
Db 697 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGC 756  
Qy 301 TGGCATTCGGCTGTGGCCCTTGAAGAGCATTTGATTAAGAGATTCCTCATTTCT 360  
Db 757 TGGCATTCGGCTGTGGCCCTTGAAGAGCATTTGATTAAGAGATTCCTCATTTCT 816  
Qy 361 TCGGAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGCTCTCTCTTCCGCTCC 420  
Db 757 TCGGAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGCTCTCTCTTCCGCTCC 876  
Qy 421 AAGAACCCCAATAGTAGGGGTCAATTGGGCTGTGGCCATTTAGCATTAAGTCCAG 480  
Db 877 AAGAACCCCAATAGTAGGGGTCAATTGGGCTGTGGCCATTTAGCATTAAGTCCAG 936  
Qy 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTAACAGCAACATCATGATCTG 540  
Db 937 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTAACAGCAACATCATGATCTG 996  
Qy 541 AGTGAACAAGACTTGTTCAAATATTTCAATGAGGCTTGTGCTTCAATGCTCAGAGCA 600  
Db 997 AGTGAACAAGACTTGTTCAAATATTTCAATGAGGCTTGTGCTTCAATGCTCAGAGCA 1056  
Qy 601 AGGTCCATGATGACATAGTAAGAGTCAACTGAGCCATGATCAGCCGACACCA 660  
Db 1057 AGGTCCATGATGACATAGTAAGAGTCAACTGAGCCATGATCAGCCGACACCA 1116  
Qy 661 GAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGGAGAGAGG 720  
Db 1117 GAAAGCACTATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGGAGAGAGG 1176  
Qy 721 ATTGATGAGCCCACTTTACAAATCTTACAGTAATGTCAGGAGAGAGCTTGAATAG 780  
Db 1177 ATTGATGAGCCCACTTTACAAATCTTACAGTAATGTCAGGAGAGAGCTTGAATAG 1236  
Qy 781 CTGCTGAAGAGCTCAAGAGTCACTTGGCCAAAGCCCGGGTGGTGGCTTCTGTAG 840  
Db 1237 CTGCTGAAGAGCTCAAGAGTCACTTGGCCAAAGCCCGGGTGGTGGCTTCTGTAG 1296  
Qy 841 GGCATGACGATGAGAGAGTCTGCTGATGAGCAGCCTGGGCTTATGAGGAGATTT 900  
Db 1297 GGCATGACGATGAGAGAGTCTGCTGATGAGCAGCCTGGGCTTATGAGGAGATTT 1356

QY 541 AGTGAAGACTCTGTCAATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGGCA 600  
DB 688 AGTGAAGACTCTGTCAATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGGCA 747  
QY 601 AGTGCATGTGTGACATAGTGAAGAGTCACTGACCTTATGTATCAGCCGTACACACA 660  
DB 748 AGGGCCATGTGTGACATAGTGAAGAGTCACTGACCTTATGTATCAGCCGTACACACA 807  
QY 661 GAAGGCAACTATGTGAAGAAAGTGGATGGAGCCCTTCAAGATATGTACAGGAAGAAAGG 720  
DB 808 GAAGGCAACTATGTGAAGAAAGTGGATGGAGCCCTTCAAGATATGTACAGGAAGAAAGG 867  
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DB 868 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGCAGACCTTGTATAG 927  
QY 781 CTGCTGAAGAGTCACTCAAGTCACTTGCCTCAAGGCCCGGGTGTGCTTCTGTGAG 840  
DB 928 CTGCTGAAGAGTCACTCAAGTCACTTGCCTCAAGGCCCGGGTGTGCTTCTGTGAG 987  
QY 841 GGATGACGGTGAAGAGTCTGTGATGAGCCATGAGAGGCTTGGGTCTAGTGGAGAAATT 900  
DB 988 GGATGACGGTGAAGAGTCTGTGATGAGCCATGAGAGGCTTGGGTCTAGTGGAGAAATT 1047  
QY 901 CTGCTTCTGGGACAGGA 917  
DB 1048 CTGCTTCTGGGACAGTGA 1064

RESULT 11  
ARI45364 4207 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 1 from patent US 6211353.  
DEFINITION ARI45364  
ACCESSION ARI45364  
VERSION ARI45364.1 GI:15107231  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4207)  
AUTHORS Burnette,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mglurs  
JOURNAL Patent: US 6211353-A 1 03-APR-2001;  
FEATURES  
Location/Qualifiers  
source 1..4207  
BASE COUNT 1011 a 1120 c 1112 g 964 t

Query Match 48.9%; Score 891.4; DB 6; Length 4207;  
Best Local Similarity 98.3%; Pred. No. 2.5e-226;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGTCCTTCTGTGATCTGTCACTTACTTTTGAAGAAGATGCCGTGGAGT 60  
DB 457 AAAATGTCCTTCTGTGATCTGTCACTTACTTTTGAAGAAGATGCCGTGGAGT 516  
QY 61 GCAAGTCAGTGAAGAGAGGTGTGTGCTCACTGCTGGGTGACATCATTTATGAGCT 120  
DB 517 GCAAGTCAGTGAAGAGAGGTGTGTGCTCACTGCTGGGTGACATCATTTATGAGCT 576  
QY 121 CTCTTTTCTGTTCATCACTGCTCACTGTGTGAGCAAACTTCAATGAGAGAAAGTGTGGGCA 180  
DB 577 CTCTTTTCTGTTCATCACTGCTCACTGTGTGAGCAAACTTCAATGAGAGAAAGTGTGGGCG 636  
QY 181 GTCGTAAGCAGTATGSCATTTCAAGAGTGAAGGCCATGTGCTACCTCTGAAAGATC 240  
DB 637 GTCGTAAGCAGTATGSCATTTCAAGAGTGAAGGCCATGTGCTACCTCTGAAAGATC 696  
QY 241 AATTGACAGCCCACTCTTGTGCCCAACATCACTGAGGCTGTGAGATTAAGGGAATCTCTGC 300  
DB 697 AATTGACAGCCCACTCTTGTGCCCAACATCACTGAGGCTGTGAGATTAAGGGAATCTCTGC 756

QY 301 TGGCATTCGGCTGTGGCCCTAGAGCAGACATTTGAGTTGATTAAGAGATTCCTCATTTCT 360  
DB 757 TGGCATTCGGCTGTGGCCCTAGAGCAGACATTTGAGTTGATTAAGAGATTCCTCATTTCT 816  
QY 361 TCGAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGCTCTCTCTTCTTCCGCTCC 420  
DB 817 TCGAAGAGAAAGAGGCTTGGTATGCTGTGTGATGAGCTCTCTCTTCTTCCGCTCC 876  
QY 421 AAGAACCCATAGTAGGGTCAATTGGGCTGTGTTCAGTTCTTTAGCCATTCAGGTCAG 480  
DB 877 AAGAACCCATAGTAGGGTCAATTGGGCTGTGTTCAGTTCTTTAGCCATTCAGGTCAG 936  
QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACCATCATGATCTG 540  
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QY 541 AGTGAAGACTCTGTCAATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGGCA 600  
DB 997 AGTGAAGACTCTGTCAATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGGCA 1056  
QY 601 AGTGCATGTGTGACATAGTGAAGAGTACACTGACCTTATGTATCAGCCGTACACACA 660  
DB 1057 AGGGCCATGTGTGACATAGTGAAGAGTACACTGACCTTATGTATCAGCCGTACACACA 1116  
QY 661 GAAGGCAACTATGTGAAGAAAGTGGATGGAGCCCTTCAAGATATGTCAAGGAAGAAAGG 720  
DB 1117 GAAGGCAACTATGTGAAGAAAGTGGATGGAGCCCTTCAAGATATGTCAAGGAAGAAAGG 1176  
QY 721 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGCAGACCTTGTATAG 780  
DB 1177 ATTGATGCGCCCACTCTTACAAATCTACATATGACAGGAGCAGACCTTGTATAG 1236  
QY 781 CTGCTGAAGAGTCACTCAAGTCACTTGCCTCAAGGCCCGGGTGTGCTTCTGTGAG 840  
DB 1237 CTGCTGAAGAGTCACTCAAGTCACTTGCCTCAAGGCCCGGGTGTGCTTCTGTGAG 1296  
QY 841 GGATGACGGTGAAGAGTCTGTGATGAGCCATGAGAGGCTTGGGTCTAGTGGAGAAATT 900  
DB 1297 GGATGACGGTGAAGAGTCTGTGATGAGCCATGAGAGGCTTGGGTCTAGTGGAGAAATT 1356  
QY 901 CTGCTTCTGGGACAGGA 917  
DB 1357 CTGCTTCTGGGACAGTGA 1373

RESULT 12  
ARI45365 4207 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 3 from patent US 6211353.  
DEFINITION ARI45365  
ACCESSION ARI45365  
VERSION ARI45365.1 GI:15107232  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4207)  
AUTHORS Burnette,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mglurs  
JOURNAL Patent: US 6211353-A 3 03-APR-2001;  
FEATURES  
Location/Qualifiers  
source 1..4207  
BASE COUNT 1010 a 1121 c 1112 g 964 t

Query Match 48.9%; Score 891.4; DB 6; Length 4207;  
Best Local Similarity 98.3%; Pred. No. 2.5e-226;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGTCCTTCTGTGATCTGTCACTTACTTTTGAAGAAGATGCCGTGGAGT 60  
|||||

FCGEMTVRLMMARLGLVGEELLGREDPAIFIEIKSNLSIMEDRRKCOGRFLQGF  
 GDILHSESVILHMPDLNLELSSGPITGDRRLI"  
 BASE COUNT 276 a 253 c 306 g 275 t  
 ORIGIN

Query Match 60.9%; Score 1110; DB 6; Length 1110;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-285;  
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 ATGGCTCTGCTGATCGTGCAGTCTTCTTTGAAGAAGATGCCGGGAGGCA 60  
 64 CAGTCCAGTGAAGAGGAGTGTGCTCAATGCTGGGTGACATATTATGAGCTCTC 123  
 61 CAGTCCAGTGAAGAGGAGTGTGCTCAATGCTGGGTGACATATTATGAGCTCTC 120  
 124 TTTTCTGTTCAATCCAGCTTCTGTGAGCAAGTTCAATGAGAAAGTGGGGCAGTC 183  
 121 TTTTCTGTTCAATCCAGCTTCTGTGAGCAAGTTCAATGAGAAAGTGGGGCAGTC 180  
 184 CCGTAACAGTATGGCATTTCAAGAGTGAAGGCCATGCTGATACCTCGAAAGATCAAT 243  
 181 CCGTAACAGTATGGCATTTCAAGAGTGAAGGCCATGCTGATACCTCGAAAGATCAAT 240  
 244 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAAGGATTCCTGCTGG 303  
 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAAGGATTCCTGCTGG 300  
 304 CATTCGGCTGTGGCCCTTGAAGCAGAGCATTGATTAAGATTCCTCATTTCTTCG 363  
 301 CATTCGGCTGTGGCCCTTGAAGCAGAGCATTGATTAAGATTCCTCATTTCTTCG 360  
 364 GAAGAGAAAGAGGCTTGTGATGCTCTGTGATGAGTCCCTCTTCTTCCGCTCAAG 423  
 361 GAAGAGAAAGAGGCTTGTGATGCTCTGTGATGAGTCCCTCTTCTTCCGCTCAAG 420  
 424 AACCCCATAGTAGGGGCTATTGGGCTGTGCTCAGTCTTTAGCATTCAAGTCCAGAT 483  
 421 AACCCCATAGTAGGGGCTATTGGGCTGTGCTCAGTCTTTAGCATTCAAGTCCAGAT 480  
 484 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATGAT 543  
 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATGATGAT 540  
 544 GAAAGACTCTGTTCAAAATTTTCAAGAGGCTGTGCTCAGATGCTCAGCAGGCAAG 603  
 541 GAAAGACTCTGTTCAAAATTTTCAAGAGGCTGTGCTCAGATGCTCAGCAGGCAAG 600  
 604 TCCATGCTGACATAGTAGGAGTGAAGCTGACCTATGATCAGCCGTACACAGAA 663  
 601 TCCATGCTGACATAGTAGGAGTGAAGCTGACCTATGATCAGCCGTACACAGAA 660  
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 661 GGGCACTATGAGAAAGTGGATGGAAGCTTCAAAAGATATGTCAGGGAAGAGGAT 720  
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 781 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCCGGGTGTGCTTCTCTGAGAGGC 840  
 844 ATGACGCTGAGAGATCTGCTGATGAGCAGTGGCTGTAGTGAAGAAATTTCTG 903  
 841 ATGACGCTGAGAGATCTGCTGATGAGCAGTGGCTGTAGTGAAGAAATTTCTG 900  
 904 CTTCCTGGGCGAGGAAACAGATGCCATTTTATGAGATCTCAAGAAACAGATCTATGG 963  
 901 CTTCCTGGGCGAGGAAACAGATGCCATTTTATGAGATCTCAAGAAACAGATCTATGG 960

QY 964 GAAGACAGAAAGAAATGCCAAGGTGCTCTTCAAGGTTTGGAGACATATTACAGA 1023  
 DB 961 GAAGACAGAAAGAAATGCCAAGGTGCTCTTCAAGGTTTGGAGACATATTACAGA 1020  
 QY 1024 AGTAGTCCGCTGCTGCTGCAATGCCAGCCTCTGAATTTAGAGTCAAGTTCAGGCCCC 1083  
 DB 1021 AGTAGTCCGCTGCTGCTGCAATGCCAGCCTCTGAATTTAGAGTCAAGTTCAGGCCCC 1080  
 QY 1084 ATCAGTGAATGAGGAGCAGGCTCATCTAA 1113  
 DB 1081 ATCAGTGAATGAGGAGCAGGCTCATCTAA 1110

RESULT 10  
 AR270570  
 LOCUS AR270570 4078 bp DNA linear PAT 10-APR-2003  
 DEFINITION Sequence 1133 from patent US 6500938.  
 ACCESSION AR270570  
 VERSION AR270570.1 GI:29701804  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4078)  
 AUTHORS Au-Young,J. and Sellhammer,J.J.  
 TITLE Composition for the detection of signaling pathway gene expression  
 JOURNAL Patent: US 6500938-A 1133 31-DEC-2002;  
 FEATURES  
 source 1..4078  
 /organism="unknown"  
 BASE COUNT 994 a 1074 c 1076 g 934 t  
 ORIGIN

Query Match 48.9%; Score 891.4; DB 6; Length 4078;  
 Best Local Similarity 98.3%; Pred. No. 2.5e-226;  
 Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAATGGCTCTGTTGATCCGTGAGTCTTCTTTGAAGAAGATGCCGGGAGT 60  
 DB 148 AAAATGGCTCTGTTGATCCGTGAGTCTTCTTTGAAGAAGATGCCGGGAGT 207  
 QY 61 GCACAGTCCAGTGAAGAGGAGTGTGCTCAGATGCTGGGTGACATCATATTATGAGCT 120  
 DB 208 GCACAGTCCAGTGAAGAGGAGTGTGCTCAGATGCTGGGTGACATCATATTATGAGCT 267  
 QY 121 CTCTTTTCTGTTATCAACAGCTTACTGTGAGCAAGTTCAATGAGAAAGTGTGGGCA 180  
 DB 268 CTCTTTTCTGTTATCAACAGCTTACTGTGAGCAAGTTCAATGAGAAAGTGTGGGCG 327  
 QY 181 GTCCGGAACAGTATGGCAATTCAGAGAGTGAAGCCATGCTGATACCTGGAAGGATC 240  
 DB 328 GTCCGGAACAGTATGGCAATTCAGAGAGTGAAGCCATGCTGATACCTGGAAGGATC 387  
 QY 241 AATTGACGCCCACTCTTGGCCCAATCACTGAGCTGTGAGATTAAGGATTCCTG 300  
 DB 388 AATTGACGCCCACTCTTGGCCCAATCACTGAGCTGTGAGATTAAGGATTCCTG 447  
 QY 301 TGGCATTCGGCTGTGAGCCCTTGAAGCAGAGCATTGATTAAGAGATTCCTCATTTCT 360  
 DB 448 TGGCATTCGGCTGTGAGCCCTTGAAGCAGAGCATTGATTAAGAGATTCCTCATTTCT 507  
 QY 361 TCGGAAGAGAGAGGCTTGTGATGCTCTGTGATGAGTCTCTCTCTTCTCCGCTCC 420  
 DB 508 TCGGAAGAGAGAGGCTTGTGATGCTCTGTGATGAGTCTCTCTCTTCTCCGCTCC 567  
 QY 421 AAGAAGCCCAATGATGAGGCTCATTTGGGCTGTGATTCAGTTCTTTAGCCATTCAGTCCAG 480  
 DB 568 AAGAAGCCCAATGATGAGGCTCATTTGGGCTGTGATTCAGTTCTTTAGCCATTCAGTCCAG 627  
 QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAAGCAACATCATGATCTG 540  
 DB 628 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAAGCAACATCATGATCTG 687



QY 361 TGGGAAGGAGAGAGGCTTGGATGCTGCTGGGA TGGCTCTCTCTTCCTCCGCTCC 420  
 Db 722 TCGGAAGGAGAGAGGCTTGGATGCTGCTGGGA TGGCTCTCTCTTCCTCCGCTCC 781  
 QY 421 AAGAGCCCACTAGTAGGGGCTCATTTGGGCTGCTTCCAGTTCTTTAGCCATTCAGTCCAG 480  
 Db 782 AAGAGCCCACTAGTAGGGGCTCATTTGGGCTGCTTCCAGTTCTTTAGCCATTCAGTCCAG 841  
 QY 481 AATTTCCTCAGCTTTTCAACATACCTCAGATTGCTTACAGAACCATCATCATGATCTG 540  
 Db 842 AATTTCCTCAGCTTTTCAACATACCTCAGATTGCTTACAGAACCATCATCATGATCTG 901  
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 Db 902 AAGTCAAGAGCTGCTTCAAAATATTTCAATGAGGGTTGTGCTTCAAGTGTCCAGAGGCA 961  
 QY 601 AGGTCCATGCTGAGCATAGTGAAGAGTCAACTGACCTATGATACGCCGTACACACA 660  
 Db 962 AGGTCCATGCTGAGCATAGTGAAGAGTCAACTGACCTATGATACGCCGTACACACA 1021  
 QY 661 GA----- 662  
 Db 1022 GAAGGTTCAAGCTATTCTCATGCTCAGCTCAGAGAGCTAGGCTGCTTCAACTCT 1081  
 QY 663 ----- 662  
 Db 1082 TGGCTCAGAGTATCTGCTGCTTGGGCTTCCAAATTGCTGGGATTTAGGGCATGAGCC 1141  
 QY 663 -----A 663  
 Db 1142 ACCGACGACCCGGCCAGTCCGATCTTGAACACTCTTGAAGTGTCTTCTGATTTTA 1201  
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 Db 1202 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGGGAAGAGGATTT 1261  
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 DEFINITION Sequence 3 from Patent W002070708.  
 ACCESSION AX709349  
 VERSION AX709349.1 GI:29564891  
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 REFERENCE  
 1 Batee,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
 Glutamate receptor modulatory proteins and nucleic acids encoding  
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AX068371.1 GI:12578536
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Schwarz, D.A. and Maki, R.A.
Metabotropic glutamate receptors and methods of use therefor
Patent: WO 0102566-A 6 11-JAN-2001;
Neurocrine Biosciences, Inc. (US)

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REFERENCE
AUTHORS      1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE         1 Mammalia; Buthera; Primates; Catarrhini; Homnidae; Homo.
JOURNAL
FEATURES
source        1 Schwarz, D. A. and Maki, R. A.
               Metabotropic glutamate receptors and methods of use therefor
               Patent: WO 0102566-A 1 11-JUN-2001;
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241 AATTCAGACCCCAACAATTCTTCCCCA...GTTGGATC 60L

301 TGGCATTGCGCTGTGACCCAGAGCACCAATTTA..... 681

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 ACCESSION AX068370  
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 REFERENCE 1  
 AUTHORS Schwarz, D.A. and Maki, R.A.  
 TITLES Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 5 11-JAN-2001;  
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 ACCESSION AX068376  
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 AUTHORS Schwarz,D.A. and Maki,R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 11 11-JAN-2001;  
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 DB 962 AGTCAATGTGACATATGTAAGAGGTAACTGACCTATGCTACAGCCGATCAACACA 1021  
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 DB 1022 GAAAGCACTATGAGAAAGTGGATGAAAGCTTCAAAAGATATGTCAGGAAAGAGG 1081  
 QY 721 ATTTGATGCGCCACTCTTACAAATCTACAGTATGACAGGGAGGAGGAGCTTTGATAG 780  
 DB 1082 ATTTGATGCGCCACTCTTACAAATCTACAGTATGACAGGGAGGAGGAGCTTTGATAG 1141  
 QY 781 CTGCTGAAGAGTCAAGTCACTTGGCCCAAGGCCCGGGTGTGGCTTACTTCTTGAG 840  
 DB 1142 CTGCTGAAGAGTCAAGTCACTTGGCCCAAGGCCCGGGTGTGGCTTACTTCTTGAG 1201  
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 DB 1202 GGCATGACGGTGAAGAGTCTGATGACCATGAGGCGCTGGGCTTAAAGGAGAAATT 1261  
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 DB 1262 CTGCTTCTGGGCAAGGAAACCATGTGCATCTTATTAAGATCTCAAGAACACATCTTA 1272  
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 DB 1334 CCGATCACTGACTGAGGAGCAGGCTCATCTAATTTCTGAGTGAATTAATCTGCAATTAT 1393  
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Db	1899	ATCCGTAATGTGCTCTTCAACCTCCTCTCAAGGCGCTACTCTTTGGTGATTCATCTCGA	1958
Qy	1621	CCAGAGACAAATCAGAAATGTGTTATCTGCTGTGGGAACCCCTTATCCCAATAAAGCC	1680
Db	1959	CCAGAGACAAATCAGAAATGTGTTATCTGCTGTGGGAACCCCTTATCCCAATAAAGCC	2018
Qy	1681	TCTTCCTGTGCTTATCAAAACAGGACAAATAGGTCGTTTATAGTCTTAAATTCATT	1740
Db	2019	TCTTCCTTATGCTTATCAAAACAGGACAAATAGGTCGTTTATAGTCTTAAATTCATT	2078
Qy	1741	CTAATGTTATTAACCTCATTATTTGTTTACTATTAATGTGTAATAACAAAA	1800
Db	2079	CTAATGTTATTAACCTCATTATTTGTTTACTATTAATGTGTAATAACCTTAAAA	2138
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RESULT 4			
AX068368	AX068368	2349 bp	DNA linear PAT 25-JAN-2001
LOCUS	Sequence 3 from Patent WO0102566.		
DEFINITION	AX068368		
ACCESSION	AX068368.1	GI:12578534	
VERSION			
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	Schwartz,D.A. and Maki,R.A.		
AUTHORS	Metabotropic glutamate receptors and methods of use therefor		
TITLE	Patent: WO 0102566-A 3 11-JAN-2001;		
JOURNAL	Neurocrine Biosciences, Inc. (US)		
FEATURES	Location/Qualifiers		
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Query Match	88.6%; Score 1615.6; DB 6; Length 2349;		
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Matches 1805; Conservative 1; Mismatches 5; Indels 177; Gaps 1;			
Qy	1	AAATGTCCTTCTGTGATCTGTGACGTCTTACTTTTGAAGAAGATGTCGGGAGT	60
Db	362	AAATGTCCTTCTGTGATCTGTGACGTCTTACTTTTGAAGAAGATGTCGGGAGT	421
Qy	61	GCACAGTCAGATGAGAGAGGGGTGGCTCACATGCTGGTGACATCTTATTTGAGCT	120
Db	422	GCAACGTCCAGTGAAGAGAGGGGTGGCTCACATGCTGGTGACATCTTATTTGAGCT	481
Qy	121	CTCTTTCTGTTCATCACACGCTTACTGTGTGACGAAGTTCATGTGAGAGAAAGTGTGGGCA	180
Db	482	CTCTTTCTGTTCATCACACGCTTACTGTGTGACGAAGTTCATGTGAGAGAAAGTGTGGGCA	541
Qy	181	GTCGTGAACAGTATGTGCAATTCAGAGAGTGAAGGCCATGCTGCATACCCGTGGAAGATC	240
Db	542	GTCGTGAACAGTATGTGCAATTCAGAGAGTGAAGGCCATGCTGCATACCCGTGGAAGATC	601
Qy	241	AATTCAGACCCCACTCTTGCCCAATCACTGAGGCTGTGAGATTAAGGAATTCCTGC	300
Db	602	AATTCAGACCCCACTCTTGCCCAATCACTGAGGCTGTGAGATTAAGGAATTCCTGC	661
Qy	301	TGGCAATTCGGCTGTGGCCCTAGAGCAGAGCATTAAGTTCATTAAGAGATTCCTCATTTCT	360
Db	662	TGGCAATTCGGCTGTGGCCCTAGAGCAGAGCATTAAGTTCATTAAGAGATTCCTCATTTCT	721
Qy	361	TTCGAAGAAGAGAGGCTTGGTATGCTCTGTGATGGCTTCCTCTTCTTCCGCTCC	420

Db	722	TCGAAAGAGAAAGAGCGTTGGTGTGCTCTGTGGATGGCTCTCCTCTTCCGCTCC	781
Qy	421	AAGAAGCCCATAGTAGAGGGTCAATGGGCTGGTTCAGTTCTTAAAGCATTCAGGTCAAG	480
Db	782	AAGAAGCCCATAGTAGAGGGTCAATGGGCTGGTTCAGTTCTGTAAGCATTCAGGTCCAG	841
Qy	481	AATTTGCTCCAGCTTTTCAATATACCTCAGATTCCTTAACAGAACCATATGATCTGTG	540
Db	842	AATTTGCTCCAGCTTTTCAATATACCTCAGATTCCTTAACAGAACCATATGATCTGTG	901
Qy	541	AGTGCACAAGCTCTGTTCAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGACA	600
Db	902	AGTGCACAAGACTCTGTTCAAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGACA	961
Qy	601	AGGTCCATGTGTGACATATGTGAAGAGGTACAATGGACCTATGTATCAGCCGTACACA	660
Db	962	AGGTCCATGTGTGACATATGTGAAGAGGTACAATGGACCTATGTATCAGCCGTACACA	1021
Qy	661	GA-----	662
Db	1022	GAAAGTTCAAGCTATTCATGCTCAGCTCAGCCACCTCAGAGAGCTAGGTCTTCAACTCT	1081
Qy	663	-----	662
Db	1082	TGGCCTCAAGTGAATCTGCTGCTTTGGCCTTCCAAATTTGCTGGATTATGGGACATGAGCC	1141
Qy	663	-----	663
Db	1142	ACCAACAGACCCGGCCAGTGGCCGACTTGAACAACACTTTGAGGTGCTTCTGATTTTTA	1201
Qy	664	GGCAACTATGAGAAAGTGGGATGGAAGCTTCAAAGTATGTCAAGCGAAGAAAGGATT	723
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Qy	724	TGCATGCGCCCACTCTTACAAAATCTAACAGTAAATGACGGGAGCAGAGCTTTGATAAAGCTG	783
Db	1262	TGCATGCGCCCACTCTTACAAAATCTAACAGTAAATGACGGGAGCAGAGCTTTGATAAAGCTG	1322
Qy	784	CTGAAGAACTCAACAATCACTTGCSCCAAGGCCCGGGTGTGTGCTTACTTGTGAAGGCG	843
Db	1322	CTGAAGAAAGCTCAACAATCACTTGCSCCAAGGCCCGGGTGTGTGCTTACTTGTGAAGGCG	1381
Qy	844	ATGACGGTGAAGGTCGTGCTGATGAGCCATGAGGCGCTGGGTCTAATGGGAGAAATTTCTG	903
Db	1382	ATGACGGTGAAGGTCGTGCTGATGAGGCCATGAGGCGCTGGGTCTAATGGGAGAAATTTCTG	1441
Qy	904	CTTCTGGGAGGGGAACAGATGCCATCTTTATGAGATCTCAAGAAACAGACATCCTATGG	963
Db	1442	CTTCTGGGAGGGGAACAGATGCCATCTTTATGAGATCTCAAGAAACAGACATCCTATGG	1501
Qy	964	GAAACAGAAAGAAATGCCAAGGTGCTTCCCTTCAGGGTTTGGAGACATATTTACACAGA	1023
Db	1502	GAAACAGAAAGAAATGCCAAGGTGCTTCCCTTCAGGGTTTGGAGACATATTTACACAGA	1561
Qy	1024	AGTGAATCCGTGCTGTGCTGACATGCCCCAGCTCTGAATCTAGAGCTCAGTTCAAGGCCCC	1083
Db	1562	AGTGAATCCGTGCTGTGCTGACATGCCCCAGCTCTGAATCTAGAGCTCAGTTCAAGGCCCC	1621
Qy	1084	ATCACTGGAACGAGGGGACAGGCTCATCTAATTCGATGGAATNTAATCTGCAATTATAT	1143
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Qy	1144	GAAAGCAACAGTCATATCTTCTGATGTGAGATTGGAAGCAATTTGTATGTGATGTGAC	1203
Db	1682	GAAAGCAACAGTCATATCTTCTGATGTGAGATTGGAAGCAATTTGTATGTGATGTGAC	1741
Qy	1204	CGTCAAAATGCGCCCATATCACTGCAACCTAACAAAGTTTCTTGATGGGGTGCTCAG	1263
Db	1742	CGTCAAAATGCGCCCATATCACTGCAACCTAACAAAGTTTCTTGATGGGGTGCTCAG	1801
Qy	1264	ACTTTTCACTCTTGGAAGTATTAATCTGGGAGGTCAATGTGGGGCACTTTGGAAATTTGGGCT	1323
Db	1802	ACTTTTCACTCTTGGAAGTATTAATCTGGGAGGTCAATGTGGGGCACTTTGGAAATTTGGGCT	1861



Db	2042	TCCTCCCTTATGSCCTTATCAACAGAGCAAAATAGGTCGCTTTATGCTTGAATTCAGTT	2101
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LOCUS	AX068374	2149 bp	DNA linear PAT 25-JAN-2001
DEFINITION	Sequence 9 from Patent WO0102566.		
ACCESSION	AX068374		
VERSION	AX068374.1	GI:12578538	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Schwarz, D.A. and Maki, R.A.		
TITLE	Metabotropic glutamate receptors and methods of use therefor		
JOURNAL	Patent: WO 0102566-A 9 11-JAN-2001; Neurocrine Biosciences, Inc. (US)		
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ORIGIN			
Query Match	95.8%; Score 1746.6; DB 6; Length 2149;		
Best Local Similarity	98.4%; Pred. No. 0;		
Matches 1782; Conservative 1; Mismatches 5; Indels 23; Gaps 1			
Qy	1	AAAAATGCGCTTCCTGTTGATCCTGTCAGTCAGTCTTATTTGAAAGAGATGTCGGTGGAGT	60
Db	362	AAAAATGTCCTTCCTGTTGATCCTGTCAGTCTTATTTGAAAGAGATGTCGGTGGAGT	421
Qy	61	GCACAGTCCAGTGAAGAGAGGGTGGCTCACTGCTGGTGAATTTATTTGAGCT	120
Db	422	GCACAGTCCAGTGAAGAGAGGGTGGCTCACTGCTGGTGAATTTATTTGAGCT	481
Qy	121	CTCTTTTCTGTTCAATCAACAGCTTCTGTGACGAAGTTCAATGAGAGAAAGTGTGGGCA	180
Db	482	CTCTTTTCTGTTCAATCAACAGCTTCTGTGACGAAGTTCAATGAGAGAAAGTGTGGGCA	541
Qy	181	GTCGGTGAACAGTATGGAATTCAGAGAGTGAAGAGGCAATGTCATACCTGGAAAGATC	240
Db	542	GTCGGTGAACAGTATGGAATTCAGAGAGTGAAGAGGCAATGTCATACCTGGAAAGATC	601
Qy	241	AATTGAGACCCCACTCTTTGCCCCAATCACTGAGCTGTGAGATTAAGGATTCCTGC	300
Db	602	AATTGAGACCCCACTCTTTGCCCCAATCACTGAGCTGTGAGATTAAGGATTCCTGC	661
Qy	301	TGGCATTGGCTGTGGCCCTTGAAGCAGAGCATTTGATTCATTAAGATTCCTCATTTCT	360
Db	662	TGGCATTGGCTGTGGCCCTTGAAGCAGAGCATTTGATTCATTAAGATTCCTCATTTCT	721
Qy	361	TGGGAAGGAGAAAGGGCTGGTATGCTGTGAGATGAGTCTCTCTCTTCCTTCGGTCC	420
Db	722	TGGGAAGGAGAAAGGGCTGGTATGCTGTGAGATGAGTCTCTCTCTTCCTTCGGTCC	781
Qy	421	AAGAAGCCCATAGTAGGGGTCACTTGGGCTGGTTCAGTCTTTAGCCATTGAGGTCAG	480
Db	782	AAGAAGCCCATAGTAGGGGTCACTTGGGCTGGTTCAGTCTTTAGCCATTGAGGTCAG	841
Qy	481	AATTTGCTCAGCTTTTCAACATACCTCAGATTTCTTACTCAGAACCAATCATGATCTG	540

Db	842	AAATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGGAAACCATCATGATCTG	901
Qy	541	AGTGCACAGACTCTGTTCAAAATATTTCAATGAGGTTGTGCTTCAGATGCTCAGCAGCA	600
Db	902	AGTGACAAAGACTCTGTTCAAAATATTTCAATGAGGTTGTGCTTCAGATGCTCAGCAGCA	961
Qy	601	AGGTCCATGGTGCACATATGAAAGAGGTACAACCTGCAGCTATGATACAGCCGTACACACA	660
Db	962	AGGTCCATGGTGCACATATGAAAGAGGTACAACCTGCATATGATATCAGCCGTACACACA	1021
Qy	661	GAAGGCAACATATGAGAAATGAGGATGGAAGCCTTCAAGATATGTCAAGCGAAGAAAGG	720
Db	1022	GAAGGCAACATATGAGAAATGAGGATGGAAGCCTTCAAGATATGTCAAGCGAAGAAAGG	1081
Qy	721	ATTTCATCGCCCACTCTTAACAAATCTCACATATCAGATATCAGGAGCAGAGCTTTGATAG	780
Db	1082	ATTTCATCGCCCACTCTTAACAAATCTCACATATCAGATATCAGGAGCAGAGCTTTGATAG	1141
Qy	781	CTGCTGAAGAGCTCACAAATCCTGGCCCAAGGCCGGGGTGGGGCTACTTCTGAG	840
Db	1142	CTGCTGAAGAGCTCACAAATCCTGGCCCAAGGCCGGGGTGGGGCTACTTCTGAG	1201
Qy	841	GGCATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCGCTGGCTCTAGTGGAGAAATTT	900
Db	1202	GGCATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCGCTGGCTCTAGTGGAGAAATTT	1261
Qy	901	CTGCTTCTGGGCAAGGGAACGAGATGCCATCTTAATGAGATCTCAAGAAACAGATCCTA	960
Db	1262	CTGCTTCTGGGCAAGGGAACGAGATGCCATCTTAATGAGATCTCAAGAAACAGATCCTA	1321
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Qy	1021	AGAAGTAGTCCGGTCTGCTGCACATGCCAGCGCTCGAATCTAGAGCTCAGTTCAGGG	1080
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Qy	1081	CCCATCACTGAGCTGAGGGAACAGGCTCATCTAAATTCAGATGATATTACTCTGCAATAT	1140
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Qy	1141	AATGAAAGCAACAGTCAATCTTCTGATGAGAAATTTGAAACATTTGATTTGGAAGT	1200
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Qy	1261	CAGACTTTCACCTCTGGCAAGTATTACTGGGAGTGCATGTGGGGGACTCTTGGAAATTTG	1320
Db	1599	CAGACTTTCACCTCTGGCAAGTATTACTGGGAGTGCATGTGGGGGACTCTTGGAAATTTG	1658
Qy	1321	GCTTTCGGTGTGTTGTAATAGTACCTGAAAGGGAAGTAACGAATGCAATATATATGGA	1380
Db	1659	GCTTTCGGTGTGTTGTAATAGTACCTGAAAGGGAAGTAACGAATGCAATATATATGGA	1718
Qy	1381	GAGAGGGAACCTTTAATCTTTGGGATTTGTAAGAACGACATTCAGTGCAGTCTTTAAC	1440
Db	1719	GAGAGGGAACCTTTAATCTTTGGGATTTGTAAGAACGACATTCAGTGCAGTCTTTAAC	1778
Qy	1441	ACCTCCCAAGTTACATGCAAGTATGTCCCAAGACCTACCAACCAATGATGATATTTCTCG	1500
Db	1779	ACCTCCCAAGTTACATGCAAGTATGTCCCAAGACCTACCAACCAATGATGATATTTCTCG	1838
Qy	1501	GATTGTAGAGTAGAAGCTGTAGGCTTGTGATGTTAATCAAGCTCCCTATATATAC	1560
Db	1839	GATTGTAGAGTAGAAGCTGTAGGCTTGTGATGTTAATCAAGCTCCCTATATATAC	1898
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QY	1801	AAAAAAAAAAAAAAAAAAAAA	1823
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RESULT 2			
LOCUS	AX068372	2172 bp	DNA
DEFINITION	Sequence 7 from Patent WO0102566.		linear
ACCESSION	AX068372		
VERSION	AX068372.1		
KEYWORDS	GI:12578537		
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Bukacinska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Schwarz, D.A. and Maki, R.A.		
TITLE	Metabotropic glutamate receptors and methods of use therefor		
JOURNAL	Patent: WO 0102566-A 7 11-JAN-2001;		
FEATURES	Neurocrine Biosciences, Inc. (US)		
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BASE COUNT	554 a 488 c 544 g 586 t		
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Query Match	98.9%; Score 1802.6; DB 6; Length 2172;		
Best Local Similarity	99.7%; Pred. No. 0;		
Matches 1805; Conservative	1; Mismatches 5; Indels 0; Gaps 0;		
QY	1	AAAAATGCTCTTCTGTGATCCTGTCACTCTTACTTTTGAAGAAGATGCTCGGGAGT	60
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Db	422	GCACAGTCCAGTGAGAGAGGGGTGGTCTCAATGCTGGGTGACATCATTTATTTGAGCT	481
QY	121	CTCTTTCTGTTCATCACCAGCTTACTGTGACCAAGTTCATGAGAGAAATGTGGGGCA	180
Db	482	CTCTTTCTGTTCATCACCAGCTTACTGTGACCAAGTTCATGAGAGAAATGTGGGGCA	541
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QY	241	AATTCAAGCCACACTCTTGCACATCACTGGCTGTGAGATTAAGGATTCCTGTC	300
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QY	301	TGGCATTCGGCTGTGGCCCTTAGAGCAGACATTTGATTCATTAAGATTCCTCATTTCT	360
Db	662	TGGCATTCGGCTGTGGCCCTTAGAGCAGACATTTGATTCATTAAGATTCCTCATTTCT	721
QY	361	TCCGAGAAGAGAGGGCTTGTATGCTCTGTGATGGCTCTGCTCTTCTTCGCTCC	420
Db	722	TCCGAGAAGAGAGGGCTTGTATGCTCTGTGATGGCTCTGCTCTTCTTCGCTCC	781
QY	421	AAGAAGCCATAGTAGAGGTCATTGGGCTTGTCAAGTCTTTAGGCATTCAGGTCCAG	480
Db	782	AAGAAGCCATAGTAGAGGTCATTGGGCTTGTCAAGTCTTTAGGCATTCAGGTCCAG	841
QY	481	AATTGCTCCAGCTTTTCAACATCTTCAGATTGCTTACAGCAACATCATGAGATCTG	540
Db	842	AATTGCTCCAGCTTTTCAACATCTTCAGATTGCTTACAGCAACATCATGAGATCTG	901
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Db	902	AGTGAACAAGCTCTGTTCAAAATATTTATGAGGGTTGTGCTTCAAGATGCTCAGACAGCA	961

QY	601	GGGTCACATGGTGGACATATGGAAGAAGGTACACCTGGACCTATGTATACAGCCCTACACA	660
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QY	661	GAAGGCAACTATGAGAGAAAGTGGATGGAAGCCTTCAAAAGATATGTGACGCAAGAAAGG	720
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Db	1082	ATTTCATCGCCCACTCTTACAAATCTACATATGACAGGGAGCGAGCTTTGATAG	1141
QY	781	CTGCTGAAGAGCTCACAGTCACTTTCGCCAAGGCCCGGGGTGGGCTCTCTTGAG	840
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QY	901	CTGCTTCTGGCAGAGGAACCAAGTGCATCTTATGAGATCTCAAGAACAGATCCTA	960
Db	1262	CTGCTTCTGGCAGAGGAACCAAGTGCATCTTATGAGATCTCAAGAACAGATCCTA	1321
QY	961	TGGGAAGACAGAAAAAATGCGAAGGTGCTCTCTTCAAGGTTTTGAGACATATTCAC	1020
Db	1322	TGGGAAGACAGAAAAAATGCGAAGGTGCTCTCTTCAAGGTTTTGAGACATATTCAC	1381
QY	1021	AGAAGTAGTCCGTGCTGTGACATATGCCAGCCTCTGAATCTAGAGCTCAGTTCAGGG	1080
Db	1382	AGAAGTAGTCCGTGCTGTGACATATGCCAGCCTCTGAATCTAGAGCTCAGTTCAGGG	1441
QY	1081	CCCATCACTGAGCTGAGGAGACAGGCTCATCTAATCTGAGTGATATTACTCTGCATTA	1140
Db	1442	CCCATCACTGAGCTGAGGAGACAGGCTCATCTAATCTGAGTGATATTACTCTGCATTA	1501
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Db	1562	GACCGTCAAAAATGGGCCCATATATCACTGCAACACCTCAAGTTTCTTGCATGGGGTGCT	1621
QY	1261	CAGACTTTCACCTCTGGCAAGTATTACTGSGAAGGTCCATGTGGGGGACCTTGGAAATGG	1320
Db	1622	CAGACTTTCACCTCTGGCAAGTATTACTGSGAAGGTCCATGTGGGGGACCTTGGAAATGG	1681
QY	1321	GCTTTCGGGTGTTGTATTAAGTACTGGAAGGGAAGATCAGAAATGGCAATATATATGGA	1380
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QY	1381	GAGGAGGAGACTTTAGTCTTGGGATGTTTAAAGACGACATTCAGTGCAGTCTTTAC	1440
Db	1742	GAGGAGGAGACTTTAGTCTTGGGATGTTTAAAGACGACATTCAGTGCAGTCTTTAC	1801
QY	1441	ACCTCCCACTTACCTGCAGTATGTGCCAAGACTTACCAACCAATGTAGATTAATTC	1500
Db	1802	ACCTCCCACTTACCTGCAGTATGTGCCAAGACTTACCAACCAATGTAGATTAATTC	1861
QY	1501	GATTGTGAAGCTGAAGACTGTGAGCTTGTGATGTTAATCAAAAGTCCCTATATAC	1560
Db	1862	GATTGTGAAGCTGAAGACTGTGAGCTTGTGATGTTAATCAAAAGTCCCTATATAC	1921
QY	1561	ATCCCTAATGCTCCCTTCAACGCTCCCTCAGGCTATCTTTGCTGTATTCATCTG	1620
Db	1922	ATCCCTAATGCTCCCTTCAACGCTCCCTCAGGCTATCTTTGCTGTATTCATCTG	1981
QY	1621	CCAGAGCAATATGAAGATGTGTTATCTGCTGAGAACCCCTTATCCCATAAAGCC	1680
Db	1982	CCAGAGCAATATGAAGATGTGTTATCTGCTGAGAACCCCTTATCCCATAAAGCC	2041
QY	1681	TCTTCCTTGCTTATCAAAACAGACAAATAGGCTCTGTTTATGTCTTGAAATGCA	1740

JOURNAL Patent: WO 02070708-A 1 12-SEP-2002;  
FEATURES Myeth (US)  
Source Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 121 CTCTTTCTGTTCATCAACAGCTTCTGTGACGAGTTCATGAGAGAGTGGGCA 180  
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DB 1741 CTATGTTTATTAACATCATTTATGTTGTTTATTAATGTTGTTTAAATGTTGTTTAA 1800

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:51:47 ; Search time 6887.99 Seconds  
(without alignments)  
10827.282 Million cell updates/sec

Title: US-10-027-923-1

Perfect score: 1823  
Sequence: 1 aaatggtcctctctgtgat.....aaaaaaaaaaaaaaaaaaaaa 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

GenEmbl: \*  
1: gb\_da: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_cm: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
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9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
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15: gb\_da: \*  
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17: em\_hum: \*  
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19: em\_mu: \*  
20: em\_om: \*  
21: em\_ov: \*  
22: em\_or: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rtd: \*  
36: em\_htg\_man: \*  
37: em\_htg\_vtc: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1822.6	100.0	1823	6	AX709347	AX709347 Sequence
2	1802.6	98.9	2172	6	AX068372	AX068372 Sequence
3	1746.6	95.8	2149	6	AX068374	AX068374 Sequence
4	1615.6	88.6	2349	6	AX068368	AX068368 Sequence
5	1576.6	86.5	2064	6	AX068376	AX068376 Sequence
6	1559.6	85.6	2326	6	AX068370	AX068370 Sequence
7	1413.6	77.5	2251	6	AX068366	AX068366 Sequence
8	1389.6	76.2	2241	6	AX068371	AX068371 Sequence
9	1110	60.9	1110	6	AX709349	AX709349 Sequence
10	891.4	48.9	4078	6	AR270570	AR270570 Sequence
11	891.4	48.9	4207	6	AR145364	AR145364 Sequence
12	891.4	48.9	4207	6	AR145365	AR145365 Sequence
13	891.4	48.9	4303	6	AR145366	AR145366 Sequence
14	891.4	48.9	4303	6	AR145367	AR145367 Sequence
15	891.4	48.9	4518	6	AX548892	AX548892 Sequence
16	891.4	48.9	4518	9	HUMMGRES5A	D28538 Human mRNA
17	891.4	48.9	4614	9	HUMMGRES5B	D28539 Human mRNA
18	888.2	48.7	3282	6	AR038828	AR038828 Sequence
19	888.2	48.7	3282	6	AR038845	AR038845 Sequence
20	888.2	48.7	3282	6	AR256861	AR256861 Sequence
21	888.2	48.7	3282	6	121438	121438 Sequence
22	888.2	48.7	4085	6	AR038826	AR038826 Sequence
23	888.2	48.7	4085	6	AR038843	AR038843 Sequence
24	888.2	48.7	4085	6	AR256859	AR256859 Sequence
25	888.2	48.7	4085	6	121436	121436 Sequence
26	888.2	48.7	4181	6	AR038827	AR038827 Sequence
27	888.2	48.7	4181	6	AR038844	AR038844 Sequence
28	888.2	48.7	4181	6	AR256860	AR256860 Sequence
29	888.2	48.7	4181	6	121437	121437 Sequence
30	770.8	42.3	1472	9	BC001862	BC001862 Homo sapi
31	769.2	40.2	1470	9	AF521869	AF521869 Homo sapi
32	739.4	39.18	3918	10	RATMGCLR	D10881 Rattus norv
33	681.6	37.4	146921	2	AC130357	AC130357 Homo sapi
34	681.6	37.4	173032	9	AC130364	AC130364 Homo sapi
35	681.6	37.4	173795	2	AC130336	AC130336 Homo sapi
36	670.6	36.8	203298	2	AC073113	AC073113 Homo sapi
37	668	36.6	79253	9	AC107937	AC107937 Homo sapi
38	666	36.5	2163	9	AB037682	AB037682 Homo sapi
39	659.2	36.2	152269	9	AC136759	AC136759 Homo sapi
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42	647.2	35.5	163591	2	AC011829	AC011829 Homo sapi
43	646.4	35.5	106316	9	AP000626	AP000626 Homo sapi
44	644.6	35.4	36055	2	AP005815	AP005815 Homo sapi
45	644.6	35.4	39852	9	AP005814	AP005814 Homo sapi

## ALIGNMENTS

RESULT 1	AX709347	1823 bp	DNA	linear	PAT 04-APR-2003
LOCUS	AX709347				
DEFINITION	Sequence 1 from Patent WO02070708.				
ACCESSION	AX709347				
VERSION	AX709347.1	GI:29564889			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
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	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE					
AUTHORS	Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.B.				
TITLE	Glutamate receptor modulatory proteins and nucleic acids encoding them				

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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 268)  
 AUTHORS Aufferay, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Denizès, M.D., Duprat, S., Hougatte, R., Uméau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouliot, Y., Sebasteian-Kabackich, C. and Tessier, A.  
 TITLE IMAGE: molecular integration of the analysis of the human genome and its expression  
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
 MEDLINE 95277534  
 PUBMED 7757816  
 COMMENT Contact: Genethon  
 Genexpress-Genethon  
 Genethon Centre de recherche sur le Genome Humain  
 1 rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
 Tel: 33169412800  
 Fax: 33160778698  
 Email: Genexpress@genethon.fr  
 Single read.  
 Genexpress\_library\_id: G; Genexpress\_sequence\_id: y1c-0bc11  
 Seq primer: (-21)M13 universal.  
 Location/Qualifiers  
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 BASE COUNT 70 a 61 c 67 g 1 others  
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 Best Local Similarity 100.0%; Pred. No. 0;  
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 DB 167 TATGTACGACGAGGAGGATTTCATCGCCACTTTACAAATCTACAGTATGACAG 226  
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 DB 227 GGAGCAGAGCTTTGATTAAGTCTGCTGAAGAAGCTCACAGTCA 268

RESULT 15  
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 DEFINITION BX282658 NIH MGC 119 Homo sapiens cDNA clone IMAGE998G0711417;  
 ACCESSION IMAGE:5167902, mRNA sequence.  
 VERSION BX282658  
 KEYWORDS EST.  
 SOURCE BX282658.1 GI:28613056  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 516)  
 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radetof, U., Schneider, D. and Korn, B.  
 TITLE Human Unigeneset - RZPD3

JOURNAL Unpublished  
 COMMENT Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGE998G0711417.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl/cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13u, Primer sequence: CGTTTAAACACGCGCCAGT.  
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 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 QY 61 GCACAGTCCAGTGAGAGAGGGTGTGCTCACATGC 97  
 DB 428 GCACAGTCCAGTGAGAGAGGGTGTGCTCACATGC 464

Search completed: December 14, 2003, 23:43:35  
 Job time: 4166.78 secs

DEFINITION wb68b11.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2310813 3' similar to SW:BTUT\_HUMAN Q13410 BUTYROPHILIN PRECURSOR ;, mRNA sequence.

ACCESSION AF55261

VERSION AF55261.1 GI:4739240

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 455)

AUTHORS Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGP98A225727. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human UnigeneSet - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/ClonCards/cgi-bin/showLib.pl.cgi/responseLibNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de

FEATURES

source

1..455

/organism="Homo sapiens"

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/clone="IMAGE:2310813"

/issue\_type="pooled germ cell tumors"

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/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 138 a 82 c 111 g 124 t

ORIGIN

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DB 350 TTACTGTCAGTATGTCCTCAAGACCTACCAACATGATGATTTCTGGATTGGAAG 291

QY 1511 CTGAACCTGAGCTTGTGATGTTAATCAAGCTCCCTATATACCAATCCCTAATT 1570

DB 290 CTGAACCTGAGCTTGTGATGTTAATCAAGCTCCCTATATACCAATCCCTAATT 231

QY 1571 GCTCCTTTCACCTCTCTCAGGCTATCTTTTCTGT 1608

DB 230 GCTCCTTTCACCTCTCTCAGGCTATCTTTTCTGT 193

RESULT 13

LOCUS BX116917 494 bp mRNA linear EST 07-FEB-2003

DEFINITION BX116917 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2310813, mRNA sequence.

ACCESSION BX116917

VERSION BX116917.1 GI:27840301

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 494)

AUTHORS Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGP98A225727. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human UnigeneSet - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/ClonCards/cgi-bin/showLib.pl.cgi/responseLibNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de

FEATURES

source

1..494

/organism="Homo sapiens"

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/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 118 a 118 c 105 g 153 t

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DB 210 TTACTGTCAGTATGTCCTCAAGACCTACCAACATGATGATTTCTGGATTGGAAG 269

QY 1511 CTGAACCTGAGCTTGTGATGTTAATCAAGCTCCCTATATACCAATCCCTAATT 1570

DB 270 CTGAACCTGAGCTTGTGATGTTAATCAAGCTCCCTATATACCAATCCCTAATT 329

QY 1571 GCTCCTTTCACCTCTCTCAGGCTATCTTTTCTGT 1608

DB 330 GCTCCTTTCACCTCTCTCAGGCTATCTTTTCTGT 367

RESULT 14

LOCUS F05449 268 bp mRNA linear EST 19-FEB-1995

DEFINITION HSCOBc11 normalized infant brain cDNA Homo sapiens cDNA clone c-0bc11, mRNA sequence.

ACCESSION F05449

VERSION F05449.1 GI:669265

KEYWORDS EST.

SOURCE Homo sapiens (human)

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 DB 608 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATTAAGGATTCCTG 667  
 QY 301 TGGCATTGGCTGTGGCCCTTGAAGACAGCATTTGATTCTTAAGAGATTCCTCATTTCT 360  
 DB 668 TGGCATTGGCTGTGGCCCTTGAAGACAGCATTTGATTCTTAAGAGATTCCTCATTTCT 727  
 QY 361 TC 362  
 DB 728 TC 729  
 RESULT 10  
 BI826234 664 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603075928F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5167902 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI826234 GI:15937784  
 VERSION BI826234.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 1 (bases 1 to 664)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L14M1417 row: 9 column: 07  
 High quality sequence stop: 662.  
 Location/Qualifiers  
 1. 664  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5167902"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"  
 /clone\_11b="NIH\_MGC\_119"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 site\_2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC library."  
 BASE COUNT 151 a 177 c 179 g 157 t  
 ORIGIN  
 Query Match 6.2%; Score 113; DB 12; Length 664;  
 Best Local Similarity 100.0%; Pred.No. 0;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 181 GTCCGTGAACAGATGAGCATTTGAGAGAGGAGCCATGCTGATACCTGGAAGATC 240  
 DB 547 GTCCGTGAACAGATGAGCATTTGAGAGAGGAGCCATGCTGATACCTGGAAGATC 606  
 QY 241 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATTAAGGATTC 293  
 DB 607 AATTGAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGTGATTAAGGATTC 659

RESULT 11  
 AI950429/c 452 bp mRNA linear EST 08-MAR-2000  
 LOCUS wq35601.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2473249 3',  
 DEFINITION similar to SW-BUTY\_HUMAN Q13410 BUTYROPHILIN PRECURSOR, mRNA  
 sequence.  
 ACCESSION AI950429 GI:5742739  
 VERSION AI950429  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NCI-CGAP http://www.nci.nih.gov/ncicgap.  
 1 (bases 1 to 452)  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/btrp/image/image.html  
 Insert Length: 607 Std Error: 0.00  
 Seg primer: -40UP from Gibco.  
 Location/Qualifiers  
 1. 452  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2473249"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_11b="NCI CGAP GC6"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI CGAP GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneids  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 139 a 81 c 109 g 122 t 1 others  
 ORIGIN

Query Match 5.9%; Score 107; DB 9; Length 452;  
 Best Local Similarity 99.4%; Pred.No. 0;  
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1451 TTACACTGAGATGATGTCGAGACCTTACCAACATGATGATTTCTGTGATGGAAG 1510  
 DB 349 TTACACTGAGATGATGTCGAGACCTTACCAACATGATGATTTCTGTGATGGAAG 290  
 QY 1511 CTAGAACTGTAGCTTCTGTGATGTTAATCAAGCTCCCTTATATACCATCCCTAAT 1570  
 DB 289 CTAGAACTGTAGCTTCTGTGATGTTAATCAAGCTCCCTTATATACCATCCCTAAT 230  
 QY 1571 GCTCCTTCACTCCTCTCAGGCTATCTTTGTGCTGT 1608  
 DB 229 GCTCCTTCACTCCTCTCAGGCTATCTTTGTGCTGT 192  
 RESULT 12  
 AI655261/c 455 bp mRNA linear EST 17-DEC-1999  
 LOCUS AI655261



Qy	1631	ATCGAAATGCTTATATCGTGTGGGAACCCCTTATCCATTAAGCCCTTCCTGT	1690
Db	464	ATCGAAATGCTTATATCGTGTGGGAACCCCTTATCCATTAAGCCCTTCCTGT	405
Qy	1691	GCCTTATCAACAGGACCAATAGGTTCTGTTTATGCTTGAATGCACTTCAATGTAT	1750
Db	404	GCCTTATCAACAGGACCAATAGGTTCTGTTTATGCTTGAATGCACTTCAATGTAT	345
Qy	1751	TAAACTCATTTATGTGTTACTATTAATGATGCTTAAA	1789
Db	344	TAAACTCATTTATGTGTTACTATTAATGATGCTTAAA	306

RESULT	8
LOCUS	T78107
DEFINITION	T78107 392 bp mRNA linear EST 07-MAR-1995
LOCUS	yc88a01..r1 Soares infant brain 11N8 Homo sapiens cDNA clone
DEFINITION	IMAGE:23998.5' similar to SP:JC2132 JC2132 METABOTROPIC GLUTAMATE
LOCUS	RECEPTOR 5 A - ; mRNA sequence.
DEFINITION	T78107
LOCUS	T78107.1 GI:696616
DEFINITION	EST. sapiens (human)
LOCUS	Homo sapiens
DEFINITION	Homo sapiens

REFERENCE AUTHORS	1 (bases 1 to 392) Hillier, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, M., Holman J., Johnson, W., Kohnen, J., Kunkel, R., Lawrence, C., McQuinn, D., Moore, M., Parnell, D.
----------------------	---

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
High quality sequence stops: 204  
Source: IMAGE Consortium<sup>1</sup>, LINTL.  
This clone is available royalty-free through LINTL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Seq primer: M13RPI  
High quality sequence stop: 204.

FEATURES	Location/Qualifiers
source	1. .392

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:396345"
/db_xref="taxon:9606"
/clone="IMAGE:23998"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_11b="Soares infant brain IN1B"
/note="Organ: whole brain; Vector: LambdaB; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AAGTCAGAGAAATTCGCGCGCAGAAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the LambdaB vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Paciencia Bonafido."

```

Query Match 7.7%; Score 141; DB 14; Length 392;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 141; Conservative 0; Indels 0; Gaps 0;

Qy	464	TACGATTAAGGTCAGAAATTGGCTCCAGCTTTTCAACATACCTCAGATTGGTACTCAG	522
Db	74	TACCCATTAGGTCAGAAATTGGCTCCAGCTTTTCAACATACCTCAGATTGGTACTCAG	133
Qy	524	CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAAAATATTTCAATAGGGTTTGCTT	583
Db	134	CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAAAATATTTCAATAGGGTTTGCTT	192
Qy	584	CAGATGCTCAGCAGCGCAAGT	604
Db	194	CAGATGCTCAGCAGCGCAAGT	214

RESULT	9
BC031602	
LOCUS	BC031602
DEFINITION	BC031602 Homo sapiens, clone IMAGE:5167902, mRNA.
ACCESSION	BC031602
VERSION	BC031602.1 GI:21594893
KEYWORDS	HTC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1297)
REFERENCE	GenBank

**TITLE** Direct Submission  
**JOURNAL** Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Submitted (06-JUN-2002) National Cancer Institute, Office of Cancer Research

REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Günarsteine, P. H., García, A. M., Lu, X., Huiyk, S. W., Loulseged, H., Kowls, C. R., Sneed, A. J., Martin, R. G., Muzny, D. M., Nanaevati, A. N., Gibbs, R. A.

**FEATURES**

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: [http://image.llnl.gov/series/IRAK\\_plate/51.Row.a.Column.11](http://image.llnl.gov/series/IRAK_plate/51.Row.a.Column.11)

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504142

This clone has the following problem: retained intron.

Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .1297

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5167902"
/tissue_type="Brain, adult medulla"
/clone_id="NTH_MGC_119"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
BASE COUNT      343 a      301 c      325 g      328 t
ORIGIN
Query Match      7.2%  Score 131;  DB 11;  Length 1297;
Best Local Similarity 99.5%;  Pred. No. 0;
Matches 181;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0

```

Qy	181	GTCCGTGAACAGTATGCGCATTCAGAGAGTGGAGCCATGTCGTAACCCGTGAAGGATC	240
Db	548	GTCCGTGAACAGTATGCGCATTCAGAGAGTGGAGCCATGTCGTAACCCGTGAAGGATC	607

CB153433 449 bp mRNA linear EST 29-JAN-2003  
 LOCUS K-EST0210877 B1T694954 Homo sapiens cDNA clone B1T694954-28-C09 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CB153433 GI:28138427  
 VERSION CB153433.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 449)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 TITLE JOURNAL  
 COMMENT Unpublished  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongseung@mail.kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
 Location/Qualifiers  
 1..449  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="B1T694954-28-C09"  
 /sex="M"  
 /lab\_host="Top10"  
 /clone\_1b="B1T694954"  
 /note="Organ: Brain; Vector: PCNS-D2; Site: 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then deacapped  
 with tobacco acid pyrophosphatase (TAP). The deacapped  
 intact mRNA was ligated with RNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dT-tailed vector was  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA after digestion of  
 circularized with R. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by electroporation method.  
 competent cells R. coli Top10 by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."  
 full-length enriched cDNA library."
 BASE COUNT 106 a 112 c 112 g 119 t  
 ORIGIN  
 Query Match 19.0%; Score 347; DB 14; Length 449;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 123 CTTTTCGTCATCAGCAGCTTCTGTGAGCAAGATTCATGAGAGAGTGGGAGT 182  
 1 CTTTTCGTCATCAGCAGCTTCTGTGAGCAAGATTCATGAGAGAGTGGGAGT 60  
 183 CCGTGAACAGTATGAGCATTCAGAGAGAGGCGCATGCTACCTCGGAAAGATCAA 242  
 61 CCGTGAACAGTATGAGCATTCAGAGAGAGGCGCATGCTACCTCGGAAAGATCAA 120  
 243 TTGAGACCCACAGCTTGTCCCAATACAGCTGGGCTGAGATTAAGGATTCCTGCTG 302  
 121 TTGAGACCCACAGCTTGTCCCAATACAGCTGGGCTGAGATTAAGGATTCCTGCTG 180  
 303 GCATTGGCTGTGGCCCTAGAGAGAGATTAAGTTCATTAAGATTCCTCATTTCTTC 362  
 181 GCATTGGCTGTGGCCCTAGAGAGAGATTAAGTTCATTAAGATTCCTCATTTCTTC 240

363 GAGAGAGAGAGAGGCGCTTGTGATAGCTGTGAGAGGCTCTCTCTTCCGCTCCAA 422  
 241 GAGAGAGAGAGAGGCGCTTGTGATAGCTGTGAGAGGCTCTCTCTTCCGCTCCAA 300  
 423 GAGGCGCATAGTATGAGGCTATGAGGCTGTCCAGTCTTTAGGCATTGAGTCCAGAA 482  
 301 GAGGCGCATAGTATGAGGCTATGAGGCTGTCCAGTCTTTAGGCATTGAGTCCAGAA 360  
 483 TTGTCTCAGCTTTTCAATACCTCAGATTTGCTTACAGCAACATCATGATCTGAG 542  
 361 TTGTCTCAGCTTTTCAATACCTCAGATTTGCTTACAGCAACATCATGATCTGAG 420  
 543 TGACAAAGCTGTGTCATTAATATTCATGA 571  
 421 TGACAAAGCTGTGTCATTAATATTCATGA 449  
 RESULT 7.  
 LOCUS AO313970/c 625 bp DNA linear GSS 04-MAY-1999  
 DEFINITION RPI11-103J21.TV RPI1-11 Homo sapiens genomic clone RPI1-11-103J21,  
 genomic survey sequence.  
 ACCESSION AO313970 GI:4045433  
 VERSION AO313970.1  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 625)  
 Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K.,  
 Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.  
 Use of human BAC End Sequences for Sequence-Ready Map Building  
 Other GSSes: RPI11-103J21.TV  
 TITLE JOURNAL  
 COMMENT Unpublished  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbeet@igf.org  
 Clones are derived from the human BAC library RPI1-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (http://info@resgen.com). BAC end search page:  
 http://www.tigr.org/cdb/humgen/bac\_end\_search.html  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
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 /clone="RPI1-11-103J21"  
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 /cell\_type="Lymphocytes"  
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;  
 RPI11 Human Male BAC library"  
 RPI11 Human Male BAC library"  
 BASE COUNT 235 a 98 c 115 g 177 t  
 ORIGIN  
 Query Match 12.0%; Score 219; DB 28; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1571 GCTCTTCTACCTCTCTCAGGCTATCTTTTGGGATTCATCTGACCAAGACAA 1630  
 524 GCTCTTCTACCTCTCTCAGGCTATCTTTTGGGATTCATCTGACCAAGACAA 465

This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer M13r, Primer sequence: TTTTCACACAGGAACAGCTATGAC.

## FEATURES

## Bouyce

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE5984078034 , IMAGE:3281166"
/ribose_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/notes="Organ :lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clones
1414920-1417991 and 1509094-1522439). Subtraction by Bentic
 Soares and M. Fatima Donaldo."

```

BASE COUNT	137 a	138 c	105 g	133 e	2 others
ORIGIN					

## RIGIN

Query Match	22.6%	Score 412;	DB 13;	Length 515;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 462;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

QY	905	TTCTGGGCAAGGAAACGAGATCCGATCTTATTGAGATCTCAAGAAACGATCTTATGGG	964
Db	466	TTCTGGGCAAGGAAACGAGATCGATCTTATTGAGATCTCAAGAAACGATCTTATGGG	407
QY	965	AAGCAGAGAAAGAAATGCCAGGTGGCTTCCTTCAGGGTTTGGAGACATATTACAGAA	1022
Db	406	AAGCAGAGAAAGAAATGCCAGGTGGCTTCCTTCAGGGTTTGGAGACATATTACAGAA	347
QY	1025	GTGAGTCCGATCTGTGTCACATAGCCAGCCGCTCTGATCTTAGAGCTCAGTTCAAGGCCCA	1084
Db	346	GTGAGTCCGATCTGTGTCACATAGCCAGCCGCTCTGATCTTAGAGCTCAGTTCAAGGCCCA	287
QY	1085	TCAGTGAAGTGAAGGACAGGCTCATCTTAATCTGAGTGGAATTATCTCTGCATTATATG	1144
Db	286	TCAGTGAAGTGAAGGACAGGCTCATCTTAATCTGAGTGGAATTATCTCTGCATTATATG	227
QY	1145	AAGCCAAACGTCATATCTTCTGATGTGGAGATTGGAAGCACTTTGTATGTGATGTGAC	1204
Db	226	AAGCCAAACGTCATATCTTCTGATGTGGAGATTGGAAGCACTTTGTATGTGATGTGAC	167
QY	1205	GTCAAAATAGSCCCCATATCACTGACGAAACACTCAAGATTTCTTGATAGGGGTGCTCAGA	126
Db	166	GTCAAAATAGSCCCCATATCACTGACGAAACACTCAAGATTTCTTGATAGGGGTGCTCAGA	107
QY	1265	CTTTCACTCTGGCAAGTATTACTGGAGGTCATGTGGGGGACTCTTGAATTGGGCTT	1332
Db	106	CTTTCACTCTGGCAAGTATTACTGGAGGTCATGTGGGGGACTCTTGAATTGGGCTT	47
QY	1325	TCGGATCTTGTATTAAGTACTGGAAAGGGAAGAAATCAAAATGG	1367
Db	46	TCGGATCTTGTATTAAGTACTGGAAAGGGAAGAAATCAAAATGG	4

RESULT 5  
BG150163

0163

LOCUS	BG150163	414 bp	mRNA	linear	EST 05-FEB-2007
DEFINITION	nad46b03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3368404 3'				

similar to SW:MG85\_HUMAN p41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECURSOR. [1] ;, mRNA sequence.

ACCESSION	BG150163
VERSION	BG150163.1
	GI:12662193

KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM      Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

**REFERENCE** 1 (bases 1 to 414)  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished  
Contact: Robert Strausberg, Ph.D.

High quality sequence block: 354  
Location/Quality: 144496

### **Source**

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3368404"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_id="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and six circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneids
1414920-1417991 and 1520944-1522433). Subtraction by Bencio
soares and M.Felicia Bonaldo."

```

BASE COUNT	110 a	91 c	118 g	95 t
ORIGIN				

**ORIGIN**

Query Match	21.1%;	Score 384;	DB 10;	length 414;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 384;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	505	CCTCAGATTTGTTACTCAGCAACCATATGATCTGAGTGCACGAAGCTGTTCAAAAT	564
Db	25	CCTCAGATTTGTTACTCAGCAACCATATGATCTGAGTGCACGAAGCTGTTCAAAAT	84
QY	565	TTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCAAGTTCATGTGGACATATGTGAAG	624
Db	85	TTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCAAGTTCATGTGGACATATGTGAAG	144
QY	625	AGGTACAACTGGAACCTTATGTTATCAGCCGTACACACAAAGGCACCTATGGAGAAAGTGGG	684
Db	145	AGGTACAACTGGAACCTTATGTTATCAGCCGTACACACAAAGGCACCTATGGAGAAAGTGGG	204
QY	685	ATGGAGACCTTCAAAGAATATGTCAAGCCAGGAAGGAATTTGCATCGCCCACTTTACAA	744
Db	205	ATGGAGACCTTCAAAGAATATGTCAAGCCAGGAAGGAATTTGCATCGCCCACTTTACAA	264
QY	745	ATCTACAGTATATGCAGGGGAGCAGAGCTTTGATTAAGCTGCTGAAGAACTCACAAGTAC	804
Db	265	ATCTACAGTATATGCAGGGGAGCAGAGCTTTGATTAAGCTGCTGAAGAACTCACAAGTAC	324
QY	805	TTTGCCCAAGGCCGGGTGTGTGGCTTACTTCTGTGAAGGCATGACGGTGAAGAGTCTGCTG	864
Db	325	TTTGCCCAAGGCCGGGTGTGTGGCTTACTTCTGTGAAGGCATGACGGTGAAGAGTCTGCTG	384
QY	865	ATGGCCATGAGAGCGCTCGGCTCTA	888
Db	385	ATGGCCATGAGAGCGCTCGGCTCTA	408

## RESULT 6

Db 391 ATGAGCGCTGGGTCTAGTGGAGAAATTTCTGCTTGTGGCAGAGCAAGATGCCATC 450

Qy 931 TTATTGAGATCTCAAGAACAGCATCTTATGGAGACAGAGAAATGCAAGGTGCG 990

Db 451 TTTATTGAGATCTCAAGAACAGCATCTTATGGAGACAGAGAAATGCAAGGTGCG 510

Qy 991 TTCCTTCAG 999

Db 511 TTCCTTCAG 519

RESULT 3  
AW015382  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW015382 442 bp mRNA linear EST 10-SEP-1999  
UT-H-BIO-aat-d-06-0-UI-s1 NCI CGAP\_Sub1 Homo sapiens cDNA clone  
IMAGE:2710331.3', mRNA sequence.

AW015382  
AW015382.1 GI:5864139  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 442)  
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Straubeberg, Ph.D.  
Email: cgaaps-f@mail.nih.gov  
Oligo-dt track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. CDNA Library Preparation: M.B.  
Soares Lab clone distribution: NCI-CGAP clone distribution  
information can be found through the I.M.A.G.E.B. Consortium/ILNL at:  
www.bio.lnl.gov/bdrip/image/image.html  
Seq primer: M13 forward  
POLYA=No.

FEATURES  
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Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2710331"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_1ib="NCI CGAP Sub1"  
/note="Vector: pT773D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not 1; Site 2: Eco RI; The  
NCI CGAP Sub1 library is a subcloned library derived from  
BI. BI constitutes a mixture of 21 normalized or  
subcloned NCI CGAP libraries: NCI CGAP C04,  
NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP C010, NCI CGAP C016  
, NCI CGAP Kid5, NCI CGAP Kid12, NCI CGAP Kid3,  
NCI CGAP Kid11, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP C08,  
NCI CGAP C011, NCI CGAP Lys12, NCI CGAP Brn3, NCI CGAP Lys  
, NCI CGAP Lu24, NCI CGAP Lu19, NCI CGAP G04, NCI CGAP G06  
, NCI CGAP Brn25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with a  
driver whose composition is detailed below: NCI CGAP Kid3  
pool 1 LHAM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
Cloneids 1322376-1323911, 1456008-1456775, 1500552-1502855  
) NCI CGAP Kid5 pool 1 LHAM 3338-3342, 3722-3725,  
3776-3778 (IMAGE Cloneids 1323912-1325831,  
1471368-1472903, 1492104-1493555) NCI CGAP Lys pool 1 LHAM  
3575-3582, 3851-3854 (IMAGE Cloneids 141920-1417991,  
1520904-1522439) NCI CGAP G04 pool 1 LHAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE Cloneids 1257096-1258631,  
1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1  
LHAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneids  
985608-986759, 1101192-1101959, 1217928-1220615)  
NCI CGAP C010 pool 1 LHAM 2644-2653, 2871-2872 (IMAGE  
Cloneids 1057416-1061255, 1144584-1145351) The resulting  
subcloned library contained 530,000 recombinants.

Subtraction was performed as previously described [Bonaldo  
, Lennon & Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Genome  
Research 6, 791-806  
TAG\_LIB=NCI CGAP\_Lys12  
TAG\_TISSUE=Leiomysarcoma  
TAG\_SEQ=AATCG"

BASE COUNT 118 a 97 c 127 g 100 t

ORIGIN

Query Match 22.6%; Score 412; DB 9; Length 442;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 489 CGAGCTTTCAACATACCTCAGATGCTTACTAGACACATCATGATGATGACAA 548

Db 7 CCAGCTTTCAACATACCTCAGATGCTTACTAGACACATCATGATGATGACAA 66

Qy 549 GACTCTGTTCAATATATTTATGAGGGTGTGCTTCAATGCTCAGCAGCAAGTTCAT 608

Db 67 GACTCTGTTCAATATATTTATGAGGGTGTGCTTCAATGCTCAGCAGCAAGTTCAT 126

Qy 609 GTTGAACATATGTAAGAGGTAACATGACCTATATATACCCGTACACAGAGGCAA 668

Db 127 GTTGAACATATGTAAGAGGTAACATGACCTATATATACCCGTACACAGAGGCAA 186

Qy 669 CTATGGAAGAAAGTGGATGGAAGCCTTCAAGATATGTACAGCAAGAGGATTTGCA 728

Db 187 CTATGGAAGAAAGTGGATGGAAGCCTTCAAGATATGTACAGCAAGAGGATTTGCA 246

Qy 729 CGCCCACTTTCAATATATCTACATATGATGAGGAGAGCAAGCTTATAGCTGTGAA 788

Db 247 CGCCCACTTTCAATATATCTACATATGATGAGGAGAGCAAGCTTATAGCTGTGAA 306

Qy 789 GAAGCTCAAGTCACTGCTCCCAAGCCCGGGTGTGGCTTCTGTGAGGCAATGAC 848

Db 307 GAAGCTCAAGTCACTGCTCCCAAGCCCGGGTGTGGCTTCTGTGAGGCAATGAC 366

Qy 849 GGTGAGAGGTCTGCTGATGATGATGAGGCGCTGATGATGAGGCAATTT 900

Db 367 GGTGAGAGGTCTGCTGATGATGATGAGGCGCTGATGATGAGGCAATTT 418

RESULT 4  
BX280403/c  
LOCUS  
DEFINITION  
ACCESSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BX280403 515 bp mRNA linear EST 04-MAR-2003  
BX280403 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE998A078034 ;  
IMAGE:3281166, mRNA sequence.

BX280403  
BX280403.1 GI:28612394  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 515)  
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radet, O., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD, IMAGE998A078034.  
RZPDLIB, I.M.A.G.E.B. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/Cloncards/cgi-  
bin/showLib.pl.cgi/responseLibNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heidelberg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

infoimage.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 493.  
Location/Qualifiers

# FEATURES

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/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lys was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bernaldo."

## BASE COUNT

141 a 107 c 138 g 113 t

## ORIGIN

Query Match 27.4%; Score 499; DB 10; Length 499;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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560 AATATTTCATGAGGGTTGCTTCAAGTCTCAGACGCGAGGTCATGGTGCATAG 619  
61 AATATTTCATGAGGGTTGCTTCAAGTCTCAGACGCGAGGTCATGGTGCATAG 120  
620 TGAAGAGTCACTGACCTATGATCAGCCGTCACACAGAGGCACTATGAGAAA 679  
121 TGAAGAGTCACTGACCTATGATCAGCCGTCACACAGAGGCACTATGAGAAA 180  
680 GTGGGATGGAAGCCTTCAAGATATGTCAAGCAAGAGGATTGATGCCCACTTT 739  
181 GTGGGATGGAAGCCTTCAAGATATGTCAAGCAAGAGGATTGATGCCCACTTT 240  
740 ACAAAATCTACAGTAATGACGAGGAGCAAGCTTTGATAGCTCTGAAGAGTCA 799  
241 ACAAAATCTACAGTAATGACGAGGAGCAAGCTTTGATAGCTCTGAAGAGTCA 300  
800 GTCACTTGGCCAGGCGCGGGTGGCTACTCTGTGAGGGGATGACGGTGAAGGTC 859  
301 GTCACTTGGCCAGGCGCGGGTGGCTACTCTGTGAGGGGATGACGGTGAAGGTC 360  
860 TGCTGATGCGCATGAGCGCTGGGTCTAGTGGAGAAATTTCTGCTTGGGACGAG 919  
361 TGCTGATGCGCATGAGCGCTGGGTCTAGTGGAGAAATTTCTGCTTGGGACGAG 420  
920 CAGATGCGCATTTATTGAGATCTCAAGAAACAGCATCTTATGAGAAAGAGAAAT 979  
421 CAGATGCGCATTTATTGAGATCTCAAGAAACAGCATCTTATGAGAAAGAGAAAT 480  
980 GCCAAGGTGCTTCTTCA 998  
481 GCCAAGGTGCTTCTTCA 499

## RESULT 2

BE674422 519 bp mRNA linear EST 08-SEP-2000  
LOCUS BE674422  
DEFINITION 7e01a04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166 3.  
B3milar to SW:WERS\_HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECURSOR. ; mRNA sequence.

## ACCESSION

BE674422  
BE674422.1 GI:10034963

## KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

TISSUE

CDNA

LIBRARY

PREPARED

BY

CDNA

SEQUENCING

CENTER

CLONE

DISTRIBUTION

NCI-CGAP

CLONE

DISTRIBUTION

INFORMATION

CAN BE

FOUND

THROUGH

THE

I.M.A.G.E.

CONSORTIUM/LLNL, send email to:

infoimage.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 499.

Location/Qualifiers

1. 519

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3281166"

/tissue\_type="carcinoid"

/lab\_host="DH10B"

/clone.lib="NCI CGAP Lu24"

/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lys was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bernaldo."

## BASE COUNT

143 a 114 c 143 g 119 t

## ORIGIN

Query Match 26.8%; Score 489; DB 10; Length 519;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

511 ATTGCTTACTCAGCAACCATCATGATCTGATGACAGACTCTGTTCAATATTTCATG 570  
31 ATTGCTTACTCAGCAACCATCATGATCTGATGACAGACTCTGTTCAATATTTCATG 90  
571 AGGGTTGCTTCAAGTCTCAGACGAGGTCATGGTGCATAGTGAAGAGGTAC 630  
91 AGGGTTGCTTCAAGTCTCAGACGAGGTCATGGTGCATAGTGAAGAGGTAC 150  
631 AACTGCACTATGATACAGCCGTCACACAGAGGCAACTATGAGAAAGTGGAGTGA 690  
151 AACTGCACTATGATACAGCCGTCACACAGAGGCAACTATGAGAAAGTGGAGTGA 210  
691 GCCCTCAAGATATGTCAGGAGAGAGGATTGTCATGCCCACTTTCAAAATCTAC 750  
211 GCCCTCAAGATATGTCAGGAGAGAGGATTGTCATGCCCACTTTCAAAATCTAC 270  
751 AGTATGACAGGAGAGAGAGCTTTGATAGCTGCTGAAGAGCTCACAGTCACTTCCC 810  
271 AGTATGACAGGAGAGAGAGCTTTGATAGCTGCTGAAGAGCTCACAGTCACTTCCC 330  
811 AAGGCCCGGGTGGTGGCTTCTGTGAGAGGATGACGGTGAAGGTCGTGATGGCC 870  
331 AAGGCCCGGGTGGTGGCTTCTGTGAGAGGATGACGGTGAAGGTCGTGATGGCC 390  
871 ATGAGCGCTGCGGTCTAGTGGAGAAATTTCTGCTTGGGCAAGGAGACGATGCCATC 930

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 18:02:28 ; Search time 4158.78 Seconds  
(without alignments)  
10653.866 Million cell updates/sec

Title: US-10-027-923-1  
Perfect score: 1823  
Sequence: 1 aaatgctcctctgtgat.....aaaaaaaaaaaaaaaa 1823

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gsb\_hum:\*  
18: em\_gsb\_inv:\*  
19: em\_gsb\_pln:\*  
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24: em\_gsb\_pro:\*  
25: em\_gsb\_rtd:\*  
26: em\_gsb\_phg:\*  
27: em\_gsb\_vtl:\*  
28: gb\_gsb1:\*  
29: gb\_gsb2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499	27.4	499	10	BE467477 h266d08.x
2	489	26.8	519	10	BE674422 7601a04.x
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4	412	22.6	515	13	BX280403 BX280403

5	384	21.1	414	10	BG150163
6	347	19.0	449	14	CB153433
7	219	12.0	625	28	AO313970
8	141	7.7	392	14	T78107
9	131	7.2	1297	11	BC031602
10	113	6.2	664	12	BI826234
11	107	5.9	452	9	A1950429
12	107	5.9	455	9	A1655261
13	107	5.9	494	13	BX116917
14	102	5.6	268	14	P05449
15	97	5.3	516	13	BX282658
16	76	4.2	362	9	AM197327
17	73	4.0	456	9	A1201184
18	67	3.7	715	10	BE275390
19	67	3.7	888	13	BUL54755
20	66	3.6	667	29	AG046849
21	66	3.6	710	14	CA449274
22	63	3.5	378	28	B03872
23	60	3.3	526	28	B16405
24	60	3.3	720	28	B65629
25	60	3.3	1400	13	BQ277274
26	59	3.2	682	10	BG695213
27	59	3.2	3879	11	AK032422
28	58	3.2	690	10	BG193349
29	58	3.2	729	10	BG199987
30	57	3.1	542	28	AO586224
31	56	3.1	435	28	AO443358
32	48	2.6	649	29	AG052404
33	47	2.6	198	10	BE071193
34	43	2.4	742	12	BI093942
35	35	2.4	806	10	BF125311
36	43	2.4	871	10	BE893553
37	40	2.2	608	28	AO376196
38	40	2.2	647	10	BB625841
39	40	2.2	661	14	BY721282
40	40	2.2	1013	13	BQ070358
41	38	2.1	1201	13	BX421692
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43	33	1.8	49	9	AA590547
44	33	1.8	58	14	CA336341
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## ALIGNMENTS

RESULT 1  
LOCUS BE467477  
DEFINITION h266d08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3212943 3' similar to SM:NR05\_HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECUSOR. ; mRNA sequence.

ACCESSION BE467477  
VERSION BE467477.1 GI:9513252

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
Contact: Robert Strauberg, Ph.D.  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-367-264-7

Query Match 9.4%; Score 171; DB 3; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 524 CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAAAATTTTCATGAGGTTGTGCTT 583  
DB 890 CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAAAATTTTCATGAGGTTGTGCTT 949  
QY 584 CAGATGCTGAGCAGGCAAGTTCATGCTGAGCATAGTGAAGAGGTACACTGAGACTATG 643  
DB 950 CAGATGCTGAGCAGGCAAGTTCATGCTGAGCATAGTGAAGAGGTACACTGAGACTATG 1009  
QY 644 TATCAGCCGTACACACAGAGGCAACTATGAGAAAGTGGATGGAAGCTTCCAAAGATA 703  
DB 1010 TATCAGCCGTACACACAGAGGCAACTATGAGAAAGTGGATGGAAGCTTCCAAAGATA 1069  
QY 704 TGTACGGGAAGAGGATTTGATGCGCCCACTCTTACAAAATCTACATATGACAGGG 763  
DB 1070 TGTACGGGAAGAGGATTTGATGCGCCCACTCTTACAAAATCTACATATGACAGGG 1129  
QY 764 AGCAGAGCTTTGATTAAGCTGTGAAGAAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 823  
DB 1130 AGCAGAGCTTTGATTAAGCTGTGAAGAAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 1189  
QY 824 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTGATGGCCATGAGGCGCTGG 883  
DB 1190 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTGATGGCCATGAGGCGCTGG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

Search completed: December 14, 2003, 15:19:12  
Job time : 123.716 secs



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QY 824 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTGTGCTGATGAGCCATGAGCGCTGG 883  
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QY 884 GTCTAG 889  
Db 1250 GTCTAG 1255

RESULT 14  
US-08-486-270-7  
; Sequence 7, Application US/08486270  
; Patent No. 5807689  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hees, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,270  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4085 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGUR5A"  
US-08-486-270-7

Query Match 9.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TACCAATTCAGGTCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 523  
Db 830 TACCAATTCAGGTCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 889  
QY 524 CAACCATCATGATCTGAGTGAACAAGCTGTGTTCAATTTTCAATGAGGGTGTGCTT 583  
Db 890 CAACCATCATGATCTGAGTGAACAAGCTGTGTTCAATTTTCAATGAGGGTGTGCTT 949  
QY 584 CAGATGCTGACGAGCAAGGTCATGGTGAACATAGTGAAGAGTGAACACTGAGACCTATG 643  
Db 950 CAGATGCTGACGAGCAAGGTCATGGTGAACATAGTGAAGAGTGAACACTGAGACCTATG 1009  
QY 644 TATCAGCCGTACACACAGAAAGCAACTATGAGAAAGTGGAGTGAAGCCCTTCAAGATA 703  
Db 1010 TATCAGCCGTACACACAGAAAGCAACTATGAGAAAGTGGAGTGAAGCCCTTCAAGATA 1069  
QY 704 TGTACAGGAGAGAGGATTTGATGCCCACTTTCAAAATTTACATATGACAGGG 763  
Db 1070 TGTACAGGAGAGAGGATTTGATGCCCACTTTCAAAATTTACATATGACAGGG 1129  
QY 764 AGCAGAGCTTGAATAGCTGTGAAGAGCTCAACATGCACTTGCCCAAGGCCCGGGTGG 823  
Db 1130 AGCAGAGCTTGAATAGCTGTGAAGAGCTCAACATGCACTTGCCCAAGGCCCGGGTGG 1189  
QY 824 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTGTGCTGATGAGCCATGAGCGCTGG 883  
Db 1190 TGGCCTACTTCTGTGAGGGCATGACGGTGAAGAGTGTGCTGATGAGCCATGAGCGCTGG 1249  
QY 884 GTCTAG 889  
Db 1250 GTCTAG 1255

RESULT 15  
US-08-367-264-7  
; Sequence 7, Application US/08367264  
; Patent No. 6001581  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hees, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/367,264  
; FILING DATE: 02-JUN-1994

GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Lliew, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11

Query Match 9.4%; Score 171; DB 4; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

464 TAGGCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 523  
DB TAGGCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 889  
524 CAACCATCATGATCTGATGACAGAGCTCTGTTCAATAATTTTCATGAGGGTTGTGCTT 583  
DB CAACCATCATGATCTGATGACAGAGCTCTGTTCAATAATTTTCATGAGGGTTGTGCTT 949  
890 CAACCATCATGATCTGATGACAGAGCTCTGTTCAATAATTTTCATGAGGGTTGTGCTT 949  
584 CAGATGCTCAGCAGCAGAGCTCCATGCTGATGACATGAGAGAGTCACTGACCTATG 643  
DB CAGATGCTCAGCAGCAGAGCTCCATGCTGATGACATGAGAGAGTCACTGACCTATG 1009  
950 CAGATGCTCAGCAGCAGAGCTCCATGCTGATGACATGAGAGAGTCACTGACCTATG 1009  
644 TATCAGCGGTACACACAGAGGCAACTATGAGAGAGTGGAGTGAAGCGCTTCAAGATA 703  
DB TATCAGCGGTACACACAGAGGCAACTATGAGAGAGTGGAGTGAAGCGCTTCAAGATA 1069  
1010 TATCAGCGGTACACACAGAGGCAACTATGAGAGAGTGGAGTGAAGCGCTTCAAGATA 1069  
704 TGTGAGGAGAGAGGAGATTGATGCGCCACTCTTCAAAATCTACAGTAATGACAGGGG 763

DB 1070 TGTGAGGAGAGAGGAGATTTCATGCGCCACTTTACAAAATCTACAGTAATGACAGGGG 1129  
QY 764 AGCAGAGCTTTGATAGTCTGATGAGAGCTCAACAGTCACTTGCCCAAGCGCCGGCTG 823  
DB AGCAGAGCTTTGATAGTCTGATGAGAGCTCAACAGTCACTTGCCCAAGCGCCGGCTG 1189  
QY 824 TGGCCTACTTCTGTGAGGCGATGACGCTGATGAGAGTGTGATGAGCCATGAGCGGCTTG 883  
DB TGGCCTACTTCTGTGAGGCGATGACGCTGATGAGAGTGTGATGAGCCATGAGCGGCTTG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

RESULT 13  
US-08-072-574-7  
Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
APPLICANT: Lliew, Chen  
Pontsler, Aaron  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000.  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435.  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7

Query Match 9.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

464 TAGGCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 523  
DB TAGGCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 889  
830 TAGGCATTGAGTCCAGAAATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACAG 889  
QY 524 CAACCATCATGATCTGATGACAGAGCTCTGTTCAATAATTTTCATGAGGGTTGTGCTT 583

TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
US-08-367-264-11  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."

Query Match  
Best Local Similarity 98.8%; Score 171; DB 3; Length 3282;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TAGCCATTCAGGTCGAGATTTGCTCCAGCTTTCAACATACCTGATTGCTTACTACG 523  
DB 830 TAGCCATTCAGGTCGAGATTTGCTCCAGCTTTCAACATACCTGATTGCTTACTACG 889  
QY 524 CAACCATCATGATCTGATGACAGACTCTGTTCAAAATATTTCATGAGGGTTGCTT 583  
DB 890 CAACGACATGATCTGATGACAGACTCTGTTCAAAATATTTCATGAGGGTTGCTT 949  
QY 584 CAGATCTCAGCAGGCAAGGTCATGCTGACATAGTAAAGGTAACAATGACCTATG 643  
DB 950 CAGATCTCAGCAGGCAAGGTCATGCTGACATAGTAAAGGTAACAATGACCTATG 1009  
QY 644 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGATA 703  
DB 1010 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGATA 1069  
QY 704 TGTACGCGAAGAGGATTTGCTGCCACTTTACAAATCTACATATGACAGGG 763  
DB 1070 TGTACGCGAAGAGGATTTGCTGCCACTTTACAAATCTACATATGACAGGG 1129  
QY 764 AGCAGCTTTGATTAAGTCTGTAAGAAGCTCAAGATCTTGCCTCAAGCCGGGTG 823  
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QY 824 TGGCCATCTTCTGTAGGGGCAATGACGCTGATGAGGTCATGAGCCGCTTG 883  
DB 1190 TGGCCATCTTCTGTAGGGGCAATGACGCTGATGAGGTCATGAGCCGCTTG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

## RESULT 11

US-09-153-757-11  
Sequence 11, Application US/09153757  
Patent No. 6413764

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

Ellis, Steven B.

Liaw, Chen

Pontsler, Aaron

Johnson, Edwin C.

Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match  
Best Local Similarity 98.8%; Score 171; DB 4; Length 3282;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TAGCCATTCAGGTCGAGATTTGCTCCAGCTTTCAACATACCTGATTGCTTACTACG 523  
DB 830 TAGCCATTCAGGTCGAGATTTGCTCCAGCTTTCAACATACCTGATTGCTTACTACG 889  
QY 524 CAACCATCATGATCTGATGACAGACTCTGTTCAAAATATTTCATGAGGGTTGCTT 583  
DB 890 CAACGACATGATCTGATGACAGACTCTGTTCAAAATATTTCATGAGGGTTGCTT 949  
QY 584 CAGATCTCAGCAGGCAAGGTCATGCTGACATAGTAAAGGTAACAATGACCTATG 643  
DB 950 CAGATCTCAGCAGGCAAGGTCATGCTGACATAGTAAAGGTAACAATGACCTATG 1009  
QY 644 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGATA 703  
DB 1010 TATCAGCCGTCACACAGAAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGATA 1069  
QY 704 TGTACGCGAAGAGGATTTGCTGCCACTTTACAAATCTACATATGACAGGG 763  
DB 1070 TGTACGCGAAGAGGATTTGCTGCCACTTTACAAATCTACATATGACAGGG 1129  
QY 764 AGCAGCTTTGATTAAGTCTGTAAGAAGCTCAAGATCTTGCCTCAAGCCGGGTG 823  
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DB 1190 TGGCCATCTTCTGTAGGGGCAATGACGCTGATGAGGTCATGAGCCGCTTG 1249  
QY 884 GTCTAG 889  
DB 1250 GTCTAG 1255

## RESULT 12

US-09-459-715-11  
Sequence 11, Application US/09459715  
Patent No. 6485919

Db 1130 AGAGAGCTTTGTAAGCTGCTAAGAGCTCAAGTCACTTGCCCAAGCCGGGTGG 1189  
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Db 1190 TGCCCTGCTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCCCTGG 1249  
QY 884 GTCTAG 889  
Db 1250 GTCTAG 1255

RESULT 9  
US-08-486-270-11  
Sequence 11, Application US/08486270  
Patent No. 5807689  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontbier, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
CLASSIFICATION: 435  
FILING DATE: 02-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-486-270-11

Query Match 9.4%; Score 171; DB 1; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1,4e-65;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 464 TAGCATTCAGGTCAGAGATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
Db 830 TAGCATTCAGGTCAGAGATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 889

QY 524 CAACATCATGATCTGATGACCAAGACTCTGTTCAATATTTCATGAGGTTGCTT 583  
Db 890 CAACCATGATGATCTGATGACCAAGACTCTGTTCAATATTTCATGAGGTTGCTT 949  
QY 584 CAGATGCTCAGACGACGACAGTCTCATGTGACATAGTGAAGAGTCAACATGACCTTAG 643  
Db 950 CAGATGCTCAGACGACGACAGTCTCATGTGACATAGTGAAGAGTCAACATGACCTTAG 1009  
QY 644 TATCAGCCGTACACACAGAGGCAACTATGAGAAAGTGGATGGAAGCTTCAAGATA 703  
Db 1010 TATCAGCCGTACACACAGAGGCAACTATGAGAAAGTGGATGGAAGCTTCAAGATA 1069  
QY 704 TGTGAGCGAAGGAGGATTTGATGCGCCACTCTTACAAAATCTACAGTAATGACGGG 763  
Db 1070 TGTGAGCGAAGGAGGATTTGATGCGCCACTCTTACAAAATCTACAGTAATGACGGG 1129  
QY 764 AGCAGACTTTGATTAAGTGTGTAAGAAAGTCAACAGTCACTTGCCCAAGCCGGGTGG 823  
Db 1130 AGCAGACTTTGATTAAGTGTGTAAGAAAGTCAACAGTCACTTGCCCAAGCCGGGTGG 1189  
QY 824 TGCCCTACTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCCCTGG 883  
Db 1190 TGCCCTGCTTCTGTGAGGCGATGACGGTGTGCTGATGCGCATGAGCGCCCTGG 1249  
QY 884 GTCTAG 889  
Db 1250 GTCTAG 1255

RESULT 10  
US-08-367-264-11  
Sequence 11, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontbier, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-660-148-6

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TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4207 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: mRNA  
US-08-660-148-3

Query Match 12.2%; Score 222; DB 3; Length 4207;  
Best Local Similarity 76.3%; Pred. No. 6,9e-88;  
Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTTCAGAAATTGCTCCAGTTTCAACATACCTGAGATTGCTTACAG 523  
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QY 524 CAACCATCATGATCTGAGTGAAGAGAGCTGCTTCAAAATATTTCATGAGGGTGTGCTT 583  
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QY 584 CAGATGCTGACGAGGCAAGGTCCATGAGTGAAGAGGTAACAATGACCTATG 643  
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QY 704 TGTCAAGGAGAGAGAGGATTTGATGCGCCACTTCAAAATCTAAGATGAGAGGG 763  
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QY 884 GTCTAG 889  
DB 1340 GUCUAG 1345

## RESULT 6

US-08-660-148-4  
; Sequence 4, Application US/08660148  
; Patent No. 6211353  
; GENERAL INFORMATION:  
; APPLICANT: Burnett, J. P.  
; APPLICANT: Mayne, Nancy G.  
; APPLICANT: Sharp, Robert L.  
; APPLICANT: Snyder, Yvonne M.  
; TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
; TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,148

FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/282,853  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-9419  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4303 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 460..4095  
US-08-660-148-4

Query Match 12.2%; Score 222; DB 3; Length 4303;  
Best Local Similarity 99.1%; Pred. No. 6,9e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGTTCAGAAATTGCTCCAGTTTCAACATACCTGAGATTGCTTACAG 523  
DB 920 TAGCCATTGAGTTCAGAAATTGCTCCAGTTTCAACATACCTGAGATTGCTTACAG 979  
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DB 980 CAACCAAGATGATCTGAGTGAAGAGCTGCTTCAAAATATTTCATGAGGGTGTGCTT 1039  
QY 584 CAGATGCTGACGAGGCAAGGTCCATGAGTGAAGAGGTAACAATGACCTATG 643  
DB 1040 CAGATGCTGACGAGGCAAGGCGCATGAGTGAAGAGGTAACAATGACCTATG 1099  
QY 644 TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 703  
DB 1100 TATCAGCCGTGACACAGAAAGCACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 1159  
QY 704 TGTCAAGGAGAGAGGATTTGATGCGCCACTTCAAAATCTAAGATGAGAGGG 763  
DB 1160 TGTCAAGGAGAGAGGATTTGATGCGCCACTTCAAAATCTAAGATGAGAGGG 1219  
QY 764 AGCAGAGCTTTGTAAGCTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCGGCTGG 823  
DB 1220 AGCAGAGCTTTGTAAGCTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCGGCTGG 1279  
QY 824 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGCGCATGAGCGCTGG 883  
DB 1280 TGCCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGCGCATGAGCGCTGG 1339  
QY 884 GTCTAG 889  
DB 1340 GTCTAG 1345

## RESULT 7

US-08-660-148-6  
; Sequence 6, Application US/08660148  
; Patent No. 6211353  
; GENERAL INFORMATION:  
; APPLICANT: Burnett, J. P.  
; APPLICANT: Mayne, Nancy G.  
; APPLICANT: Sharp, Robert L.  
; APPLICANT: Snyder, Yvonne M.  
; TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
; TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
; NUMBER OF SEQUENCES: 6





Db 701 TGTGAGGAGGAGGATTTGATGATGCGCCACTTACAAATCTACAGTAATGACGGGG 760  
QY 764 AGCAGAGCTTTGATTAAGTCTGTAAGAAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 823  
Db 761 AGCAGAGCTTTGATTAAGTCTGTAAGAAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 820  
QY 824 TGGCTACTTCTGTGAGGGGATGACGGGTGAGAGGTCTGCTGATGAGGCCATGAGGGCCTGG 883  
Db 821 TGGCTACTTCTGTGAGGGGATGACGGGTGAGAGGTCTGCTGATGAGGCCATGAGGGCCTGG 880  
QY 884 GTCTAG 889  
Db 881 GTCTAG 886

RESULT 2  
US-09-695-481-5  
; Sequence 5, Application US/09695481  
; Patent No. 6534287  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/09/695,481  
; CURRENT FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 3129  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric  
; OTHER INFORMATION: molecule comprising portions of human mGluR4 and  
; OTHER INFORMATION: the human calcium receptor.  
; NAME/KEY: CDS  
; LOCATION: ( )..(3129)  
US-09-695-481-5

Query Match 12.2%; Score 222; DB 4; Length 3129;  
Best Local Similarity 99.1%; Pred. No. 7,1e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
Db 461 TAGCCATTGAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 520  
QY 524 CAACCATCATGAGTCTGAGTGAAGAAGCTCTGTTCAAAATTTTCATGAGGGTGTGCTT 583  
Db 521 CAACCATCATGAGTCTGAGTGAAGAAGCTCTGTTCAAAATTTTCATGAGGGTGTGCTT 580  
QY 584 CAGATGCTCAGCAGGCAAGGTCATGCTGAGCATAGTGAAGAGGTACAATGCACTATG 643  
Db 581 CAGATGCTCAGCAGGCAAGGTCATGCTGAGCATAGTGAAGAGGTACAATGCACTATG 640  
QY 644 TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 703  
Db 641 TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
QY 704 TGTGAGGAGGAGGAGGATTTGATGCTGCGCCACTTTTCAAAATTTTCAAGTAATGCAAGGG 763  
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QY 764 AGCAGAGCTTTGATTAAGTCTGTAAGAAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 823  
Db 761 AGCAGAGCTTTGATTAAGTCTGTAAGAAGCTCAACAAGTCACTTGCCCAAGGCCGGGTGG 820

QY 824 TGGCTACTTCTGTGAGGGGATGACGGGTGAGAGGTCTGCTGATGAGGCCATGAGGGCCTGG 883  
Db 821 TGGCTACTTCTGTGAGGGGATGACGGGTGAGAGGTCTGCTGATGAGGCCATGAGGGCCTGG 880  
QY 884 GTCTAG 889  
Db 881 GTCTAG 886

RESULT 3  
US-09-016-434-1133  
; Sequence 1133, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1133:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4078 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1408051  
US-09-016-434-1133

Query Match 12.2%; Score 222; DB 4; Length 4078;  
Best Local Similarity 99.1%; Pred. No. 7e-88;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TAGCCATTGAGGTCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 523  
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QY 524 CAACCATCATGAGTCTGAGTGAAGAAGCTCTGTTCAAAATTTTCATGAGGGTGTGCTT 583  
Db 671 CAACCATCATGAGTCTGAGTGAAGAAGCTCTGTTCAAAATTTTCATGAGGGTGTGCTT 730  
QY 584 CAGATGCTCAGCAGGCAAGGTCATGCTGAGCATAGTGAAGAGGTACAATGCACTATG 643  
Db 731 CAGATGCTCAGCAGGCAAGGTCATGCTGAGCATAGTGAAGAGGTACAATGCACTATG 790

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 14, 2003, 09:48:38 ; Search time 118.716 Seconds  
(without alignments)  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	222	12.2	2826	4 US-09-695-481-1	Sequence 1, Appl1
2	222	12.2	3129	4 US-09-695-481-5	Sequence 5, Appl1
3	222	12.2	4078	4 US-09-016-434-1133	Sequence 1133, Ap
4	222	12.2	4207	3 US-08-660-148-1	Sequence 1, Appl1
5	222	12.2	4207	3 US-08-660-148-3	Sequence 3, Appl1
6	222	12.2	4303	3 US-08-660-148-4	Sequence 4, Appl1
7	222	12.2	4303	3 US-08-660-148-6	Sequence 6, Appl1
8	171	9.4	3282	1 US-08-072-574-11	Sequence 11, Appl1
9	171	9.4	3282	1 US-08-486-270-11	Sequence 11, Appl1
10	171	9.4	3282	4 US-08-367-264-11	Sequence 11, Appl1
11	171	9.4	3282	4 US-09-153-757-11	Sequence 11, Appl1
12	171	9.4	3282	4 US-09-459-715-11	Sequence 11, Appl1
13	171	9.4	4085	1 US-08-072-574-7	Sequence 7, Appl1
14	171	9.4	4085	1 US-08-486-270-7	Sequence 7, Appl1
15	171	9.4	4085	3 US-08-367-264-7	Sequence 7, Appl1
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18	171	9.4	4181	1 US-08-072-574-9	Sequence 9, Appl1
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23	33	1.8	241	4 US-09-389-681-334	Sequence 334, App
24	33	1.8	241	4 US-09-620-4058-334	Sequence 334, App
25	33	1.8	241	4 US-09-433-8268-334	Sequence 334, App
26	33	1.8	241	4 US-09-604-287A-334	Sequence 334, App
27	33	1.8	940	2 US-08-471-717-1	Sequence 1, Appl1

28	33	1.8	981	3 US-08-915-225-1	Sequence 1, Appl1
29	33	1.8	1277	4 US-09-187-999-30	Sequence 30, Appl1
30	33	1.8	1413	4 US-09-504-445-1	Sequence 1, Appl1
31	33	1.8	1445	4 US-09-814-951A-1	Sequence 1, Appl1
32	33	1.8	1810	4 US-09-369-247-11	Sequence 11, Appl1
33	33	1.8	2051	4 US-09-399-913-52	Sequence 52, Appl1
34	33	1.8	2797	4 US-09-482-273-74	Sequence 74, Appl1
35	33	1.8	3080	4 US-09-489-041A-25	Sequence 25, Appl1
36	33	1.8	3080	4 US-09-245-281-25	Sequence 25, Appl1
37	33	1.8	3080	4 US-09-307-359B-25	Sequence 25, Appl1
38	33	1.8	3080	4 US-09-340-620A-25	Sequence 25, Appl1
39	33	1.8	3312	4 US-09-669-751-259	Sequence 259, App
40	33	1.8	3385	4 US-08-405-392-1	Sequence 1, Appl1
41	33	1.8	3385	3 US-08-487-691-1	Sequence 1, Appl1
42	33	1.8	3385	3 US-08-666-221B-3	Sequence 3, Appl1
43	33	1.8	3385	3 US-08-666-221B-9	Sequence 9, Appl1
44	33	1.8	3385	4 US-08-189-738A-1	Sequence 1, Appl1
45	33	1.8	3637	1 US-08-445-640-3	Sequence 3, Appl1

#### ALIGNMENTS

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RESULT 1
US-09-695-481-1
; Sequence 1, Application US/09695481
; Patent No. 6534287
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOLAND, LAURA
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: NPS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(2826)
US-09-695-481-1

Query Match 12.2%; Score 222; DB 4; Length 2826;
Best Local Similarity 99.1%; Pred. No. 7.1e-88;
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 464 TGGCCATTAGAGTCCGAAATTGCTCAGCTTTTGAACCTACCTGAGTTGCTTACG 523
DB 461 TAGCCATTAGAGTCCGAAATTGCTCAGCTTTTGAACCTACCTGAGTTGCTTACG 520
QY 524 CAACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583
DB 521 CAACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
QY 584 CAGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 643
DB 581 CAGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 640
QY 644 TATCAGCCTTACACACAGAGCACTATGAGAAAGTGGATGGAAGGCTTCAAGATA 703
DB 641 TATCAGCCTTACACACAGAGCACTATGAGAAAGTGGATGGAAGGCTTCAAGATA 700
QY 704 TGTACAGAGAGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 763
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1100 UATCAGCCCGGCAACACAGAAAGGCAACUAGAGAGAAAGUGGAGAGCCUUCACAAAGADA 1159
QY 704 TGTCAAGCGAAGAAAGGATTTGCATGCGCCCACTCTTACAAAATCTACAGTAATGCAAGGG 763
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 764 AGCAGAGCTTTGATTAAGCTGCTGAAAGGCTCACAAAGTCACTTGCCCAAGGCCCGGGTGG 823
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1280 UGGCCUGCUCUGAGGCGCAUGACGGUGAGAGGUCUGCUGAUGGCCCAUGAGGCGCCUGG 1339
QY 884 GTCTAG 889
Db :|||:
1340 GUCUAG 1345
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Job time : 531.208 secs



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CC |||||  
DB 1814 GAGGACCTTATGCTGGATGTTTAAAGACGATTCAGTGTCTTTACACC 1873  
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DB 2054 GAGACAAATCAGAAATGTTTATCTGCTGTGGAAACCCCTTATCCATTAAGCCCTCT 2113  
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QY 1684 TCTTGTGCTTATCAACGAGCAATAGTCTGTTTATGCTTGAATGCTATCTA 1743  
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DB 2114 TCTTGTGCTTATCAACGAGCAATAGTCTGTTTATGCTTGAATGCTATCTA 2173  
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QY 1744 ATGTATTAATACTCACTTATGTTACTATTAAATGCTTAACCAAAAAA 1803  
CC |||||  
DB 2174 ATGTATTAATACTCACTTATGTTACTATTAAATGCTTAACCAAAAAA 2233  
CC |||||  
QY 1804 AAAAAAA 1811  
CC |||||  
DB 2234 AAAAAAA 2241  
CC |||||

## RESULT 10

ACAS6535  
ID ACAS6535 standard; cDNA; 4078 BP.

ACAS6535;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1133.

Human; Probe; ss; array element; Parkinson's disease;

signalling pathway population; cancer; adenocarcinoma; leukaemia;

immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-0016434.

30-JAN-1998; 98US-0016434.

'INCY-') INCYTE GENOMICS INC.

Au-Young J, Selthamer J;

MPI, 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a

microarray for monitoring the expression of a number of target

polynucleotides -

Claim 1; SEQ ID NO 1133; 65bp; English.

The invention relates to a combination which, comprises a number of

polynucleotide probes comprising a sequence selected from one of the 1490

sequences mentioned in the specification. The combination is useful as an

of target polynucleotides. The microarray is particularly useful in the  
diagnosis and treatment of cancer and immunopathology and neuropathology.  
The microarray is useful in diagnostics and treatment regimens, drug  
discovery and development, toxicological and carcinogenicity studies,  
forensics and pharmacogenomics. The microarray is also useful for  
monitoring progression of diseases and for developing sophisticated  
profiles for the effects of currently available therapeutic drugs. The  
combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
and genomic fragments and in research and diagnostic applications. The  
array can detect changes in expression in a large number of genes coding  
for different signalling pathway populations which can be used to diagnose  
various diseases including cancer e.g. adenocarcinoma and leukaemia,  
immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
and Parkinson's disease. The present sequence represents a polynucleotide  
probe of the invention.  
Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from USPTO  
at [seqdata.uspto.gov/sequence.html?DocID=06500938B1](http://seqdata.uspto.gov/sequence.html?DocID=06500938B1).

SO Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other;

Query Match 48.9%; Score 891.4; DB 25; Length 4078;

Best Local Similarity 98.3%; Pred. No. 1.3e-215;

Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAAAAATGCTCTTCTGTTGATTCCTGTCAGCTTATTTGAAAGAAAGATGCTGGAGT 60  
DB 148 AAAAAATGCTCTTCTGTTGATTCCTGTCAGCTTATTTGAAAGAAAGATGCTGGAGT 207  
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QY 61 GCAAGTCCAGTGAAGAGAGAGGAGTGTGCTCAATGCTGGGTGATCATTTATGAGCT 120  
DB 208 GCAAGTCCAGTGAAGAGAGAGGAGTGTGCTCAATGCTGGGTGATCATTTATGAGCT 267  
CC |||||  
QY 121 CTCCTTCTGTTTATGATCAGCAAGCTTGTGAGCAAGATTCATGAGAGAAAGTGGGCA 180  
DB 268 CTCCTTCTGTTTATGATCAGCAAGCTTGTGAGCAAGATTCATGAGAGAAAGTGGGCG 327  
CC |||||  
QY 181 GTCCCTGGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGATACCTCTGAGAAAGATC 240  
DB 328 GTCCCTGGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGATACCTCTGAGAAAGATC 387  
CC |||||  
QY 241 AATTGAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGAGATTCCTGC 300  
DB 388 AATTGAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGAGATTCCTGC 447  
CC |||||  
QY 301 TGGCATTTGGCTGTGAGCCCTTAAGAGAGCATTTAGTCAATTAAGAGATTCCTCATTTCT 360  
DB 448 TGGCATTTGGCTGTGAGCCCTTAAGAGAGCATTTAGTCAATTAAGAGATTCCTCATTTCT 507  
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QY 361 TCGGAAGAGAGAGAGGCTTTGTATGCTCTGTGAGATGAGTCTCTCTCTCCGCTCC 420  
DB 508 TCGGAAGAGAGAGAGGCTTTGTATGCTCTGTGAGATGAGTCTCTCTCTCCGCTCC 567  
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DB 568 AAGAAGCCATAGTAGGGGTCAATTTGGGCTGTGAGTTCAGTTCTTACCAATTCAGTCCAG 627  
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QY 481 AATTGCTCAGCTTTTCAACATCACTCAATGCTTCACTCAAGCAACATCATGATGATCTG 540  
DB 628 AATTGCTCAGCTTTTCAACATCACTCAATGCTTCACTCAAGCAACATCATGATGATCTG 687  
CC |||||  
QY 541 AGTGACAAAGCTCTGTTCAATTTTCAATGAGGCTGTGCTCAATGCTCAAGGCA 600  
DB 688 AGTGACAAAGCTCTGTTCAATTTTCAATGAGGCTGTGCTCAATGCTCAAGGCA 747  
CC |||||  
QY 601 AGGTCCATGCTGAGCATAGTGAAGAGTCACTGAGCCATGATCATGAGCCGATCAACA 660  
DB 748 AGGTCCATGCTGAGCATAGTGAAGAGTCACTGAGCCATGATCATGAGCCGATCAACA 807  
CC |||||  
QY 661 GAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATATGTCAGAGAAAGAGG 720  
DB 808 GAAAGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATATGTCAGAGAAAGAGG 867  
CC |||||







Pt	US8211353-B1.
XX	03-APR-2001.
XX	07-JUN-1996; 96US-0660148.
PF	29-JUL-1994; 94US-0282853.
XX	(ELIL ) LILLY & CO ELI.
XX	Burnett JP, Mayne NG, Sharp RL, Snyder YM,
XX	WPI; 2001-289639/30.
DR	P-P5DB; AAE01156.
XX	New isolated nucleic acids for producing human metabotropic glutamate
PT	receptors, which are useful for modulating the presynaptic release of
PT	glutamate or the postsynaptic sensitivity of the neuronal cell to
PT	glutamate excitation -
XX	Claim 2; Column 43-46; 53pp; English.
PS	The present sequence is a mRNA encoding human metabotropic glutamate
CC	receptor, mGluR5. L-glutamate, the most abundant neurotransmitter in
CC	the central nervous system (CNS), mediates excitatory pathway in
CC	mammals. L-glutamate is referred to as excitatory amino acid (EAA) and
CC	the receptors that respond to glutamate are EAA receptors. The receptors
CC	are useful for modulating the presynaptic release of glutamate and the
CC	postsynaptic sensitivity of the neuronal cell to glutamate excitation.
XX	Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;
SQ	
Query Match	48.9%; Score 891.4; DB 22; Length 4207;
Best Local Similarity	73.9%; Pred. No. 1.4e-215;
Matches 678; Conservative 223; Mismatches 16; Indels 0; Gaps 0;	
Oy	1 AAAATGGCTTCCTGTGATCTCGTCACTCTTGAAGAAAGAAGATTCCGTGGGAGT 60
Dd	457 AAAUVGGGCCUUCGUUGAUUCUGUCAUCUUUAAGAAAGAAGUUCGUGGAGU 516
Oy	61 GCACAGTGCATGAGAGAGAGGGTGAGCTCATATGCTGGGTGACATCATTTATTTGAGACT 120
Dd	517 GCACAGTGCATGAGAGAGAGGGTGGTGGTCCGAGCAUCCGGGUGACAUAUUAUUGAGACU 576
Oy	121 CTCTTTTCTGTTCATCACCAAGCTTACTGTGACGAAATTCAATGAGAGAACTGTGGGCA 180
Dd	577 CUUUUUUUGUUCACACACAGCUUUGAACAAGUUCAUUGAGAGAAUGUGGGGCG 636
Oy	181 GTCCGTGAACAGTATAGCATTCAGAGATGAGAGGCAATGCTGATACCCTGGAAAAGATC 240
Dd	637 GUCCGUGAACAGUUAAGGCAUUCAGAGAGGAGGCGACAGCCGACAAUCCUGGAAAGAUUC 696
Oy	241 AATTGAGACCCCACTCTTGCCCAACATCACTGGGCTGTGAGATTAAGGATTCCTGC 300
Dd	697 AAUUCAGACCCCACTCTTGCCCAACATCACTGGGCTGTGAGATTAAGGATTCCTGC 756
Oy	301 TGGCATTTGGCTGTGGCCCTTAGAGACAGCATTTGAGTTCAATAAGAGATTCCTCTCATTTCT 360
Dd	757 UGGCAUUGGGGCGUGGGCCCUAGAGCAGCAUUGAGUUCAUAAAGAUUCCUUCU 816
Oy	361 TTGGGAAGAGAAAGGGGCTGGTATAGCTGTGAGATGAGCTCTCTCTTCCCTCCGCTCC 420
Dd	817 UCAGAGAGAGAAAGGGGCTGGTATAGCTGTGAGATGAGCTCTCTCTTCCCTCCGCTCC 876
Oy	421 AAGAAGCCCATATGAGGGGTCAATTTGGGCTGTGAGTTCTTTTGAAGCATTCAGGTCCAG 480
Dd	877 AAGAAGCCCATATGAGGGGTCAATTTGGGCTGTGAGTTCTTTTGAAGCATTCAGGTCCAG 936
Oy	481 AATTGCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGACCAACATCATGAGATCTG 540
Dd	937 AAUUTGCTCCAGCTTTTCAACATACCTGAGATTGCTTACTGACCAACATCATGAGATCTG 996
Oy	541 AGTGAACAAGATCTGTTCAAATATTTCATGAGGGTTGTGCTTCAAGATGCTCAGCAGGCA 600

[illegible]



XX  
DR WPI; 2001-289639/30.  
XX  
PT New isolated nucleic acids for producing human metabotropic glutamate  
PT receptors, which are useful for modulating the presynaptic release of  
PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
PT glutamate excitation -  
XX  
PS Disclosure; Column 23-34; 53pp; English.  
XX  
CC The present sequence is a cDNA mutant encoding human metabotropic  
CC glutamate receptor, mGluR5B. L-glutamate, the most abundant  
CC neurotransmitter in the central nervous system (CNS), mediates excitatory  
CC pathway in mammals. L-glutamate is referred to as excitatory amino acid  
CC (EAA) and the receptors that respond to glutamate are EAA receptors. The  
CC receptors are useful for modulating the presynaptic release of glutamate  
CC and the postsynaptic sensitivity of the neuronal cell to glutamate  
CC excitation.  
XX  
SQ Sequence 4303 BP; 1043 A; 1139 C; 1144 G; 977 T; 0 other:  
  
Query Match 48.9%; Score 891.4; DB 22; Length 4303;  
Best Local Similarity 98.3%; Pred. No. 1.4e-215;  
Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
  
QY 1 AAAATGCTCTCTCTGATCCCTGATCTTACTTTTGAAGAAGATGCCGGAGT 60  
DB 457 AAAATGCTCTCTCTGATCCCTGATCTTACTTTTGAAGAAGATGCCGGAGT 516  
QY 61 GCACAGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 120  
DB 517 GCACAGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 576  
QY 121 CTCTTTCTGTTATCAACCAAGCTACTGTGACGAAGTTCAAGAGAGAGAGAGT 180  
DB 577 CTCTTTCTGTTATCAACCAAGCTACTGTGACGAAGTTCAAGAGAGAGAGT 636  
QY 181 GTCCGTGAAGATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
DB 637 GTCCGTGAAGATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 696  
QY 241 AATTGAGCCCACTCTTGTCCCAATCACTGAGAGAGAGAGAGAGAGAGATC 300  
DB 697 AATTGAGCCCACTCTTGTCCCAATCACTGAGAGAGAGAGAGAGAGATC 756  
QY 301 TGGCATTGCGCTGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGATCT 360  
DB 757 TGGCATTGCGCTGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGATCT 816  
QY 361 TCGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCC 420  
DB 817 TCGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCC 876  
QY 421 AAGAAGCCATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 480  
DB 877 AAGAAGCCATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 936  
QY 481 AATTGCTCAGCTTTTCAACATACCTCAAGTGTCTTACAGCAACCATCATGATCTG 540  
DB 937 AATTGCTCAGCTTTTCAACATACCTCAAGTGTCTTACAGCAACCATCATGATCTG 996  
QY 541 AGTGAACAAGACTCTGTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGAGT 600  
DB 997 AGTGAACAAGACTCTGTTCAAAATATTTTCAAGAGAGAGAGAGAGAGAGT 1056  
QY 601 AGGTCAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 660  
DB 1057 AGGTCAATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1116  
QY 661 GAAGGCAACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 720  
DB 1117 GAAGGCAACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1176

QY 721 ATTGATGAGCCCACTCTTACAAAATCTACAGTAAATGAGAGAGAGAGAGATTAAG 780  
DB 1177 ATTGATGAGCCCACTCTTACAAAATCTACAGTAAATGAGAGAGAGAGAGATTAAG 1236  
QY 781 CTGCTGAAGAAGCTCAAGAGTCACTTGCCTAAGAGAGAGAGAGAGAGAGAGT 840  
DB 1237 CTGCTGAAGAAGCTCAAGAGTCACTTGCCTAAGAGAGAGAGAGAGAGAGT 1296  
QY 841 GGCATGACGCTGAGAGAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGATTT 900  
DB 1297 GGCATGACGCTGAGAGAGTCTGATGAGAGAGAGAGAGAGAGAGAGATTT 1356  
QY 901 CTGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTT 917  
DB 1357 CTGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTT 1373  
  
Search completed: December 14, 2003, 10:19:23  
Job time : 549.208 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 04:35:06 ; Search time 118.716 Seconds  
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6777.889 Million cell updates/sec

Title: US-10-027-923-1

Sequence: 1823  
1 aaatgctctctctgtgat.....aaaaaaaaaaaaaaaaaaaaa 1823

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq:\*  
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6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891.4	48.9	4078	4 US-09-016-434-1133	Sequence 1133, Ap
2	891.4	48.9	4207	3 US-08-660-148-1	Sequence 1, Appl
3	891.4	48.9	4207	3 US-08-660-148-3	Sequence 3, Appl
4	891.4	48.9	4303	3 US-08-660-148-4	Sequence 4, Appl
5	891.4	48.9	4303	3 US-08-660-148-6	Sequence 6, Appl
6	888.4	48.7	2826	4 US-09-695-481-1	Sequence 1, Appl
7	888.4	48.7	3129	4 US-09-695-481-5	Sequence 5, Appl
8	888.4	48.7	3282	1 US-08-072-574-11	Sequence 11, Appl
9	888.2	48.7	3282	1 US-08-486-270-11	Sequence 11, Appl
10	888.2	48.7	3282	4 US-09-153-757-11	Sequence 11, Appl
11	888.2	48.7	3282	4 US-09-153-757-11	Sequence 11, Appl
12	888.2	48.7	3282	4 US-09-459-715-11	Sequence 11, Appl
13	888.2	48.7	4085	1 US-08-072-574-7	Sequence 7, Appl
14	888.2	48.7	4085	1 US-08-486-270-7	Sequence 7, Appl
15	888.2	48.7	4085	3 US-08-367-264-7	Sequence 7, Appl
16	888.2	48.7	4085	4 US-09-153-757-7	Sequence 7, Appl
17	888.2	48.7	4085	4 US-09-459-715-7	Sequence 7, Appl
18	888.2	48.7	4181	1 US-08-072-574-9	Sequence 9, Appl
19	888.2	48.7	4181	1 US-08-486-270-9	Sequence 9, Appl
20	888.2	48.7	4181	3 US-08-367-264-9	Sequence 9, Appl
21	888.2	48.7	4181	4 US-09-153-757-9	Sequence 9, Appl
22	888.2	48.7	4181	4 US-09-459-715-9	Sequence 9, Appl
23	458.2	25.1	3321	1 US-08-486-270-1	Sequence 1, Appl
24	458.2	25.1	3321	3 US-08-367-264-1	Sequence 1, Appl
25	458.2	25.1	3321	4 US-09-153-757-1	Sequence 1, Appl
26	458.2	25.1	3321	4 US-09-459-715-1	Sequence 1, Appl
27	458.2	25.1	3582	4 US-08-538-526-2	Sequence 2, Appl

28	458.2	25.1	4074	4 US-09-016-434-1475	Sequence 1475, Ap
29	449.2	24.6	3219	4 US-08-687-289A-3	Sequence 3, Appl
30	449.2	24.6	3219	4 US-09-435-897-3	Sequence 3, Appl
31	449.2	24.6	3384	2 US-08-687-289A-1	Sequence 1, Appl
32	449.2	24.6	3384	4 US-09-435-897-1	Sequence 1, Appl
33	449.2	24.6	4300	1 US-08-041-538-1	Sequence 1, Appl
34	449.2	24.6	4300	1 US-08-463-642-1	Sequence 1, Appl
35	449.2	24.6	4300	1 US-08-455-602-1	Sequence 1, Appl
36	449.2	24.6	4300	2 US-08-465-157-1	Sequence 1, Appl
37	449.2	24.6	4300	5 PCT-US91-09422-1	Sequence 1, Appl
38	449.2	24.6	5236	5 PCT-US91-09422-16	Sequence 16, Appl
39	444.4	24.4	3219	2 US-08-687-289A-4	Sequence 4, Appl
40	444.4	24.4	3219	4 US-09-435-897-4	Sequence 4, Appl
41	437.4	24.0	3330	1 US-08-072-574-1	Sequence 1, Appl
42	144.2	7.9	4095	5 PCT-US91-09422-18	Sequence 18, Appl
43	143.6	7.9	2736	3 US-08-617-785-1	Sequence 1, Appl
44	143.6	7.9	2736	4 US-09-817-464-1	Sequence 0, Appl
45	143.6	7.9	3431	4 US-09-641-318-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-09-016-434-1133  
Sequence 1133, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Sellhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4078 base pairs  
TYPE: nucleic acid  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1408051  
US-09-016-434-1133  
Query Match 48.9%; Score 891.4; DB 4; Length 4078;  
Best Local Similarity 98.3%; Pred. No. 3.3e-211;

	Matches	901	Conservative	0	Mismatches	16	Indels	0	Gaps	0
OY	1	AAATAGTCTCTCTGTGATCTCTGACAGTCTTACTTTGAAAGAAAGTCCGTGGAGT	60							
Db	148	AAAATGGCTCTCTGTGATCTCTGACAGTCTTACTTTGAAAGAAAGTCCGTGGAGT	207							
OY	61	GCAAGTCAAGTGAAGAGGAGGTGGCTCACTGTCGGGACATCATTTTASAGT	120							
Db	208	GCAAGTCAAGTGAAGAGGAGGTGGCTCACTGTCGGGACATCATTTTASAGT	267							
OY	121	CTCTTTCTGTTCACTCAACGCTTACTGTGACGAAGTTCATGAGAGAGTGGGCA	180							
Db	268	CTCTTTCTGTTCACTCAACGCTTACTGTGACGAAGTTCATGAGAGAGTGGGCG	327							
OY	181	GTCCGTGAACAGTATNGGCAATTGAGAGTGAAGGCCATGCTGCAATCCCTGAAAGATC	240							
Db	328	GTCCGTGAACAGTATNGGCAATTGAGAGTGAAGGCCATGCTGCAATCCCTGAAAGATC	387							
OY	241	AATTGAGACCCCACTCTGTCGCAACATCACTGAGGCTGTGATTAAGGATTCCTGAC	300							
Db	388	AATTGAGACCCCACTCTGTCGCAACATCACTGAGGCTGTGATTAAGGATTCCTGAC	447							
OY	301	TGGCATTCGGCTGTGAGCCCTTGAAGCAGAGCATTTGAGTTCAATAGATTCCTCATTTCT	360							
Db	448	TGGCATTCGGCTGTGAGCCCTTGAAGCAGAGCATTTGAGTTCAATAGATTCCTCATTTCT	507							
OY	351	TGCGAAGAGGAAGAGGCTTGGTATGCTCTGTGATAGTCTCTCTTCTTCCGCTCC	420							
Db	508	TCAGAAGAGGAAGAGGCTTGGTATGCTCTGTGATAGTCTCTCTTCTTCCGCTCC	567							
OY	421	AAGAAGCCCATAGTAGGGGTCATTGGGCTGGTCTCAAGTCTTTAGCCATTGAGGTCAG	480							
Db	568	AAGAAGCCCATAGTAGGGGTCATTGGGCTGGTCTCAAGTCTTTAGCCATTGAGGTCAG	627							
OY	481	AATTGCTCCAGCTTTTCAACATACCTGAGATTCCTACTCAGCAACCATCATGATCTG	540							
Db	628	AATTGCTCCAGCTTTTCAACATACCTGAGATTCCTACTCAGCAACCATCATGATCTG	687							
OY	541	AGTGCATGATCTCTGTTCAAAATTTTCAATGAGGCTTGGCTTCAGATGCTCAAGAGCA	600							
Db	688	AGTGCATGATCTCTGTTCAAAATTTTCAATGAGGCTTGGCTTCAGATGCTCAAGAGCA	747							
OY	601	AGTGCATGATGACATAGTAGAAGGATCAACACTGATGTATCAGCCGTACACA	660							
Db	748	AGGCGCATAGTGAACATATGTGAAGGATCAACTGACCTTATGTATCAGCCGTACACA	807							
OY	661	GAAGGCATATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAAGCAAGAGG	720							
Db	808	GAAGGCATATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAAGCAAGAGAGG	867							
OY	721	AATTGCAATCGCCCATCTTTCAAAATCTACGTATATGACAGGGGACACAGCTTATATAG	780							
Db	868	AATTGCAATCGCCCATCTTTCAAAATCTACGTATATGACAGGGGACACAGCTTATATAG	927							
OY	781	CTGCTGAAGAAAGCTCAACAATCTATGCGCAAGGCCGGGTGTGGCTTACTTCTGTAG	840							
Db	928	CTGCTGAAGAAAGCTCAACAATCTATGCGCAAGGCCGGGTGTGGCTTACTTCTGTAG	987							
OY	841	GGCATGACGGTGAAGGCTCTGCTGATGSCCATGAGGCGCTGGGTCTATGTTGAGAAATTT	900							
Db	988	GGCATGACGGTGAAGGCTCTGCTGATGSCCATGAGGCGCGTGGGTCTATGCGGAGAAATTT	1047							
OY	901	CTGCTTTGGGCAAGGA 917								
Db	1048	CTGCTTTGGGCAAGGA 1064								

RESULT 2  
US-08-660-148-1  
; Sequence 1, Application US/08660148  
; Patent No. 6211353  
; GENERAL INFORMATION:  
; APPLICANT: Burnett, J. P.

	APPLICANT:	Mayne, Nancy G.
	APPLICANT:	Sharp, Robert L.
	APPLICANT:	Snyder, Yvonne M.
	TITLE OF INVENTION:	EXCITATORY AMINO RECEPTOR PROTEIN AND
	TITLE OF INVENTION:	RELATED NUCLEIC ACID COMPOUNDS
	NUMBER OF SEQUENCES:	6
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE:	Eli Lilly and Company
	STREET:	Lilly Corporate Center
	CITY:	Indianapolis
	STATE:	Indiana
	COUNTRY:	United States of America
	ZIP:	46285
	COMPUTER READABLE FORM:	
	MEDIUM TYPE:	Floppy disk
	COMPUTER:	IBM PC compatible
	OPERATING SYSTEM:	PC-DOS/MS-DOS
	SOFTWARE:	Patentin Release #1.0, Version #1.25
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER:	US/08/660,148
	FILING DATE:	
	CLASSIFICATION:	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	US/08/282,853
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Gayle, Paul J.
	REGISTRATION NUMBER:	36,808
	REFERENCE/DOCKET NUMBER:	X-9419
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	(317) 276-0756
	TELEFAX:	(317) 276-3861
	INFORMATION FOR SEQ ID NO:	1:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	4207 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	single
	TOPOLOGY:	linear
	MOLECULE TYPE:	CDNA
	FEATURE:	
	NAME/KEY:	CDS
	LOCATION:	460..3999
	US-08-660-148-1	
	Query Match	48.9%; Score 891.4; DB 3; Length 4207;
	Best Local Similarity	98.3%; Pred. No. 3.3e-211;
	Matches 901; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
Dy	1	AAATGGCTTCGTTGATCGTGCAGCTTACTTTTGAAAGAAGATGCCGTGGAGT 60
Dd	457	AAAATGGCTTCGTTGATCGTGCAGCTTACTTTTGAAAGAAGATGCCGTGGAGT 516
Dy	61	GCAAGTCAGTAGAGAGAGGGGTGGCTCACATGCTGGGTGAACATCATTTTGAAGT 120
Dd	517	GCAAGTCAGTAGAGAGAGGGGTGGCTCACATGCCGGGTGACATCATTTTGAAGT 576
Dy	121	CTCTTTCTGTTCATCACAGCTTAAGTGGAGCAAGTTCAATGAGGAAGTGTGGSCA 180
Dd	577	CTCTTTCTGTTCATCACAGCTTAAGTGGAGCAAGTTCAATGAGGAAGTGTGGSCG 636
Dy	181	GTCGGTGAACGATATGGATTCAGAGATGAGAGCCATGCTGCATACCTTGAAAGATC 240
Dd	637	GTCGGTGAACGATATGGATTCAGAGATGAGAGCCATGCTGCATACCTTGAAAGATC 696
Dy	241	AATTCAGCCCCCACTCTTGCCCAACATCACATGGGGCTGTGAGATAAGGATTCCTGC 300
Dd	697	AATTCAGCCCCCACTCTTGCCCAACATCACATGGGGCTGTGAGATAAGGATTCCTGC 756
Dy	301	TGGCATTCGGCTGTGGCCCTTGAAGCAGAGCATTTGATTAAGATTCCTCATTTTCT 360
Dd	757	TGGCATTCGGCTGTGGCCCTTGAAGCAGAGCATTTGATTAAGATTCCTCATTTTCT 816
Dy	361	TGGAGAAGAGAGGGCTGTGATGCTGTGTGATGGCTCTCTCTTCTTCCGCTTC 420

```

Db      817  TCAGAGAGAGAGAGAGGCTTGTAAGCTGTGTGATGGCTCTCTCTCTTCCGCTCC  876
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Db      877  AAGAAGCCCATAGTAGAGGCTCATTGGGCTGTGCTCCAGTCTTGAAGCCATTCAAGTCCAG  936
QY      481  AATTGCTCCAGCTTTTCAACATACCTCCAGATTCCTTACTAGAGCAACATATAGATCTG  540
Db      937  AATTGCTCCAGCTTTTCAACATACCTCCAGATTCCTTACTAGAGCAACATAGATGATCTG  996
QY      541  AGTGCACAAGA CTCTGTTCAAAATATTTTCAATGAGGTTGTGCTCTAGATGTCCAGAGCA  600
Db      997  AGTGCACAAGACTCTGTTCAAAATATTTTCAATGAGGTTGTGCTCTAGATGTCCAGAGCA  1056
QY      601  AGTCCATGCTGTGACATATGTAGAGAGTACAACTGGAACCTATGTATCAGCCGTACACA  660
Db      1057  AGGCGCATGTGGTGA CATGTAGAGAGGTACAACTGGAACCTATGTATCAGCCGTACACA  1116
QY      661  GAAGGCAACTATGTAGAGAAAGTGGGATGGAGACCTTTCAAAAGTATGTACGCGAAGAGG  720
Db      1117  GAAGGCAACTATGTAGAGAAAGTGGGATGGAGACCTTTCAAAAGTATGTACGCGAAGAGG  1176
QY      721  ATTGCATATGCCCACTCTTACAAAATCCAGTATGACAGGAGGACAGACTTTGATAG  780
Db      1177  ATTGCATATGCCCACTCTTACAAAATCCAGTATGACAGGAGGACAGACTTTGATAG  1236
QY      781  CTGCTGAAGAGCTTCACAAAGTCACTTGGCCCAAGGCCCGGTGTGTGCTTACTTGTGAG  840
Db      1237  CTGCTGAAGAGAGCTTCACAAAGTCACTTGGCCCAAGGCCCGGTGTGTGCTTACTTGTGAG  1296
QY      841  GGCATGACGGTGAAGAGTCTGCTGATGCGCATGAGGCGCTTGGGTCTTAGTGGAGAAATT  900
Db      1297  GGCATGACGGTGAAGAGTCTGCTGATGCGCATGAGGCGCTTGGGTCTTAGTGGAGAAATT  1356
QY      901  CTGCTTCTGGGACAGGGA  917
Db      1357  CTGCTTCTGGGACAGTGA  1373

RESULT 3
US-08-660-148-3
: Sequence 3, Application US/08660148
: Patent No. 621153
: GENERAL INFORMATION:
: APPLICANT: Burnett, J. P.
: APPLICANT: Mayne, Nancy G.
: APPLICANT: Sharp, Robert L.
: APPLICANT: Snyder, Yvonne M.
: TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
: TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Eli Lilly and Company
: STREET: Lilly Corporate Center
: CITY: Indianapolis
: STATE: Indiana
: COUNTRY: United States of America
: ZIP: 46285
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/660,148
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/282,853
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gaylo, Paul J.

```

Query Match	48.9%	Score 891.4	DB 3	Length 4207
Best Local Similarity	73.9%	Pred. No. 3.3e-211		
Matches 678	Conservative 223	Mismatches 16	Indels 0	Gaps 0
REGISTRATION NUMBER: 36,808 REFERENCE/DOCKET NUMBER: X-9419 TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 276-0756 TELEFAX: (317) 276-3861 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 4207 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: mRNA US-08-660-148-3				
QY	1	AAAATGCTCTCTGTTGATCTCTGTCACTCTTATTTGAAAGAAAGATGTCCTGGAGAGT	60	
DB	457	AAAATGCTCTCTGTTGATCTCTGTCACTCTTATTTGAAAGAAAGATGTCCTGGAGAGT	516	
QY	61	GCAAGTCCAGTGAAGAGAGGAGTGGTGGCTCAATGCTGGAGTGCATCTTATTTGAGACT	120	
DB	517	GCAAGTCCAGTGAAGAGAGGAGTGGTGGCTCAATGCTGGAGTGCATCTTATTTGAGACT	576	
QY	121	CTCTTTTCTGTTCTATCAACAGACGCTTCTGTGACGAACTTCAATGAGAGAAAGTGGAGCA	180	
DB	577	CTCTTTTCTGTTCTATCAACAGACGCTTCTGTGACGAACTTCAATGAGAGAAAGTGGAGCA	636	
QY	181	GTCCTGTAACATGATGAGCATTTCAAGAGTGAAGGCTTCTGCTGATACCTTGGAAAGATC	240	
DB	637	GTCCTGTAACATGATGAGCATTTCAAGAGTGAAGGCTTCTGCTGATACCTTGGAAAGATC	696	
QY	241	AATTCAGACCCCAACATCTTGGCCCAATCACTGAGGCTGTGATTAAGGATTTCTGAC	300	
DB	697	AATTCAGACCCCAACATCTTGGCCCAATCACTGAGGCTGTGATTAAGGATTTCTGAC	756	
QY	301	TGGCATTCGAGTGTGAGCCCTAGAGCAGAGCATTTGAGTTCAATAGAGATTTCTGATTTCT	360	
DB	757	TGGCATTCGAGTGTGAGCCCTAGAGCAGAGCATTTGAGTTCAATAGAGATTTCTGATTTCT	816	
QY	361	TGCGAAGAGAGAGAGGCTTGGATGCTGTGTGATGAGTGGCTCTCTCTTCTCTTCCGCTCC	420	
DB	817	TGCGAAGAGAGAGAGGCTTGGATGCTGTGTGATGAGTGGCTCTCTCTTCTCTTCCGCTCC	876	
QY	421	AAGAGGCCCATATGATGAGGGTCAATTGGGCTGAGTTCAGTTCTTTAGGCAATTCAAGTCCAG	480	
DB	877	AAGAGGCCCATATGATGAGGGTCAATTGGGCTGAGTTCAGTTCTTTAGGCAATTCAAGTCCAG	936	
QY	481	AATTGCTCCAGCTTTTCAACATCACTCTCAGATTGCTTACTCAGCAACCATCATGATGATCTG	540	
DB	937	AATTGCTCCAGCTTTTCAACATCACTCTCAGATTGCTTACTCAGCAACCATCATGATGATCTG	996	
QY	541	AGTGAACAAGACTCTGTCTCAATAATTCTATGAGGTTGTGCTTCAAGTCTCAGCAGGCA	600	
DB	997	AGTGAACAAGACTCTGTCTCAATAATTCTATGAGGTTGTGCTTCAAGTCTCAGCAGGCA	1056	
QY	601	AGGTCATATGATGAGCATATGAGAAAGAGTCAACTGACCTATGATATGATATGATATGATG	660	
DB	1057	AGGTCATATGATGAGCATATGAGAAAGAGTCAACTGACCTATGATATGATATGATATGATG	1116	
QY	661	GAAAGCAACTATGAGAGAAAGTGGATGGAAGCTTCAAAAGATATATGACGCAAGAAAGG	720	
DB	1117	GAAAGCAACTATGAGAGAAAGTGGATGGAAGCTTCAAAAGATATATGACGCAAGAAAGG	1176	
QY	721	ATTTCATTCGCCCCCTCTTACAAATTTACATGATATGCAAGGAGGAGCAGAGCTTGTATAG	780	
DB	1177	ATTTCATTCGCCCCCTCTTACAAATTTACATGATATGCAAGGAGGAGCAGAGCTTGTATAG	1236	
QY	781	CTGCTGAAGAACTCAACAATCTTTCGCCAAGGCTCGGAGTGTGCTACTTCTGTGAG	840	
DB	1237	CTGCTGAAGAACTCAACAATCTTTCGCCAAGGCTCGGAGTGTGCTACTTCTGTGAG	1296	





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COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GAYLO, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-660-148-6

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Query Match 48.9%; Score 891.4; DB 3; Length 4303;

Best Local Similarity 73.9%; Pred. No. 3,3e-211; Matches 678; Conservative 223; Mismatches 16; Indels 0; Gaps 0;

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DB 457 AAATGCTCTTGTGTGATCTGTCACTTTTGAAGAAGATGCTCGTGGAGT 516
QY 61 GCACATCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 517 GCACATCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 576
QY 121 CTCTTTCTGTTTCATGACCAAGCTTCTGTCGAAAGTTATGAGAGGAGGAGG 180
DB 577 CUCUUUCUUGUUAUACCAAGCTTCTGTCGAAAGTTATGAGAGGAGGAGG 636
QY 181 GTCCGTGAACAGTATGAGGATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 637 GTCCGTGAACAGTATGAGGATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 696
QY 241 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAATTAAGGAGTTCC 300
DB 697 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAATTAAGGAGTTCC 756
QY 301 TGGCATTTGGGCTGTGGCCCTTGAAGAGAGGATTCATTAAGATTCCTCATTT 360
DB 757 TGGCATTTGGGCTGTGGCCCTTGAAGAGAGGATTCATTAAGATTCCTCATTT 816
QY 361 TCGGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 817 TCGGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 876
QY 421 AAGAAGCCCACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 877 AAGAAGCCCACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATATGAT 540
DB 937 AATTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATATGAT 996
QY 541 AGTGAACAAGCTGTCTTCAATATTTTCATGAGGAGGAGGAGGAGGAGGAGG 600
DB 997 AGTGAACAAGCTGTCTTCAATATTTTCATGAGGAGGAGGAGGAGGAGGAGG 1056

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QY 601 AGTTCATGTTGAGACATAGTGAAGGTTCAATGTGACCTATGTATCAGCCGTA 660
DB 1057 AGTTCATGTTGAGACATAGTGAAGGTTCAATGTGACCTATGTATCAGCCGTA 1116
QY 661 GAAGGACATATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 1117 GAAGGACATATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1176
QY 721 AATTGATGCCCCACTTCTTACAAATCTAAGTATGACAGGAGGAGGAGGAGG 780
DB 1177 AATTGATGCCCCACTTCTTACAAATCTAAGTATGACAGGAGGAGGAGGAGG 1236
QY 781 CTGCTGAAGAAGCTCAAGTCACTTGGCCCAAGGCCCCGGGTGTGCTTCTG 840
DB 1237 CTGCTGAAGAAGCTCAAGTCACTTGGCCCAAGGCCCCGGGTGTGCTTCTG 1296
QY 841 GGCATGACGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 1297 GGCATGACGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1356
QY 901 CTGCTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 917
DB 1357 CTGCTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1373

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# RESULT 6

US-09-695-481-1  
Sequence 1, Application US/09695481  
Patent No. 6534287

GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: LEVINTHAL, CYNTHIA  
APPLICANT: STOROHAN, LAURA  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: KRAPCHO, KAREN J.  
APPLICANT: NPS PHARMACEUTICALS, INC.  
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
FILE REFERENCE: 1094.2.6  
CURRENT APPLICATION NUMBER: US/09/695,481  
CURRENT FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/161,481  
PRIOR FILING DATE: 1999-10-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2826  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2826)

US-09-695-481-1

Query Match 48.7%; Score 888.4; DB 4; Length 2826;

Best Local Similarity 98.2%; Pred. No. 1.6e-210; Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 1 ATGCTCTTCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCT 60
QY 64 CAGTCAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123
DB 61 CAGTCAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 124 TTTTCTGTTTCATCACAGGCTCTGTGAGCAAGTTTATGAGAGGAGGAGGAG 183
DB 121 TTTTCTGTTTCATCACAGGCTCTGTGAGCAAGTTTATGAGAGGAGGAGGAG 180
QY 184 CGTGAACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
DB 181 CGTGAACAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

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Oy	244	TCAGACCCCA	CACTCTGGCC	CCAAACAT	CA	CACTGGCG	CTGTGA	GA	TAAGGA	ATTCCT	CTGG	303
Dd	241	TCAGACCCCA	CACTCTGGCC	CCAAACAT	CA	CTGGCG	CTGTGA	GA	TAAGGA	ATTCCT	CTGG	300
Oy	304	CATTGGCTGT	GGCCCTTA	GAGCAG	AGCAT	TGA	ATTGAT	TA	AAGATT	CCCTCAT	TTTCTTG	363
Dd	301	CATTGGCTGT	GGCCCTTA	GAGCAG	AGCAT	TGA	ATTGAT	TA	AAGATT	CCCTCAT	TTTCTTG	360
Oy	364	GAAAGGAA	GAGGCTTG	TATGCT	CTGTG	GANTGG	CTCTCC	CTCTCT	CTTCCG	CTCCAG	423	
Dd	361	GAAAGGAA	GAGGCTTG	TATGCT	CTGTG	GANTGG	CTCTCC	CTCTCT	CTTCCG	CTCCAG	420	
Oy	424	AAGCCCAT	ATGATG	GGGTCA	TTTG	GGCTTG	CTCA	GTCTTG	TAGCCAT	TTCAG	483	
Dd	421	AAGCCCAT	ATGATG	GGGTCA	TTTG	GGCTTG	CTCA	GTCTTG	TAGCCAT	TTCAG	480	
Oy	484	TTGCTCCAG	CTTTTCA	CACTCA	CTTCA	ATTGCT	TACT	CA	GCAC	CAATCAT	GTGAGT	543
Dd	481	TTGCTCCAG	CTTTTCA	CACTCA	CTTCA	ATTGCT	TACT	CA	GCAC	CAATCAT	GTGAGT	540
Oy	544	GACAAGACT	CTGTTC	AAATATT	TCAT	GAGGGT	TG	CCCTT	CAGATG	CTCAG	CGGCAAG	603
Dd	541	GACAAGACT	CTGTTC	AAATATT	TCAT	GAGGGT	TG	CCCTT	CAGATG	CTCAG	CGGCAAG	600
Oy	604	TCCATGTG	TGACAT	AGTGA	AGGTACA	CTGCA	CTTAT	GTAT	CAGCC	GTACA	CA	663
Dd	601	GCCATGTG	TGACAT	AGTGA	AGGTACA	CTGCA	CTTAT	GTAT	CAGCC	GTACA	CA	660
Oy	664	GGCAACTAT	GAGAA	AGTGGAT	TGA	AGCTTCA	AA	AGATAT	GT	CA	GCGAAG	723
Dd	661	GGCAACTAT	GAGAA	AGTGGAT	TGA	AGCTTCA	AA	AGATAT	GT	CA	GCGAAG	720
Oy	724	TGCATCGCC	CACTCTT	ACAAAT	CTAC	AGTAAT	GCAG	GGGAG	CA	GAGCTT	GA	783
Dd	721	TGCATCGCC	CACTCTT	ACAAAT	CTAC	AGTAAT	GCAG	GGGAG	CA	GAGCTT	GA	780
Oy	784	CTGAAGA	AGCTCA	CAAGTCA	CTTG	CCCAAG	CCCG	GGTGTG	GCCT	ACTTCT	GTGA	843
Dd	781	CTGAAGA	AGCTCA	CAAGTCA	CTTG	CCCAAG	CCCG	GGTGTG	GCCT	ACTTCT	GTGA	840
Oy	844	ATGACGTG	TAGAG	GGTGTG	CTGAT	GGCCTA	GTAG	AGGCG	CTTG	GTGG	GA	903
Dd	841	ATGACGTG	TAGAG	GGTGTG	CTGAT	GGCCTA	GTAG	AGGCG	CTTG	GTGG	GA	900
Oy	904	CTTCTGG	CGAGGA	917								
Dd	901	CTTCTGG	CGAGGA	914								

RESULT 7  
 US-09-695-481-5  
 Sequence 5, Application US/09695481  
 Patent No. 6534287  
 GENERAL INFORMATION:  
 APPLICANT: STORMANN, THOMAS M.  
 APPLICANT: LEVINTHAL, CYNTHIA  
 APPLICANT: STORJOHANN, LAURA  
 APPLICANT: HAMMERLAND, LANCE G.  
 APPLICANT: KRAPCHO, KAREN J.  
 APPLICANT: NPS PHARMACEUTICALS, INC.  
 TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
 FILE REFERENCE: 1094.2.6  
 CURRENT APPLICATION NUMBER: US-09/695,481  
 CURRENT FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: 60/161,481  
 PRIOR FILING DATE: 1999-10-25  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 5  
 LENGTH: 3129  
 TYPE: DNA  
 ORGANISM: Artificial Sequence

Db 901 CTTCTGGGAGTGA 914

## RESULT 8

US-08-072-574-11  
Sequence 11, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 900719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULAR TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-072-574-11

Query Match 48.7%; Score 888.2; DB 1; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTGTGATCTGTGATCTTGAAGAAGATGTCCTGGAGAT 60  
DB 367 AAAATGCTCTTGTGATCTGTGATCTTGAAGAAGATGTCCTGGAGAT 426  
QY 61 GCAAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
DB 427 GCAAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486  
QY 121 CTCTTTCTGTTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
DB 487 CTCTTTCTGTTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546  
QY 181 GTCCGTAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
DB 547 GTCCGTAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 606

QY 241 AATTGAG 300  
DB 607 AATTGAG 666  
QY 301 TGGCATTGAG 360  
DB 667 TGGCATTGAG 726  
QY 361 TCGAAG 420  
DB 727 TCGAAG 786  
QY 421 AAG 480  
DB 787 AAG 846  
QY 481 AATTGCTCAGCTTTTCAACATGCTGAGATGCTTCAAGAGAGAGAGAGAGAG 540  
DB 847 AATTGCTCAGCTTTTCAACATGCTGAGATGCTTCAAGAGAGAGAGAGAGAG 906  
QY 541 AGTGAAG 600  
DB 907 AGTGAAG 966  
QY 601 AGGTGATGAG 660  
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QY 661 GAAGGAG 720  
DB 1027 GAAGGAG 1086  
QY 721 AATTGATGAG 780  
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QY 841 GGCATGAG 900  
DB 1207 GGCATGAG 1266  
QY 901 CTGCTTCTGGAG 960  
DB 1267 CTGCTTCTGGAG 1326

## RESULT 9

US-08-486-270-11  
Sequence 11, Application US/08486270  
Patent No. 5807689

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-486-270-11

Query Match 48.7%; Score 888.2; DB 1; Length 3282;

Best Local Similarity 98.0%; Pred. No. 1,9e-210;

Matches 89; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 60  
DB 367 AAAATGCTCTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 426  
QY 61 GCACAGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
DB 427 GCACAGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486  
QY 121 CTCTTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 180  
DB 487 CTCTTTCTGTTGATCTGTGCTTACTTTTGAAGAAGATGCTGGAGT 546  
QY 181 GTCCGTGAACAGTATGTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
DB 547 GTCCGTGAACAGTATGTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGATC 606  
QY 241 AATTGACAGCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGC 300  
DB 607 AATTGACAGCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGATTCCTGC 666  
QY 301 TGGCATTCGGCTGGCCCTAGAGCAGAGCATTGAGTTCAATTAAGAGATTCCTCATTTCT 360  
DB 667 TGGCATTCGGCTGGCCCTAGAGCAGAGCATTGAGTTCAATTAAGAGATTCCTCATTTCT 726  
QY 361 TCGAAGATC 420  
DB 727 TCGAAGATC 786  
QY 421 AAGAAGCCCATAG 480  
DB 787 AAGAAGCCCATAG 846  
QY 481 AATTGCTCAGCTTTCAACATCTCAATTTGCTTACTCAGCAACATCATGATCTG 540  
DB 847 AATTGCTCAGCTTTCAACATCTCAATTTGCTTACTCAGCAACATCATGATCTG 906  
QY 541 AGTGACAGAAGCTCTGTTCAATATTTGATGAGGGTTGTGCTTCAATGCTCAGCAGCA 600  
DB 907 AGTGACAGAAGCTCTGTTCAATATTTGATGAGGGTTGTGCTTCAATGCTCAGCAGCA 966

QY 601 AGTCCATGATGAGCATAGTGAAGAGAGTCAACTGACCTATGATATCAGCCGTACACACA 660  
DB 967 AGGCGCATGATGAGCATAGTGAAGAGAGTCAACTGACCTATGATATCAGCCGTACACACA 1026  
QY 661 GAAGGCACTATGAG 720  
DB 1027 GAAGGCACTATGAG 1086  
QY 721 AATTGATGAGCCCACTTCAAAATCTACAGTAAGCAGGAGAGAGAGAGAGAGAGAGAGAG 780  
DB 1087 AATTGATGAGCCCACTTCAAAATCTACAGTAAGCAGGAGAGAGAGAGAGAGAGAGAGAG 1146  
QY 781 CTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGAGTGGCTACTTCTGTGAG 840  
DB 1147 CTGCTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGAGTGGCTACTTCTGTGAG 1206  
QY 841 GGCATGACGGTGAAGAGTCTGTGATGAGCATGAGAGCCTGGCTTAAGTGGAGAAATT 900  
DB 1207 GGCATGACGGTGAAGAGTCTGTGATGAGCATGAGAGCCTGGCTTAAGTGGAGAAATT 1266  
QY 901 CTGCTTCTGGCAGGGA 917  
DB 1267 CTGCTTCTGGCAGTGA 1283

RESULT 10  
US-08-367-264-11  
Sequence 11, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
APPLICANT: Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "variant of MGLUR5A with truncated 3' end."  
US-08-367-264-11

Query Match  
Best Local Similarity 98.0%; Score 888.2; DB 3; Length 3282;  
Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTCAGTCTTACCTTTGAAAGAGATGTCGGTGGAGT 60  
DB AAAATGCTCTTCTGTTGATCTGTCAGTCTTACCTTTGAAAGAGATGTCGGTGGAGT 426  
QY 61 GCAAGCTCAGTGAAG 120  
DB GCAAGCTCAGTGAAG 486  
QY 121 CTCTTTCTGTTCACTCAGCAGCTTCTGTCAGAGAGTTCATGAGAGAGAGAGAGAG 180  
DB CTCTTTCTGTTCACTCAGCAGCTTCTGTCAGAGAGTTCATGAGAGAGAGAGAGAG 546  
QY 181 GTCCGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
DB GTCCGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606  
QY 241 AATTGAG 300  
DB AATTGAG 666  
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QY 781 CTGCTGAAG 840  
DB CTGCTGAAG 1206  
QY 841 GGCATGAG 900  
DB GGCATGAG 1266  
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DB 1267 CTGCTTCTGGGAG 1283

RESULT 11  
US-09-153-757-11  
Sequence 11, Application US/09153757  
Patent No. 6413764  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Law, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09153,757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match  
Best Local Similarity 98.0%; Score 888.2; DB 4; Length 3282;  
Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGCTCTTCTGTTGATCTGTCAGTCTTACCTTTGAAAGAGATGTCGGTGGAGT 60  
DB AAAATGCTCTTCTGTTGATCTGTCAGTCTTACCTTTGAAAGAGATGTCGGTGGAGT 426  
QY 61 GCAAGCTCAGTGAAG 120  
DB GCAAGCTCAGTGAAG 486  
QY 121 CTCTTTCTGTTCACTCAGCAGCTTCTGTCAGAGAGTTCATGAGAGAGAGAGAGAG 180  
DB CTCTTTCTGTTCACTCAGCAGCTTCTGTCAGAGAGTTCATGAGAGAGAGAGAGAG 546

DB 487 CTCTTTTCTGTTATATACCAAGCTTCTGTGAGCAAAAGTTTATATAGAGAAAGTGTGGGGG 546  
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DB 607 AATTGAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCCTG 666  
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DB 667 TGGCATTCGGCTGTGGCCCTAGAGACAGATTAAGTCAATTAAGATTCCTCATTTCT 726  
QY 727 TCAGAGAGAGAAAGGCTTGGTACGCTGTGAGATGAGCTCTCTCTTCTCCGCTCC 786  
DB 421 AAGAAGCCCATATAGAGGGGTCAATTTGGGCTGTGAGATTCCTCATTTCT 480  
QY 787 AAGAAGCCCATATAGAGGGGTCAATTTGGGCTGTGAGATTCCTCATTTCT 846  
DB 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACCATCATGATCTG 540  
QY 847 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGCAACCATCATGATCTG 906  
DB 541 AGTGAACAAGCTGTGTTCAAAATATTTCTAGAGGGGTGTGCTTCAATGCTCAGAGGCA 600  
QY 907 AGTGAACAAGCTGTGTTCAAAATATTTCTAGAGGGGTGTGCTTCAATGCTCAGAGGCA 966  
DB 601 AGGTCCATGTTGACATATGAGAAAGGTATCAATCTGACCTTATATACAGCCCTACACACA 660  
QY 967 AGGTCCATGTTGACATATGAGAAAGGTATCAATCTGACCTTATATACAGCCCTACACACA 1026  
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QY 1027 GAAGCACTATGAGAAAGGTATGAGAAAGGTATGAGAAAGGTATGAGAAAGGTATGAGAAAGGT 1086  
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QY 1087 AATTGATGCGCCACTCTTCAAAATATTTCTAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1146  
DB 781 CTGCTGAAGAGCTCAACATCTTCCCAAGGCTGGGTGTGAGTCTTCTGTGAG 840  
QY 1147 CTGCTGAAGAGCTCAACATCTTCCCAAGGCTGGGTGTGAGTCTTCTGTGAG 1206  
DB 841 GGCATGACGCTGAGAGAGGTCTGTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 1207 GGCATGACGCTGAGAGAGGTCTGTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1266  
DB 901 CTGCTTCTGGGCAAGGA 917  
QY 1267 CTGCTTCTGGGCAAGTA 1283

## RESULT 12

US-09-459-715-11

; Sequence 11, Application US/09459715

; Patent No. 6485919

; GENERAL INFORMATION:

; APPLICANT: Daggett, Lorrie

; Ellis, Steven B.

; Liaw, Chen

; Pontesler, Aaron

; Johnson, Edwin C.

; Hess, Stephen D.

; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,

; NUCLEIC ACIDS ENCODING SAME AND USBS THEREOF

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

; STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11  
Query Match 48.7%; Score 888.2; DB 4; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 1.9e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 AAAATGTCCTTCTGTTGATTCCTGTCAGTCTTACTTTTGAAGAAAGATGTCCTGGAGT 60  
DB 367 AAATGTCCTTCTGTTGATTCCTGTCAGTCTTACTTTTGAAGAAAGATGTCCTGGAGT 426  
QY 61 GCACAGTCCAGTGAAGAGAGGTGTGCTCAGATCTGGGTGACATCAATTAATGAGCT 120  
DB 427 GCACAGTCCAGTGAAGAGAGGTGTGCTCAGATCTGGGTGACATCAATTAATGAGCT 486  
QY 121 CTCTTTTCTGTTGATACCAAGCTTACTGTGAGAGAGTTCAATGAGAGAGAGTGTGGGCA 180  
DB 487 CTCTTTTCTGTTGATACCAAGCTTACTGTGAGAGAGTTCAATGAGAGAGAGTGTGGGCG 546  
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DB 667 TGGCATTCGGCTGTGGCCCTAGAGACAGATTAAGTCAATTAAGATTCCTCATTTCT 726  
QY 727 TCAGAGAGAGAAAGGCTTGGTACGCTGTGAGATGAGCTCTCTCTTCTCCGCTCC 786  
DB 421 AAGAAGCCCATATAGAGGGGTCAATTTGGGCTGTGAGATTCCTCATTTCT 480  
QY 787 AAGAAGCCCATATAGAGGGGTCAATTTGGGCTGTGAGATTCCTCATTTCT 846



QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGAACCATCATGATCTG 540  
DB 847 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGAACCATCATGATCTG 906  
QY 541 AGTGAACAAGCTCTGTTCATTAATTTTCATGAGGGTGTGCTTCAGATGCTCAGACGCA 600  
DB 907 AGTGAACAAGCTCTGTTCATTAATTTTCATGAGGGTGTGCTTCAGATGCTCAGACGCA 966  
QY 601 AGGTCCATGCTGACATAGTGAAGAGGTACATCTGACCTATATATACGCCGTACACCA 660  
DB 967 AGGGCCATGCTGACATAGTGAAGAGGTACATCTGACCTATATATACGCCGTACACCA 1026  
QY 661 GAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGAATATGTCAAGGAAGAAAGG 720  
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QY 721 ATTGTCATGCCCCACTCTTTACAAATCTACATATATGACAGGAGGAGGAGCTTTGATAAG 780  
DB 1087 ATTGTCATGCCCCACTCTTTACAAATCTACATATATGACAGGAGGAGGAGCTTTGATAAG 1146  
QY 781 CTGCTGAAGAAGCTCAACAAGTCACTTGCCCAAGGCCCGGGTGGTGCCTTACTTGTGAG 840  
DB 1147 CTGCTGAAGAAGCTCAACAAGTCACTTGCCCAAGGCCCGGGTGGTGCCTTACTTGTGAG 1206  
QY 841 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGCGCTGGGCTCAATGAGGAATTT 900  
DB 1207 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGCGCTGGGCTCAATGAGGAATTT 1266  
QY 901 CTGCTTCTGGGAGGGA 917  
DB 1267 CTGCTTCTGGGAGGGA 1283

RESULT 13  
US-08-072-574-7  
Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
TITLE OF INVENTION: HUMAN METABOLIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7  
Query Match 48.7%; Score 888.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 2e-210;  
Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 AAAATGCTCTCTGTTGATCCGTGAGCTTACTTTTGAAGAATGTCGTGGAGT 60  
DB 367 AAAATGCTCTCTGTTGATCCGTGAGCTTACTTTTGAAGAATGTCGTGGAGT 426  
QY 61 GCACAGTCCAGTGAAGAGAGGTGTGCTCAATGCTGGTGAATATATGAGCT 120  
DB 427 GCACAGTCCAGTGAAGAGAGGTGTGCTCAATGCTGGTGAATATATGAGCT 486  
QY 121 CTCTTTCTGTTCAATCAAGCTTACTGTGAACAAATTCAATGAGAAAGTGTGGGCA 180  
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QY 241 AATTGAGACCCCACTCTTGCCCAATCACACTGGCTGTGAGATTAAGGATTCCTGC 300  
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DB 667 TGGCATTCGGCTGTGGCCCTTAAGACAGAGCATTTAGATTAAGATTCCTCATTTCT 726  
QY 361 TGGGAAGAGAAAGAGGCTGTGTATGCTGTGTGATGAGTCCCTCTCTCTCTCTCC 420  
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QY 421 AAGAAGCCCATATGAGAGGCTCATTTGGGCTGTGCTCACTTTTACCATTCAGTCCAG 480  
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QY 481 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGAACCATCATGATCTG 540  
DB 847 AATTGCTCAGCTTTTCAACATACCTCAGATTTGCTTACTCAGAACCATCATGATCTG 906  
QY 541 AGTGAACAAGCTCTGTTCATTAATTTTCATGAGGGTGTGCTTCAGATGCTCAGACGCA 600  
DB 907 AGTGAACAAGCTCTGTTCATTAATTTTCATGAGGGTGTGCTTCAGATGCTCAGACGCA 966  
QY 601 AGGTCCATGCTGACATAGTGAAGAGGTACATCTGACCTATATATACGCCGTACACCA 660  
DB 967 AGGGCCATGCTGACATAGTGAAGAGGTACATCTGACCTATATATACGCCGTACACCA 1026  
QY 661 GAAGGCACTATGAGAAAGTGGATGAAAGCTTCAAGAATATGTCAAGGAAGAAAGG 720  
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QY 721 ATTGTCATGCCCCACTCTTTACAAATCTACATATATGACAGGAGGAGGAGCTTTGATAAG 780  
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DB 1147 CTGCTGAAGAAGCTCAACAAGTCACTTGCCCAAGGCCCGGGTGGTGCCTTACTTGTGAG 1206  
QY 841 GGCATGACGGTGAAGAGGTCTGCTGATGAGGAGGCGCTGGGCTCAATGAGGAATTT 900  
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QY	901	CTGCTTCTGGGCAGGGA	917
Db	1267	CTGCTTCTGGGCAGTGA	1283

RESULT 14  
IIS-08-486

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: Sequence 7, Application US/08486270
: Patent No. 5807689
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: GENERAL INFORMATION:
: APPLICANT: Daggett, Lorrie
: APPLICANT: Ellis, Steven B.
: APPLICANT: Liaw, Chen
: APPLICANT: Pontsler, Aaron
: APPLICANT: Johnson, Edwin C.
: APPLICANT: Hess, Stephen D.
: TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.
: TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
: NUMBER OF SEQUENCES: 13
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
: STREET: 444 South Flower Street, Suite 2000
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90071
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/486,270
: FILING DATE: 02-JUN-1994
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/072,574
: FILING DATE: 04-JUN-1993
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Reiter, Stephen E.
: REGISTRATION NUMBER: 31,192
: REFERENCE/DOCKET NUMBER: Pp41 9772
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-546-4737
: TELEFAX: 619-546-9392
:
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4085 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 370..3912
: OTHER INFORMATION: /product= "HUMAN MGLUR5A"
:
: US-08-486-270-7
:
: Query Match 48.7%; Score 888.2; DB 1; Length 4085;
: Best Local Similarity 98.0%; Pred. No.26-210;
: Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0
:
: Oy 1 AAAATGATCCTCTGTGTGATCTCTGCAGCTTACTTTTGAAGAAGATGTCGGTGGAGT 60
: Db 367 AAAATGATCCTCTGTGTGATCTCTGCAGCTTACTTTTGAAGAAGATGTCGGTGGAGT 426
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: Oy 61 GCACAGTCACGTGAGAGAGGGGTGGTGCATCATCTGGGTGACATCTATTATGAGCT 120
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:
: Oy 121 CTCCTTTCTGTCATCACAGAGCTCTGTGTGACGAAGTTCATGAGAGGAAGTGGGAGCA 180
: Db 487 CTCCTTTCTGTCATCACAGAGCTCTGTGTGACGAAGTTCATGAGAGGAAGTGGGAGCA 546

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QY	181	GTCCGTAAACAGATATGGCATTTCAAGAGAGTGAAGGCCCATCTGTGCATATCCCTGGAAAGGATC	240
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QY	241	AATTCAAGACCCCACTCTTTGCCCAATCACTGAGGCTGTAGATGAAGGATTTCTGC	300
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Db	667	TGGCATTCGGCTGTGGCCCTTAGAGCAGAGAGATTAGTTCATTAAGAGATTCCTCATTTCT	726
QY	361	TCGGAGAAGAGAAGGAGGCTTGATGCTCTGTGGATAGGCTCTCTCTTTCCGCTCC	420
Db	727	TCAGAAGAGAGAAGGAGGCTTGATGCTGTGTGGATGGCTCTCTCTCTTCCGCTCC	786
QY	421	AAGAGGCCCATAGTAGGGGTCATTTGGGCTGTGTTCCAGTTCTTTAGCCATTCAAGTCCAG	480
Db	787	AAGAGGCCCATAGTAGGGGTCATTTGGGCTGTGTTCCAGTTCTTTAGCCATTCAAGTCCAG	846
QY	481	AATTTTGCTCCAGCTTTTCAACATATACCTCAATTTGCTTATCTCAGCAACCATCAGATCTG	540
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QY	901	CTGCTTCAGGCAAGGA 917	
Db	1267	CTGCTTCAGGCAAGTGA 1283	

### RESULT 15

US-08-367-264-1  
Sequence 7, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
Applicant: Daggett, Lorrie  
Applicant: Ellis, Steven B.  
Applicant: Liaw, Chen  
Applicant: Pontsler, Aaron  
Applicant: Johnson, Edwin C.  
Applicant: Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Bruggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA

COUNTRY: USA  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/367,264  
 FILING DATE: 02-JUN-1994  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/072,574  
 FILING DATE: 04-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen E.  
 REGISTRATION NUMBER: 31,192  
 REFERENCE/DOCKET NUMBER: PP41 9772  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-546-4737  
 TELEFAX: 619-546-9392  
 INFORMATION FOR SEQ. ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4085 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 370..3912  
 OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
 US-08-367-264-7

Query Match 48.7%; Score 888.2; DB 3; Length 4085;  
 Best Local Similarity 98.0%; Pred. No. 2e-210;  
 Matches 899; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AAAATGTCCTCTGTGATCCCTGACGCTTCTTTGAAAGAGATGCGTGGAGT 60  
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 QY 61 GCACAGTCCAGTGAAGAGAGGAGTGTGCTCAATGCTGGGTGACATCAATTATTTGAGCT 120  
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 QY 601 AGGTCCATGATGACATGATGAGAGGTCAACTGAGCTTATGATCAAGCCGTACACCA 660  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

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Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1822.6	100.0	1823	US-10-027-923-1	Sequence 1, Appl1
2	1787.6	98.1	1788	US-09-822-830A-61	Sequence 61, Appl1
3	1110	60.9	1110	US-10-027-923-3	Sequence 3, Appl1
4	891.4	48.9	4518	US-10-225-567A-177	Sequence 177, Appl1
5	888.4	48.7	2826	US-10-346-241-1	Sequence 1, Appl1
6	888.4	48.7	3129	US-10-346-241-5	Sequence 5, Appl1
7	458.2	25.1	2634	US-09-826-509-346	Sequence 346, Appl1
8	458.2	25.1	3295	US-10-101-510-258	Sequence 258, Appl1
9	458.2	25.1	6619	US-10-225-567A-169	Sequence 169, Appl1
10	449.2	24.6	3219	US-10-300-473-3	Sequence 3, Appl1
11	449.2	24.6	3384	US-10-300-473-1	Sequence 1, Appl1
12	444.4	24.4	3219	US-10-300-473-4	Sequence 4, Appl1
13	263	14.4	687	US-10-027-632-211781	Sequence 211781, Appl1
14	263	14.4	687	US-10-027-632-211782	Sequence 211782, Appl1
15	263	14.4	687	US-10-027-632-211781	Sequence 211781, Appl1

16	263	14.4	687	US-10-027-632-211782	Sequence 211782, Appl1
17	197.8	10.9	2629	US-10-157-031-378	Sequence 378, Appl1
18	145.8	8.0	3867	US-10-255-149-1	Sequence 0, Appl1
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21	143.6	7.9	3884	US-09-820-809-14	Sequence 175, Appl1
22	143.6	7.9	3884	US-10-225-567A-175	Sequence 179, Appl1
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## ALIGNMENTS

RESULT 1  
US-10-027-923-1  
Sequence 1, Application US/10027923  
Publication No. US20020142330A1  
GENERAL INFORMATION:  
APPLICANT: Brian Galtner Bates  
APPLICANT: Kamalaka Gulukota  
APPLICANT: Yuhong Xie  
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
FILE REFERENCE: NUCLEIC ACID MOLECULES AND USES THEREFOR  
CURRENT FILING DATE: 2001-12-21  
CURRENT APPLICATION NUMBER: US/10/027,923  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/257,589  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1823  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4)..(1110)  
US-10-027-923-1  
Query Match 100.0%; Score 1822.6; DB 14; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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Sequence 61, Application US/09822830A  
Patent No. US20020142952A1  
GENERAL INFORMATION:  
APPLICANT: Genetics Institute, Inc.  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fechtel, Kim  
APPLICANT: Agostino, Michael J.  
APPLICANT: Howes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakari  
APPLICANT: Graham, James R.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6402  
CURRENT APPLICATION NUMBER: US/09/822,830A  
CURRENT FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/195,604  
NUMBER OF SEQ ID NOS: 631  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 61  
LENGTH: 1788  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-830A-61

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RESULT 3  
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; Sequence 3, Application US/10027923  
; Publication No. US20020142330A1  
; GENERAL INFORMATION:  
; APPLICANT: Brian Galcher Bates  
; APPLICANT: Kamalaka Gulukota  
; APPLICANT: Yuhong Xie  
; APPLICANT: Janet Elizabeth Paulsen  
; TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND  
; FILE REFERENCE: GNN-024  
; CURRENT APPLICATION NUMBER: US/10/027,923  
; PRIOR APPLICATION NUMBER: 2001-12-21  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1110  
; TYPE: DNA

ORGANISM: Homo sapiens  
 FEATURE: NAME/KEY: CDS  
 LOCATION: (1)..(1110)  
 US-10-027-923-3

Query Match 60.9%; Score 1110; DB 14; Length 1110;  
 Best Local Similarity 100.0%; Pred. No. 5,5e-296;  
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 ATGGTCTTGTGATCTGTGATCTTATTTTGAAGAAGTGTCCGTGGAGTGA 63
DB 1 ATGGTCTTGTGATCTGTGATCTTATTTTGAAGAAGTGTCCGTGGAGTGA 60
QY 64 CAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 61 CAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 124 TTTTCTGTATCCAGAGCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAG 183
DB 121 TTTTCTGTATCCAGAGCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 184 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 243
DB 181 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240
QY 244 TCAGAACCCACACTCTTGTCCCAATCACTGGGCTGTGAGATTAAGAGAT 303
DB 241 TCAGAACCCACACTCTTGTCCCAATCACTGGGCTGTGAGATTAAGAGAT 300
QY 304 CATTGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 363
DB 301 CATTGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 360
QY 364 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 423
DB 361 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420
QY 424 AAGCCCATAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 483
DB 421 AAGCCCATAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
QY 484 TTGCTCAGCTTTTCAACATCACTCAGATTTGCTTACTCAGAACCATCATGAT 543
DB 481 TTGCTCAGCTTTTCAACATCACTCAGATTTGCTTACTCAGAACCATCATGAT 540
QY 544 GACAAAGCTGTGTTCAAAATTTTATGAGAGAGAGAGAGAGAGAGAGAGAT 603
DB 541 GACAAAGCTGTGTTCAAAATTTTATGAGAGAGAGAGAGAGAGAGAGAGAT 600
QY 604 TCCATGTGAGATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 663
DB 601 TCCATGTGAGATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 660
QY 664 GGCAACATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 723
DB 661 GGCAACATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 720
QY 724 TGCATGCCACTCTTCAAAATTTTATGAGAGAGAGAGAGAGAGAGAGAGAT 783
DB 721 TGCATGCCACTCTTCAAAATTTTATGAGAGAGAGAGAGAGAGAGAGAGAT 780
QY 784 CTGAAGAGAGTCAAGATCACTTGCAGAGAGAGAGAGAGAGAGAGAGAGAT 843
DB 781 CTGAAGAGAGTCAAGATCACTTGCAGAGAGAGAGAGAGAGAGAGAGAGAT 840
QY 844 ATGACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 903
DB 841 ATGACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 900
QY 904 CTTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 963
DB 901 CTTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 960

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QY 964 GAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1023
DB 961 GAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1020
QY 1024 AGTGAATCCGTGTGTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAT 1083
DB 1021 AGTGAATCCGTGTGTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAT 1080
QY 1084 ATCACTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1113
DB 1081 ATCACTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1110

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## RESULT 4

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US-10-225-567A-177
; Sequence 177, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent version 3.1
; SEQ ID NO 177
; LENGTH: 4518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-177

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Query Match 48.9%; Score 891.4; DB 15; Length 4518;

Best Local Similarity 98.3%; Pred. No. 3.8e-235;

Matches 901; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1 AAATGATCTTCTGTGATCTGTGATCTTATTTTGAAGAAGTGTCCGTGGAGT 60
DB 148 AAATGATCTTCTGTGATCTGTGATCTTATTTTGAAGAAGTGTCCGTGGAGT 207
QY 61 GCAAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 120
DB 208 GCAAGTCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 267
QY 121 CTCCTTTTGTGATCAACAGAGCTACTGTGAGAGAGAGAGAGAGAGAGAT 180
DB 268 CTCCTTTTGTGATCAACAGAGCTACTGTGAGAGAGAGAGAGAGAGAGAT 327
QY 268 CTCCTTTTGTGATCAACAGAGCTACTGTGAGAGAGAGAGAGAGAGAGAT 327
DB 181 GTCCTGAAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAT 240
QY 328 GTCCTGAAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAT 387
DB 241 AATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 300
QY 388 AATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 447
DB 301 TGGCATTTGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAT 360
QY 448 TGGCATTTGGCTGTGGCCCTAGAGAGAGAGAGAGAGAGAGAGAGAT 507
DB 361 TCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420
QY 508 TCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 567
DB 421 AAGAGCCCATAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
QY 568 AAGAGCCCATAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 627
DB

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QY 481 AATTGCTCCAGCTTTTCAACATACCTCAGATTGCTTAAGTCAAGCAACATCATGATCTG 540  
DB 628 AATTGCTCCAGCTTTTCAACATACCTCAGATTGCTTAAGTCAAGCAACATCATGATCTG 687  
QY 541 AGTGACAAGACTCTGTTCAATATTTTCAAGAGGTTGTGCTTCAATGCTCAGCAGGCA 600  
DB 688 AGTGACAAGACTCTGTTCAATATTTTCAAGAGGTTGTGCTTCAATGCTCAGCAGGCA 747  
QY 601 AGGTCAATGATGAGTCAATGAGAGGTTCAACTGAGCCATGATGATGAGCCGATCAACA 660  
DB 748 AGGGCCATGATGAGTCAATGAGAGGTTCAACTGAGCCATGATGATGAGCCGATCAACA 807  
QY 661 GAAGGCACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCAGGAAAGAGG 720  
DB 808 GAAGGCACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCAGGAAAGAGG 867  
QY 721 ATTGTCATGCCCCACTCTTCAAAATCTACATGATGAGAGGAGAGAGCTTTGATAG 780  
DB 868 ATTGTCATGCCCCACTCTTCAAAATCTACATGATGAGAGGAGAGAGCTTTGATAG 927  
QY 781 CTGCTGAGAGAGCTCAAGTCACTTGCCCAAGCCCGGTGCTGCTTCTGTTAG 840  
DB 928 CTGCTGAGAGAGCTCAAGTCACTTGCCCAAGCCCGGTGCTGCTTCTGTTAG 987  
QY 841 GGCATGACCGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGAGTCAAGTGAAGATT 900  
DB 988 GGCATGACCGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGAGTCAAGTGAAGATT 1047  
QY 901 CTGCTTCTGGGAGGGA 917  
DB 1048 CTGCTTCTGGGAGTGA 1064

## RESULT 5

US-10-346-241-1  
; Sequence 1, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STOROHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: US/09/695,481  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2826  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2826)  
US-10-346-241-1

Query Match 48.7%; Score 888.4; DB 13; Length 2826;  
Best Local Similarity 98.2%; Pred. No. 1.9e-234;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 ATGGTCTCTGTGATCTCTGTCAGTCTTAATTTTAAAGAAATGTCCTGGAGATGCA 63  
DB 1 ATGGTCTCTGTGATCTCTGTCAGTCTTAATTTTAAAGAAATGTCCTGGAGATGCA 60  
QY 64 CAGTCCAGTGAAGAGGAGTGTGCTCAATGCTGGTGAACATTAATTGAGCTCTC 123

DB 61 CAGTCCAGTGAAGAGGAGTGTGCTCAATGCTGGTGAACATTAATTGAGCTCTC 120  
QY 124 TTTTCTGTCATCACAGGCTTACTGTGAGCAAGTTCAAGAGGAAAGTGTGGGCGATC 183  
DB 121 TTTTCTGTCATCACAGGCTTACTGTGAGCAAGTTCAAGAGGAAAGTGTGGGCGATC 180  
QY 184 CGTGAACAGTATGAGCTTTCAGAGAGTGAAGCCATGCTCATACCTCTGAAAGATCAAT 243  
DB 181 CGTGAACAGTATGAGCTTTCAGAGAGTGAAGCCATGCTCATACCTCTGAAAGATCAAT 240  
QY 244 TCAAGCCCAACACTTTCGCCAATCAATCAGCTGGCTGTGAAGTAAGGATTCCTGCTGG 303  
DB 241 TCAAGCCCAACACTTTCGCCAATCAATCAGCTGGCTGTGAAGTAAGGATTCCTGCTGG 300  
QY 304 CATGGGCTGTGGCCCTTAAGAGAGCATTTAGTTTATAGAGATTCCTCATTTTCTTG 363  
DB 301 CATGGGCTGTGGCCCTTAAGAGAGCATTTAGTTTATAGAGATTCCTCATTTTCTTG 360  
QY 364 GAAGAGAGAGAGGCTTGGTATGCTCTGTGAGATGAGCTCTCTCTCTCTCTCTCCAG 423  
DB 361 GAAGAGAGAGAGGCTTGGTATGCTCTGTGAGATGAGCTCTCTCTCTCTCTCTCCAG 420  
QY 424 AAGCCCATGATGAGGCTCATTTGGCCCTGCTTCAATTCATTCAGTCCAGAT 483  
DB 421 AAGCCCATGATGAGGCTCATTTGGCCCTGCTTCAATTCATTCAGTCCAGAT 480  
QY 484 TTGCTCCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACCATCATGATCTGAT 543  
DB 481 TTGCTCCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACCATCATGATCTGAT 540  
QY 544 GACAAGACTCTGTTCAAAATATTTCAATGAGGTTGCTTCAAGATGCTCAGCAGGAGG 603  
DB 541 GACAAGACTCTGTTCAAAATATTTCAATGAGGTTGCTTCAAGATGCTCAGCAGGAGG 600  
QY 604 TCCATGCTGAGCATGATGAGAGTGAAGTCAATGAGCCATATGATCAGCCGTACACAGAA 663  
DB 601 GGCATGCTGAGCATGATGAGAGTGAAGTGAAGTCAATGAGCCATATGATCAGCCGTAC 660  
QY 664 GGCATGCTGAGCATGATGAGAGTGAAGTGAAGTGAAGTCAATGAGCCATATGATCAG 723  
DB 661 GGCATGCTGAGCATGATGAGAGTGAAGTGAAGTGAAGTCAATGAGCCATATGATCAG 720  
QY 724 TGCATGCCCCACTCTTCAAAATATTTCAAGTAAATGAGGAGAGAGGCTTTGATAGCTG 783  
DB 721 TGCATGCCCCACTCTTCAAAATATTTCAAGTAAATGAGGAGAGAGGCTTTGATAGCTG 780  
QY 784 CTGAAGAAAGCTCAAGTCACTTGGCCCAAGGCGCGGTGTGAGCTTCTGTGAGGCG 843  
DB 781 CTGAAGAAAGCTCAAGTCACTTGGCCCAAGGCGCGGTGTGAGCTTCTGTGAGGCG 840  
QY 844 ATGACGCTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGGTCTTATGAGAGATTTCTG 903  
DB 841 ATGACGCTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGGTCTTATGAGAGATTTCTG 900  
QY 904 CTTTGGGAGGGA 917  
DB 901 CTTTGGGAGTGA 914

## RESULT 6

US-10-346-241-5  
; Sequence 5, Application US/10346241  
; Publication No. US20030157647A1  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STOROHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/10/346,241

```

CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US/09/695,481
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/161,481
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 5
LENGTH: 3129
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Chimeric
OTHER INFORMATION: molecule comprising portions of human mglur5d and
OTHER INFORMATION: the human calcium receptor.
FEATURE:
NAME/KEY: CDS
LOCATION: ( )...(3129)
US-10-346-241-5

Query Match      48.7%; Score 888.4; DB 13; Length 3129;
Best Local Similarity 98.2%; Pred. No. 2e-234;
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4  AAGGCTCTGTTGATCTGTGCTCTTCTTGAAGAAGATGCCGAGGAGTGA 63
DB 1  AAGGCTCTGTTGATCTGTGCTCTTCTTGAAGAAGATGCCGAGGAGTGA 60
QY 64  CAGTCCAGTGAAGAGAGGAGTGTGGCTCACAATGCTGGGTGACATATTATTTGAGCTCTC 123
DB 61  CAGTCCAGTGAAGAGAGGAGTGTGGCTCACAATGCTGGGTGACATATTATTTGAGCTCTC 120
QY 124  TTTTCTGTTATCAACCAAGCTTCTGTGAGAGAACTTATGAGAGAAAGTGTGGGCGATC 183
DB 121  TTTTCTGTTATCAACCAAGCTTCTGTGAGAGAACTTATGAGAGAAAGTGTGGGCGATC 180
QY 184  CGTGAACAGTATGAGCATTTCAAGAGAGTGAAGGCAATGCTGCAATCCCTGAAAGATCAAT 243
DB 181  CGTGAACAGTATGAGCATTTCAAGAGAGTGAAGGCAATGCTGCAATCCCTGAAAGATCAAT 240
QY 244  TCAGACCCCACTCTTGTCCCAACATCACTGGGCTGTGATGAAGAGATTCCTGTCTGG 303
DB 241  TCAGACCCCACTCTTGTCCCAACATCACTGGGCTGTGATGAAGAGATTCCTGTCTGG 300
QY 304  CATTCGGCTGTGGCCCTTGAAGAGAGATTTGATTTTCCCTCATTTCTTCTG 363
DB 301  CATTCGGCTGTGGCCCTTGAAGAGAGATTTGATTTTCCCTCATTTCTTCTG 360
QY 364  GAAGAGAGAGAGGCTGTGATGCTGTGGATGGCTCTCTCTTCTTCCGCTCCAG 423
DB 361  GAAGAGAGAGAGGCTGTGATGCTGTGGATGGCTCTCTCTTCTTCCGCTCCAG 420
QY 424  AAGCCATAGTAGGGGCTATTGGGCTGTGCTCAAGTTCTTGAAGCATTCAGGTCAGAA 483
DB 421  AAGCCATAGTAGGGGCTATTGGGCTGTGCTCAAGTTCTTGAAGCATTCAGGTCAGAA 480
QY 484  TTGCTCAGACTTTTCAACATCTCAAGATTTCTTCAAGAACATCAATGATCTGAGT 543
DB 481  TTGCTCAGACTTTTCAACATCTCAAGATTTCTTCAAGAACATCAATGATCTGAGT 540
QY 544  GACAAGACTGTCTCAATATATTTCATGAGGGTGTGGCTTCAATGCTCAGCAGGCAAG 603
DB 541  GACAAGACTGTCTCAATATATTTCATGAGGGTGTGGCTTCAATGCTCAGCAGGCAAG 600
QY 604  TCCATGCTGATCATATGAGAGATCAACTGAGCTTATGATCAGGCTTACACAGAA 663
DB 601  TCCATGCTGATCATATGAGAGATCAACTGAGCTTATGATCAGGCTTACACAGAA 660
QY 664  GGCAATCATGAGAGAAAGTGGATGAAAGCTTCAAGATATGTCAAGGAGAGAGGATTT 723
DB 661  GGCAATCATGAGAGAAAGTGGATGAAAGCTTCAAGATATGTCAAGGAGAGAGGATTT 720
QY 724  TGATGCGCCACTCTTCAAAATCTACAGTAATGAGGAGAGAGAGCTTTGATTAAGCTG 783

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DB 721  TGATGCGCCACTCTTCAAAATCTACAGTAATGAGGAGAGAGAGCTTTGATTAAGCTG 780
QY 784  CTGAAGAGCTCAAGAGTCACTTCCCAAGGCCCGGATGTGCTTCTGTGAGGCG 843
DB 781  CTGAAGAGCTCAAGAGTCACTTCCCAAGGCCCGGATGTGCTTCTGTGAGGCG 840
QY 844  ATGACGGTGAAGAGTGTGATGAGGATGAGGCGCTGGTCTGATGAGAGAAATTTCTG 903
DB 841  ATGACGGTGAAGAGTGTGATGAGGATGAGGCGCTGGTCTGATGAGAGAAATTTCTG 900
QY 904  CTTCTGGGCAAGGGA 917
DB 901  CTTCTGGGCAAGTGA 914

RESULT 7
US-09-826-509-346
Sequence 346, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruhnsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 346
LENGTH: 2634
TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-509-346

Query Match      25.1%; Score 458.2; DB 13; Length 2634;
Best Local Similarity 72.5%; Pred. No. 1.6e-115;
Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

QY 84  GGTGGCTCACATCTGTGGATCACTTATTTGAGGCTCTCTTCTTCTTCTCATACCAAGCC 143
DB 111  GGTGGCTCACATCTGTGGATCACTTATTTGAGGCTCTCTTCTTCTTCTCATACCAAGCC 170
QY 144  TACTGTGACAGAGTTCAATGAGAGAGAGTGTGGGAGTCCCTGAAACAGTATGGCATTTCA 203
DB 171  TCCGGCCGAGAAAGTCCCGAGAGAGAGTGTGGGAGATCAAGGAGACAGTATGGCATTTCA 230
QY 204  GAGAGTGAAGGCGCATGCTGATACCTTGAAGAGATCAATTCAAGACCCCACTCTTGGC 263
DB 231  GAGGATGAAGGCGCATGTTTCAACAGTTGATTAAGATCAACGCGGACCCGGTCTCTGGCC 290
QY 264  CAACATCACTGGGCTGTGAGATTAAGGATTTCTGTGCTGATTCGAGCTGTGGCCCTTGA 323
DB 291  CAACATCACTGGGCTGTGAGATTCGAGATTCGAGCTGTGGCTGTGGCTGTGGCTGTGA 350
QY 324  GCAGAGCATTTGATTAATTAAGATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 383
DB 351  ACAGAGCATTTGATTAATTAAGATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 410
QY 384  ATGC-----TCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 434
DB 411  CAACCGGTGTCTGTGTGATGAGGCGCAAGTCCCTCCCGCAGGAGCTTAAGAGCCCATTTGC 470
QY 435  AAGGATCATTTGGGCTGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 494
DB 471  GGGAGTATGATGCTTCCGCTCTCAGCTCTGTAGCAATTCAGATGCAAGAACTGTCTCAGCT 530

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QY 495 TTTCACATCATCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGTGAAGAAGCTCT 554  
 DB 531 CTTCGACATCCCGAGATGCTTATTACGCCACAAGCATGACCTGATGACAAAACCTTT 590  
 QY 555 GTTCAAAATATTTATGAGGGTGTGCTTCAATGCTCAGCAGGCAAGGTCATGCTGA 614  
 DB 591 GTACAAATCTTCTGAGGGTGTGCTTCTTCACTTTCAGGCAAGGCTCATGCTTGA 650  
 QY 615 CATAGTGAAGGATGACATGAGCCTATGATCAGCGCTACACAGAAAGGCAACTATG 674  
 DB 651 CATAGTCAAAAGCTTACATTTGACCTATGCTTCTGACATCAGACGGAAGGAATATG 710  
 QY 675 AGAAGTGGAGTGAAGCCTTCAAGATATGTCAGCGAAGGAAGGATTTGACCTG 734  
 DB 711 GAGAGCGGAGATGAGCGCTTCAAGAGCTGCGTCCAGAAAGGCTCTGATTCGCCA 770  
 QY 735 CTCTTCAAAATTTACATGATATGACGAGGAGCAGAGCTTTGATAGCTGCTGAAGA 794  
 DB 771 TTCTGCAAAATTTACAGCAACCTGCGGAGAAAGAGCTTTGACCGACTCTTGGCAA 830  
 QY 795 CACAAGTCACTTGCCCAAGGCGGGGTGCTTCTGATGAGGAGTGAACGCTGAG 854  
 DB 831 CCGAGAGAGGCTTCCCAAGGCTAGAGTGTGTCTTCTGTAAGGCAATGACAGTGC 890  
 QY 855 AGGCTGCTGATGAGCAGTGAAGGCGCTGAGTCTAGTGGAGAAATTTCTGCTTGG 914  
 DB 891 AGGACTCTTGAGGCGCATGCGGCGCTTGGCGTCTGAGGAGATTCTCACTCATGGA 950  
 QY 915 GGA 917  
 DB 951 TGA 953

## RESULT 8

US-10-101-510-258  
 ; Sequence 258, Application US/10101510  
 ; Publication No. US20030148295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAN, JACKSON  
 ; APPLICANT: WANG, YIXIN  
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
 ; FILE REFERENCE: 15117.0012  
 ; CURRENT APPLICATION NUMBER: US/10/101,510  
 ; PRIOR FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: 60/276,947  
 ; NUMBER OF SEQ ID NOS: 805  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 258  
 ; LENGTH: 3295  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-101-510-258

Query Match 25.1%; Score 458.2; DB 13; Length 3295;  
 Best Local Similarity 72.5%; Pred. No. 1.9e-115;  
 Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

QY 84 GGTGGCTCATGCTGCGGTGACATCATTTATGAGCTCTCTTCTGTTTCATCAGCAGCC 143  
 DB 481 GGTGGCCAGAAATGAGCGAGATGTCATCTTGAAGCCCTCTTCTGATCATACAGGCC 540  
 QY 144 TACTGTGAGCAAGTTCTATAGAGAAAGTGTGGGCGAGTCCGTGAACAGTATGCAATCA 203  
 DB 541 TCGGGCCGAAAGTCCCGCAGAGAGTGTGGGAGATCAGGAGAGATATGCAATCCA 600  
 QY 204 GAGAGTGAAGGCGCATGCTGATACCTCTGAAAGATCAATTCAGACCCCACTCTTGGC 263  
 DB 601 GAGGGTGAAGCCATGTTCCACAGCTTGAATAGATTAACCGGAGCCGCTCTCTGACC 660  
 QY 264 CAACATCACTGCGGTGTGATGAATGAAGATTCCTGTGCAATTCGCTGTGCGCTTAGA 323  
 DB 661 CAACATCACTGCGGTGTGATGAATGAAGATTCCTGTGCAATTCGCTGTGCGCTTAGA 720

QY 324 GCAGACATTTGATGATTAAGAGATTCCCTCATTTCTTGGAGAGAGAGGCTTGT 383  
 DB 721 ACAGAGCATTTGATGATTAAGAGATTCTTGAATTTCTTGAATGAAGAGATGAGAT 780  
 QY 384 ATGC-----TCTGTGATGAGCTCTCTCTTCTTCCGCTCCAGAAAGCCATAGT 434  
 DB 781 CAACCGGTGTGCTGACGAGCGGACCTCTCCCGCAGGAGAGACTTAAGAAAGCCATTGC 840  
 QY 435 AGGGGTCTTGGGCTGTGCTTCCAGTTCTTGAATTTCAAGTTCAGAAATTTGCTCCAGCT 494  
 DB 841 GGGAGTATGCGTCCGAGCTTCAGCTCTGATGCAATTCAGATCAAGTCAAACTGTCCAGCT 900  
 QY 495 TTTCACATACCTCAGATTGCTTACTCAGCAACCATCATGAGTGTGAGTGAAGAAGCTCT 554  
 DB 901 CTTCGACATCCCGCAATGCTTATTACGACACAGATGACCTGATGATCAAAACTTT 960  
 QY 555 GTTCAAAATATTTATGAGGGTGTGCTTCAATGCTCAGATGCTCAGAGGTCATGCTGA 614  
 DB 961 GTACAAATATCTTCTGAGGGTGTGCTTCTGACATTTGACAGGCAAGGCGCATGCTTGA 1020  
 QY 615 CATAGTGAAGGATCACTGACCTATGATATGACCGCTACACAGAAAGCACTATG 674  
 DB 1021 CATAGTCAAAAGCTTACAAATGAGCTATGCTCTGACATCCACAGAAAGGAATATG 1080  
 QY 675 AGAAGTGGAGTGAAGCCTTCAAGATATGTCAGGGAAGGAAGGATTTGACCTGCCCA 734  
 DB 1081 GGAAGCGGAATGAGCGCTTCAAGAGCTGTGCTGCCAGAAAGGCTCTGATTCGCCCA 1140  
 QY 735 CTCTTCAAAATTTACATGATATGACAGGAGAGCAGACTTTGATAGCTGCTGAAGAAGCT 794  
 DB 1141 TTCTGCAAAATTTACAGCAACCTGAGGAGAAAGACTTTGACCGACTCTTGGCAA 1200  
 QY 795 CACAAGTCACTTGCCCAAGGCGCGGTGTGCTTCTTGTAGGCGCATGACGCTGAG 854  
 DB 1201 CCGAGAGAGGCTTCCCAAGGCTAGAGTGTGTCTTCTGTAAGGCAATGACAGTGC 1260  
 QY 855 AGGCTGCTGATGAGCAGTGAAGGCGCTGAGTCTAGTGGAGAAATTTCTGCTTGG 914  
 DB 1261 AGGACTCTGAGGCGCATGCGGCGCTTGGCGTCTGAGGAGATTCTCACTCATGGA 1320  
 QY 915 GGA 917  
 DB 1321 TGA 1323

## RESULT 9

US-10-225-567A-169  
 ; Sequence 169, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lifespan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burner, Glenn C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 169  
 ; LENGTH: 6619  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-225-567A-169

Query Match 25.1%; Score 458.2; DB 15; Length 6619;  
 Best Local Similarity 72.5%; Pred. No. 2.9e-115;  
 Matches 611; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

84 GGTGGCTCACATGCTGGGATGACATCATTTATGAGCTCTGTTTCTGTTCATGACAGCC 143  
DB GGTGGCTCACATGCTGGGATGACATCATTTATGAGCTCTGTTTCTGTTCATGACAGCC 405  
QY 144 TACTGTGACGAAGTTTCATGAGAGAAAGTGTGGGAGTCCGTGAACAGTATGACATTC 203  
DB TCCGGCCGGAAGAGTCCCGAGAGAAAGTGTGGGAGATCAGGAGAGATGATGACATTC 465  
QY 204 GAGAGTGGAGCCATGCTGATACCCCTGGAAGAAAGATTCATTCAGACCCCACTTTGCC 263  
DB GAGAGTGGAGCCATGCTGATACCCCTGGAAGAAAGTTCATTCAGACCCCACTTTGCC 525  
QY 264 CAACATCACACTGGGCTGTGAGATTAAGGAAATTCCTGTGACATTCGGCTGTGGCCCTGA 323  
DB CAACATCACACTGGGCTGTGAGATTAAGGAAATTCCTGTGACATTCGGCTGTGGCCCTGA 585  
QY 324 GCAGAGCATTTGAGTTCTAAGAGATTCCTCATTTCTTCGGAAGAGAGAGAGGCTTGGT 383  
DB ACAGAGCATTTGAGTTCTAAGAGATTCCTCATTTCTTCGGAAGAGAGAGAGGCTTGGT 645  
QY 384 ATGC-----TCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 434  
DB CAACCGGTGTGCTGTGACAGCCAGTCCCTCCCGCAGAGAGAGAGAGAGAGAGAGAGAG 705  
QY 435 AGGGGTCAATGGGCTGGTCTGAGTTCTTACGATTCAGGTCAGGTCAGGTCAGGTCAGG 494  
DB GGGAGTATGCTGCTCCGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAG 765  
QY 495 TTTCACATACCTCAGATTCCTTACTGAGCAACCATGAGATTCAGTGAACAAGCTCT 554  
DB CTTCGATATCCCGAGATGCTTATTCAGCAACCATGAGATTCAGTGAACAAGCTCT 825  
QY 555 GTTCAATATTTTCAAGAGGTTGCTGCTTCAAGTCTCAGAGCAAGGTCAGGTCAGGTCAG 614  
DB GTCAATATTTTCAAGAGGTTGCTGCTTCAAGTCTCAGAGCAAGGTCAGGTCAGGTCAG 885  
QY 826 CATAGTGAAGGATGACATGACCTATGATGACAGGTCAGGTCAGGTCAGGTCAGGTCAG 674  
DB CATAGTGAAGGATGACATGACCTATGATGACAGGTCAGGTCAGGTCAGGTCAGGTCAG 945  
QY 615 AGAAGTGGATGAGACCTTCAAGATATGTCAGCAAGGAGAGAGAGAGAGAGAGAGAG 734  
DB AGAAGTGGATGAGACCTTCAAGATATGTCAGCAAGGAGAGAGAGAGAGAGAGAGAGAG 1005  
QY 946 GGAAGGAGATGAGACCTTCAAGATATGTCAGCAAGGAGAGAGAGAGAGAGAGAGAG 1005  
DB GGAAGGAGATGAGACCTTCAAGATATGTCAGCAAGGAGAGAGAGAGAGAGAGAGAGAG 1005  
QY 735 CTCTTAACAATCTACGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794  
DB CTCTTAACAATCTACGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065  
QY 1006 TTCTGAACAAATCTACGAGCAAGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAG 1065  
DB TTCTGAACAAATCTACGAGCAAGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065  
QY 795 CACAAGTCACTTGGCCCAAGGCGCGGTGAGCTTCTGTGAGGAGAGAGAGAGAGAGAG 854  
DB CACAAGTCACTTGGCCCAAGGCGCGGTGAGCTTCTGTGAGGAGAGAGAGAGAGAGAG 1125  
QY 1066 CCGAGAGAGCTTCCAGAGCTGAGTGTGTGCTTCTGTGAAGAGAGAGAGAGAGAGAG 1125  
DB CCGAGAGAGCTTCCAGAGCTGAGTGTGTGCTTCTGTGAAGAGAGAGAGAGAGAGAG 1125  
QY 855 AGGTCTGTGATGAGCAAG 914  
DB AGGTCTGTGATGAGCAAG 1185  
QY 915 GGA 917  
DB 1186 TGA 1188

RESULT 10  
US-10-300-473-3  
Sequence 3, Application US/10300473  
Publication No. US20030113873A1  
GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: STORJOHANN, LAURA L.  
APPLICANT: HAMMERLAND, LANCE G.  
APPLICANT: FULLER, FOREST H.  
APPLICANT: KAPCHIO, KAREN J.  
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING  
TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE  
TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE  
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES  
FILE REFERENCE: 072827/0909  
CURRENT APPLICATION NUMBER: US/10/300,473  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 09/435,897  
PRIOR FILING DATE: 1999-11-08  
PRIOR APPLICATION NUMBER: 08/687,289  
PRIOR FILING DATE: 1996-07-25  
PRIOR APPLICATION NUMBER: 60/001,526  
PRIOR FILING DATE: 1995-07-26  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 3219  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthesized rat  
OTHER INFORMATION: mGluR and human calcium receptor  
US-10-300-473-3  
Query Match 24.6%; Score 449.2; DB 15; Length 3219;  
Best Local Similarity 71.9%; Pred. No. 5.7e-113;  
Matches 605; Conservative 0; Mismatches 228; Indels 9; Gaps 1;  
QY 85 GTGGCTCACATGCTGGGATGACATCATTTATGAGCTCTGTTTCTGTTCATGACAGCC 144  
DB GTGGCTCACATGCTGGGATGACATCATTTATGAGCTCTGTTTCTGTTCATGACAGCC 195  
QY 145 ACTGTGACGAAGTTTCATGAGAGAAAGTGTGGGAGTCCGTGAACAGTATGACATTCAG 204  
DB ACTGTGACGAAGTTTCATGAGAGAAAGTGTGGGAGTCCGTGAACAGTATGACATTCAG 255  
QY 196 CCGAGAGAGAGATTCAG 255  
DB CCGAGAGAGAGATTCAG 315  
QY 205 AGAGTGGAGCCATGCTGATACCTGGAAGAGATCAATTCAGACCCCACTTTGCC 264  
DB AGAGTGGAGCCATGCTGATACCTGGAAGAGATCAATTCAGACCCCACTTTGCC 315  
QY 256 AGGTGAGGCGATGTTCCACAGTGTGATTAAGATTAACCGAGAGAGAGAGAGAGAG 324  
DB AGGTGAGGCGATGTTCCACAGTGTGATTAAGATTAACCGAGAGAGAGAGAGAGAG 375  
QY 316 AACATCACCTGGGCTGTGATTAAGGAGATTCCTGTGAGATTCCTGTGAGATTCCTGT 324  
DB AACATCACCTGGGCTGTGATTAAGGAGATTCCTGTGAGATTCCTGTGAGATTCCTGT 375  
QY 325 CAGAGCATGATTCATTAAGAGATTCCTCATTTCTTCGGAAGAGAGAGAGAGAGAGAG 384  
DB CAGAGCATGATTCATTAAGAGATTCCTCATTTCTTCGGAAGAGAGAGAGAGAGAGAG 435  
QY 376 CAGAGCATGATTCATTAAGAGATTCCTCATTTCTTCGGAAGAGAGAGAGAGAGAG 435  
DB CAGAGCATGATTCATTAAGAGATTCCTCATTTCTTCGGAAGAGAGAGAGAGAGAG 495  
QY 385 TGC-----TCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 434  
DB TGC-----TCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495  
QY 436 AACCGATGCTGTGATGAGCCAGAGCTTCCCGCAGAGAGAGAGAGAGAGAGAGAGAG 495  
DB AACCGATGCTGTGATGAGCCAGAGCTTCCCGCAGAGAGAGAGAGAGAGAGAGAGAG 555  
QY 436 GGGGTCAATGGGCTGGTCTCAAGTTCTTACGATTCAGGTCAGGTCAGGTCAGGTCAG 495  
DB GGGGTCAATGGGCTGGTCTCAAGTTCTTACGATTCAGGTCAGGTCAGGTCAGGTCAG 555  
QY 496 GGAAGTATGAGGCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555  
DB GGAAGTATGAGGCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615  
QY 496 TTCAACATACCTGAGATTCCTTACGAGCAACCATGAGATTCAGTGAACAAGCTTGG 555  
DB TTCAACATACCTGAGATTCCTTACGAGCAACCATGAGATTCAGTGAACAAGCTTGG 615  
QY 556 TTGCAATCCCAAGATGCTGATTCCTGCAAGAGATTAAGCTGATGATCAAAACCTTGG 615  
DB TTGCAATCCCAAGATGCTGATTCCTGCAAGAGATTAAGCTGATGATCAAAACCTTGG 675  
QY 556 TTCAATATTTTCAAGAGGTTGCTTCAAGATTCAGATGCTCAGAGAGAGAGAGAGAG 615  
DB TTCAATATTTTCAAGAGGTTGCTTCAAGATTCAGATGCTCAGAGAGAGAGAGAGAG 675  
QY 616 ATAGTGAAGGATGAG 675  
DB ATAGTGAAGGATGAG 735  
QY 676 ATAGTGAAGGATGAG 735  
DB ATAGTGAAGGATGAG 795  
QY 676 GAAAGTGGATGAG 735  
DB GAAAGTGGATGAG 795  
QY 736 GAGAGTGAATGAGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795  
DB GAGAGTGAATGAGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855  
QY 736 TCTTACAAATCTACAGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795  
DB TCTTACAAATCTACAGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855  
QY 796 TCGAGACAAATCTACAGCAATGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855  
DB TCGAGACAAATCTACAGCAATGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855

Qy	796	ACAAGTCACTTGCCCAAGGCCCGGGTGGGCTCACTTCTGTGAAGGCAATGACGGTGA	855
Db	856	CGGAGCGCGCTTCCCAAGGCCAGGGTTGTGTGCTCTTCTTGGCAAGGCATGACAGTGGG	915
Qy	856	GGTCTGCTGATGATGCCATGAGGCGCCCTGGGCTTGAATGAGGAATTTCTGCTTGGCAG	915
Db	916	GGCTTACTGATGATGCCATCGCGCGCTGGGCGGTGATGGGAGATTTCTCACTATTGGAAGT	975
Qy	916	GA 917	
Db	976	GA 977	

RESULT 11  
US-10-300-473-1

Sequence 1, Application US/10300473  
Publication No. US20030113873A1

GENERAL INFORMATION:  
APPLICANT: STORMANN, THOMAS M.  
APPLICANT: STORJOHANN, LAURA L.  
APPLICANT: HAMMERLAND, LAURA G.  
APPLICANT: FULLER, FORREST H.  
APPLICANT: KRAPCHO, KAREN J.  
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING  
TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE  
TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE  
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES  
FILE REFERENCE: 072827/0909  
CURRENT APPLICATION NUMBER: US/10/300,473  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 09/435,897  
PRIOR FILING DATE: 1999-11-08  
PRIOR APPLICATION NUMBER: 08/687,289  
PRIOR FILING DATE: 1996-07-25  
PRIOR APPLICATION NUMBER: 60/001,526  
PRIOR FILING DATE: 1995-07-26  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3384  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthesized rat  
OTHER INFORMATION: melur and human calcium receptor  
US-10-300-473-1

Query Match 24.6%; Score 449.2; DB 15; Length 3384;  
Best Local Similarity 71.9%; Pred. No. 5,9e-113;  
Matches 605; Conservative 0; Mismatches 228; Indels 9; Gaps 1

Qy	85	GTGGCTCACTGCTGGGCTGATGACATCTTATTTGAGCTCTCTTTCTGTTCATACCAAGCT	144
Db	119	GTGGCGAATGAGCAGAGATGTCTATCTCGAGCCCTCTTCTCAGTCATCACAGCT	178
Qy	145	ACTGTGACGAAGTTCATGAGAGAGATGTGGGCGCATGCCGGAACAGATGAGCATTTAG	204
Db	179	CCAAGCGAAGAGTACCCGAAAGAGTGTGGGAGATCAGGAAACATGATGTATCCAG	238
Qy	205	AGAAGTGAGGCGCATGCTGCATACCTTGAAAGATCAATTACAGCCCACTTTGCC	264
Db	239	AGGGTGAAGCGCATGTTCCACAGTTGATTAAGATTAAACGCGAACCCGGTGCTCTGCC	298
Qy	265	AACATCACTGGGCGTGTGAGTAAGGATTCCTGCTGCGCATTTCCGCTGTGGCCCTAAG	324
Db	299	AACATCACTTGGGCGATGAGATCCGGGATCTCTGCTGGCACTCTTCACTGAGTCTCGAA	358
Qy	325	CAGAGCATTTGAGTTCATAAGAGATTCCTCATTTCTTCCGAAGGAAGAGGGCTTGGTA	384
Db	359	CAGAGCATGCAATTATCATGAGATCTCCCTGATTTTCATCCGAGATGAGAGATGGGCTG	418
Qy	385	TGCG-----TCTGTGATGAGTCTCTCTCTTCCCTTCGCTCCAGAGCCCATAGTA	435

Db	419	AACGATGCGTGCCTATATGGCCAGAACCCCTGCCCTCGGAGGACCTTAAGAGGCTATTGCT	47
Qy	436	GGGGTCATTTGGGCGCTGGTTCAGTTCTTTAGCCATTGAGTCCAGAAATTTGCTCGAGCTT	49
Db	479	GGAGTATGCGGCGCTGGCTCCAGCTCTGTGGCCATTCAAGTCCAGAAATTTCTCCAGCTG	53
Qy	496	TTCAACATCTCAAGTTGGCTTACTACGAAACCATCATGATGTAGTATGACAAAGACTCTG	55
Db	539	TTGCAATCCCAAGATGCGCTATTCTTGTCCACAAAGATGAGCTTAGTGAACAAACTTTG	59
Qy	556	TTCAAAATATTTCATGAGGGTGTGGCTTCAGATGCTCAGCAGGCAAGTCCATGGTGAC	61
Db	599	TACAAATACTTCTGTAGGGTGTGCTCTTCTTGACACTTTGCAAGGCAAGGCGATGCTGAC	65
Qy	616	ATAGTGAGAGGTACACTGAGACTTATGTATACGCCGTACACACAAAGGCAACTATGGA	67
Db	659	ATAGTCAAGGTTTACAACTGAGACTTATGTCTGAGCAGTCCACACAAAGGAATTAAGCG	71
Qy	676	GAAAGTGGATGGAAGCTTCAAAAGATATGTACAGGCAAGAAAGGATTTGCTTGGCCAC	73
Db	719	GAGGTGGATGTGATCTTTCAAAGAACTGGCTGCCAAGAAAGGCGCTGCACTGGCACAC	77
Qy	736	TCTTCAAAATCTACAGTATATGACAGGGAGCAGAGCTTGATATAGCTGTGAAGAAGCTC	79
Db	779	TCCGACAAATCTTACAGCAATGCTGGCGAAGAAAGCTTTGACCGGCTCTGGCTAACTC	83
Qy	796	ACAAGTCACTTGGCCCAAGGCGCGGTGTGGCTTACTTCTGTAGAGGCAATGACGGTGA	85
Db	839	CGGAGGCGGCTTCCAAAGGCAAGGCTGTGTGCTGCTTGTGGAGGGCATGACATGGGG	89
Qy	856	GGTCTGCTGATGGCCATGAGAGCGGCTGGGTCTATAGTGGAGAAATTTGCTTGGGCA	91
Db	899	GCGTACTGAGTCCATGCGCGCGCTGGCGGTGTGGGAGAGTTCTCACTCTGAAGT	95
Qy	916	GA 917	
Db	959	GA 960	
RESULT 12			
US-10-300-473-4			
Sequence 4, Application US/10300473			
Publication No. US20030113873A1			
GENERAL INFORMATION:			
APPLICANT: STORMANN, THOMAS M.			
APPLICANT: STORJOHANN, LAURA L.			
APPLICANT: HAMMERLAND, LANCE G.			
APPLICANT: FULLER, FORREST H.			
APPLICANT: KAPACHO, KAREN J.			
TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR IDENTIFYING			
TITLE OF INVENTION: COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE			
TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE			
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS AND DISEASES			
FILE REFERENCE: 072827/0909			
CURRENT APPLICATION NUMBER: US/10/300,473			
CURRENT FILING DATE: 2003-02-21			
PRIOR APPLICATION NUMBER: 09/435,897			
PRIOR FILING DATE: 1999-11-08			
PRIOR APPLICATION NUMBER: 08/687,289			
PRIOR FILING DATE: 1996-07-25			
PRIOR APPLICATION NUMBER: 60/001,526			
PRIOR FILING DATE: 1995-07-26			
NUMBER OF SEQ ID NOS: 8			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 4			
LENGTH: 3219			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: Synthesized human			
OTHER INFORMATION: mGluR and human calcium receptor			
US-10-300-473-4			

Query Match	24.4%	Score 444.4;	DB 15;	Length 3219;
Best Local Similarity	71.5%;	Pred. No. 1.2e-11;		
Matches 602;	Conservative 0;	Mismatches 231;	Indels 9;	Gaps 1,

Oy	85	GTGGCTCA CATCTGGGGTACATCAATATATGGAGCTCTCTTTCTGTATATCAAGGCT	144
Dp	136	GTGGCGAAGATGAGACGAGATGTCAATCGAGAGCCCTCTTCTCACTCAACAGGCT	195
Oy	145	ACTGTGACGAAGTTCAATGAGAGAAAGTGTGGGCGAGTCCGTGAACGATATGGCATTCAG	204
Dp	196	CCAGCCGAGAAAGGTACCCGAAAGAAAGTGTGGGGAGATCAGGGGAAACGATATGGTATCCAG	255
Oy	205	AGAGTGGAGGGCCATCTGTGATACCTCGGAAAGGATCAATTTCAGACCCCAACCTCTGGCC	264
Dp	256	AGGTGGAGGGCCATGTTCCACAGTTGGATTAAGATTAAAGCGGAGCCGGGTCTCTGGCCC	315
Oy	265	AAACATCACA CTGGGCTGTGAGATTAAGGGAATTCCTGTGCAATTCGGCTGTGGCCCTAGAG	324
Dp	316	AACATCACTCTGGGCAAGTAGATCCGGGACCTCTGTGGGACCTTCAAGTGGCTTCGAA	375
Oy	325	CAGAGCAATTAAGTTCAATAAGAAATTCCTCAATTTCTTGGAGAGAGAAAGAGGCTTGGTA	384
Dp	376	CAGAGCAATGAATTAATCAAGAACTCCCTGAATTTTCATCCGAGATAGAAGATGGGCTTG	435
Oy	385	TGCTCTGTGTGATGGCTCTCTCTCTCTCTTCCGCTCCGATCCAAAGAGCCCATAGTA	435
Dp	436	AACCGATGCTGCTGTATGCGAGACCCTGCCCCCTGGCAGAGACTAAGAAAGCTATTTGCT	495
Oy	436	GGGGTCATTTGGGCTCTGTTCCAAGTTCTTTAAGCCATTCAAGTCCAAATTTGCTCAAGTT	495
Dp	496	GGAGTGAATCGGCTCTGGCTCCAAGCTCTGTGGCCATTCAAGTCCAGAACTTCTCCAGCTG	555
Oy	496	TTCAACATTAACCTCAGATTGCTTACTACAGAAACATATGAGATGTGAGTGAACAAGCTTG	555
Dp	556	TTTGCATATCCACAGATGCTCTATTTGTGCAACAAGCATTAAGCTGATGACAAACCTTTG	615
Oy	556	TTCAATAATTTTCATGAGGGTGTGCTTTCAGATGCTCAGCAGGCAAGTCCATGCTGAGC	615
Dp	616	TACAAATATCTCTGAGGGTTGTCCCTTGTGACATTTGCAGAGCAAGGGCCATGCTTGAC	675
Oy	616	ATATGTGAAGAGTACACATGACCTATGTATCAGCCGTACACACAGAAGCAACTATGGA	675
Dp	676	ATATGCAAAACGTTACAAATTGGAACATAATGCTCTGCACTGCAACAGAAAGGAATTTATGG	735
Oy	676	GAAATGGGATGGAAGCCCTTCAAAGATATGTGACAGCAAGAAAGGATTTGCAATGCCAC	735
Dp	736	GAGAGCGGAATGAGAGCTTTCAAAGAGCTGTGCTCCCAAGAAAGCCTCTGTATGCCCAT	795
Oy	736	TCTTACAAATATCAAGTATATCAAGGAGGAGCAGAGCTTTGATTAAGCTGTGAAGAAAGCTC	795
Dp	796	TCTGCAAAATATTACAGCAACCTCGGGGAGAAAGACTTTGACCGAATCTTGGCCCAATC	855
Oy	796	ACAAATCACTTGGCCCAAGGCCCGGGGTGAGAGGCTATCTCTGTAGAGGCATGAAGGTAGA	855
Dp	856	CGAGAGAGGCTTCCCAAGGCTTAAGATGATGTGTGCTTCTGTAAAGCAATGAAGATGCGA	915
Oy	856	GGTCTGTGATGAGCCATGAGAGCGGCTGTGGTCTAAGTGGAGAAATTTCTGCTTGGCCAGG	915
Dp	916	GGACTCTGAGGCGCATATGCGGCGCTTGGCGATGTGGGCGAAGTTTCACTCATTTGAAGT	975
Oy	916	GA 917	
Dp	976	GA 977	

RESULT 13  
US-10-027-632-211781  
; Sequence 211781, Application US/10027632  
; Publication No. US200302204075A5  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome  
 FILE REFERENCE: 108627.129  
 CURRENT APPLICATION NUMBER: US/10/027.632  
 CURRENT FILING DATE: 2002-04-30  
 CURRENT PUBLICATION NUMBER: 10/027.632

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? SEQ ID NO: 211781
? LENGTH: 687
? TYPE: DNA
? ORGANISM: Human
? FEATURES:
? NAME/KEY: misc feature
? LOCATION: (1) .. (687)
? OTHER INFORMATION: n = A,T,C or G
US-10-027-6332-211781

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Query Match	14.4%;	Score 263;	DB 13;	Length 687;
Best Local Similarity	77.5%;	Pred. No. 6.4e-62;		
Matches 317; Conservative	1;	Mismatches 91;	Indels 0;	Gaps 0;

OY	1114	TTCTGAGGGATATTACTCTGCAATTAAATGAAACCAAGCTCATATCTTCGTGATGGA	1172
Db	279	TTTGCAGTTTATCTTACTCTGCACATGACAAAGACCATGATCATATCTTCGTGATGGA	338
OY	1174	GATTTGAGAGCATTTGTATTTGATGTGACCGTCAAAATGCGCCCATATCACTGCACAA	1233
Db	339	GATTTGAGAGCATGAAAGTTGATGTGACCGTCAAAATGATCCCAATATCACTGATATAA	398
OY	1234	CTTCAAGTTTCTTGTGCAATGGGGGTCTCAGACTTTCACTCTGCGCAAGTATTACTGGGAG	1293
Db	399	TCTCAAGTTTCTTCAATGGGGGGCTGATTTTTCATATCTGCGCAATTTTATATGGGAG	458
OY	1294	GTCATGTGGGGGAGCTCTTGGCAATGGGCTTTGCGTGTGTTGTAATTAAGTACGTGAAAAGG	1353
Db	459	TTTAAACATGGGGGCACTCTTGGCAATGGGCTTTTGGTGTCTGTAAACATTAATGGAAAAG	518
OY	1354	AAGATCAGATGCGCAATATATAATGAGAGGAGGGACTCTTTAGTCTTGGAGTTGTTAAG	1413
Db	519	AAGAGACAGATGACATGATAGATGAGAGGGTGGGACTTTCTTCTTGAGATGTTAAG	578
OY	1414	AACGACATTCAGTGAAGTCTCTTTAACCACTTCCCAAGTTACATGCGAGTATGTCCCAAGA	1473
Db	579	GAGAGCACTCACTCAAGTCTCTTTACACACTTCCCACTTGTAATGCAATATGTTCCAAAGA	638
OY	1474	CTTACCAACCATGATGATTTATCTCGAATGTGTAAGCTAAACGTGGA	1522
Db	639	CTTACAGACACATGATGATTTATCTCGAATGTGTAAGGTAGACCGTGA	687

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RESULT 14
US-10-027-632-211782
; Sequence 211782, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OR INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OR INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632

```



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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211782
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(687)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-211782
```

```

Query Match      14.4%; Score 263; DB 13; Length 687;
Best Local Similarity 77.5%; Pred. No. 6,4e-62;
Matches 317; Conservative 1; Mismatches 91; Indels 0; Gaps 0;
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```

QY 1114 TTCTGATGATATTAATCTGATTAATGAAGCCCAAGTATCTTCTGATGGA 1173
DB 279 TTTCGATTTATCTTACTCTGAGCATGCAAGCCAGTAGTATCTTCTGCAATGA 338
QY 1174 GATTGGAAGCATTTGTATTTGATGATGACCGTCAAAATGCGCCCATCATCTGCAACA 1233
DB 339 GATTGGAAGCATGAAAGTTGATGATGACCCCTCAATATCCCAATATCATCTGATGAA 338
QY 1234 CCTACAAGTTTTCTTGATGAGGGGTGCTCAGACTTTCACCTCTGCAAGATTAATCTGGAG 1293
DB 399 TCTGAATGTTTTCTTCAATGAGGGGGCTGATTTTTCATATCTGGCAATTTTATGGAG 458
QY 1294 GTCCATGTGGGGGACTCTTGGAAATTTGGCTTTTGTGTTGTAATGTAATCTGAAAGGG 1353
DB 459 TTTAACATGGGGGACTCTTGGAAATTTGGCTTTTGTGTTGTAATGTAATTTGAAAGAG 518
QY 1354 AAGATTCAGATGCGCATATATATATGAGAGAGAGGACTCTTTAGTCTTGGGATTTGTAAG 1413
DB 519 AAGAGACAGATGACATGATGATGAGAGAGGAGGACTCTTTCTTCTTGGATGTGTTAG 578
QY 1414 AAGCATTCAGTGCAGTCTCTTTTACCACTCCCACTTACCTGCAATGACATGCAATGATCCCAAGA 1473
DB 579 GAGGACACTGACTGAGTCTCTTTTACCACTCCCACTTGTGAATGCAATATGTTCCAGA 638
QY 1474 CCTACCAACCATGTAGATTAATCTGATTTGGAATTTGGAAGCTGAACTGGA 1522
DB 639 CCTACGACACAGTAGATTAATCTGATTTGGAATTTGGAAGCTGGA 687
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RESULT 15  
US-10-027-632-211781

```

; Sequence 211781, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
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; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211781
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(687)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-211781
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Query Match      14.4%; Score 263; DB 14; Length 687;
Best Local Similarity 77.5%; Pred. No. 6,4e-62;
Matches 317; Conservative 1; Mismatches 91; Indels 0; Gaps 0;
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QY 1114 TTCTGATGATATTAATCTGATTAATGAAGCCCAAGTATCTTCTGATGGA 1173
DB 279 TTTCGATTTATCTTACTCTGAGCATGCAAGCCAGTAGTATCTTCTGCAATGA 338
QY 1174 GATTGGAAGCATTTGTATTTGATGATGACCGTCAAAATGCGCCCATCATCTGCAACA 1233
DB 339 GATTGGAAGCATGAAAGTTGATGATGACCCCTCAATATCCCAATATCATCTGATGAA 338
QY 1234 CCTACAAGTTTTCTTGATGAGGGGTGCTCAGACTTTCACCTCTGCAAGATTAATCTGGAG 1293
DB 399 TCTGAATGTTTTCTTCAATGAGGGGGCTGATTTTTCATATCTGGCAATTTTATGGAG 458
QY 1294 GTCCATGTGGGGGACTCTTGGAAATTTGGCTTTTGTGTTGTAATGTAATCTGAAAGGG 1353
DB 459 TTTAACATGGGGGACTCTTGGAAATTTGGCTTTTGTGTTGTAATGTAATTTGAAAGAG 518
QY 1354 AAGATTCAGATGCGCATATATATATGAGAGAGAGGACTCTTTAGTCTTGGGATTTGTAAG 1413
DB 519 AAGAGACAGATGACATGATGATGAGAGAGGAGGACTCTTTCTTCTTGGATGTGTTAG 578
QY 1414 AAGCATTCAGTGCAGTCTCTTTTACCACTCCCACTTACCTGCAATGACATGCAATGATCCCAAGA 1473
DB 579 GAGGACACTGACTGAGTCTCTTTTACCACTCCCACTTGTGAATGCAATATGTTCCAGA 638
QY 1474 CCTACCAACCATGTAGATTAATCTGATTTGGAATTTGGAAGCTGGA 1522
DB 639 CCTACGACACAGTAGATTAATCTGATTTGGAATTTGGAAGCTGGA 687
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Search completed: December 14, 2003, 10:04:46  
Job time: 609.28 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 09:35:14 ; Search time 4158.16 Seconds  
(without alignments)  
10655.460 Million cell updates/sec

Title: US-10-027-923-1  
Perfect score: 1823  
Sequence: 1 aaaaagtcctctgtgat.....aaaaaaaaaaaaaaaa 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_estbm:\*  
3: em\_estin:\*  
4: em\_estm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643	35.3	1297	11	BC031602 Homo sapi
2	628.8	34.5	710	14	CA449274 UI-H-E11-
3	511.4	28.1	515	13	BX280403 BX280403
4	509.8	28.0	519	10	BE674422 BE674422 7601a04.x

5	499	27.4	499	10	BE467477	h26608.x
6	473.2	26.0	690	10	BG193349	RG193349 RST12477
7	463.6	25.4	494	10	BX116917	BX116917 BX116917
8	445.8	24.5	449	14	CB153433	CB153433 K-EST0210
9	424.4	23.3	722	10	BG199987	BG199987 RST19284
10	424.6	23.3	449	9	AW015382	AW015382 UI-H-B10-
11	423.8	23.2	888	13	BU154755	BU154755 AGENCOURT
12	420.2	23.0	452	9	AI950429	AI950429 w35d01.x
13	417.4	22.9	667	29	AG046849	AG046849 Pan t901
14	413.8	22.7	455	9	AI655261	AI655261 w68b01.x
15	401.6	22.0	1400	13	BQ277274	BQ277274 AGENCOURT
16	400.6	22.0	414	10	BG150163	BG150163 nad4603.
17	372.2	20.4	3879	11	AK032422	AK032422 Mus muscu
18	369.8	20.2	715	10	BR275390	BR275390 601122276
19	360.8	19.8	720	28	BE5629	BE5629 CIT-HSF-202
20	340.4	18.7	362	9	AW197327	AW197327 xm38e06.x
21	315.2	17.3	625	28	AQ13970	AQ13970 RPCI11-10
22	290	15.9	664	12	B1826234	B1826234 603075928
23	289.2	15.9	682	10	BG695213	BG695213 NISC 1v13
24	281.6	15.4	657	13	BU351729	BU351729 603572561
25	281.6	15.4	669	13	BU393781	BU393781 603803380
26	275	15.1	806	10	BF125311	BF125311 601762484
27	271.6	14.9	526	28	B16405	B16405 342C10.TVB
28	268.8	14.7	378	28	BO3872	BO3872 CSR1-19b1-u
29	268.2	14.7	392	14	T78107	T78107 YC98a01.r1
30	252.2	13.8	673	13	BU390603	BU390603 603801605
31	246.8	13.5	471	14	CB730684	CB730684 AMGNNUC:N
32	228.8	12.6	439	14	CB750802	CB750802 AMGNNUC:N
33	224.2	12.3	837	28	B2181748	B2181748 CH230-388
34	219.8	12.1	435	28	AQ443358	AQ443358 HS 2231.B
35	216.2	11.9	645	12	B1858637	B1858637 603388908
36	213	11.7	960	10	BG135990	BG135990 602404035
37	195.8	10.7	871	10	BE893553	BE893553 601438128
38	194	10.6	1013	13	BQ070358	BQ070358 AGENCOURT
39	192.8	10.6	643	13	BX093574	BX093574 BX093574
40	191.6	10.5	532	29	B2930457	B2930457 CH240.36M
41	187.6	10.3	542	28	AQ586224	AQ586224 RPCI-11-4
42	185	10.1	722	28	A2815421	A2815421 2M0083H07
43	179	9.8	742	12	BI093942	BI093942 602857839
44	174	9.5	744	29	CNS03KCA	AL247981 Tetradon
45	173	9.5	681	29	CNS0300B	AL221636 Tetradon

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
BC031602	BC031602	Homo sapiens, clone IMAGE:5167902, mRNA.	BC031602.1	GI:21594893	HTC.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1297)	Strausberg, R.	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaphs-remail.nih.gov](mailto:cgaphs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: amg@bcm.tmc.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louissege, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Kuzny, D.M., Navavali,  
 A.N., Gidbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/INL at: <http://image.inl.gov>  
 Series: IRAC Plate: 51 Row: a Column: 11  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4504142  
 This clone has the following problem: retained intron.

## FEATURES

source

1. 1297  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5167902"  
 /cissue\_type="Brain, adult medulla"  
 /clone\_id="NIH MGC\_119"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"

BASE COUNT 343 a 301 c 325 g 328 t

ORIGIN

Query Match 35.3%; Score 643; DB 11; Length 1297;

Best Local Similarity 97.8%; Pred. No. 1.2e-62;

Matches 652; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

1 AAAATGCTCTTCTGTGATCTGTCACTTACTTTTGAAGAAGATGCTGGAGT 60  
 368 AAATGCTCTTCTGTGATCTGTCACTTACTTTTGAAGAAGATGCTGGAGT 427  
 61 GCACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 120  
 428 GCACATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 487  
 121 CTCCTTTCTGTTTCACTGACGCTTCTGTGAGAGAGAGAGAGAGAGAGT 180  
 488 CTCCTTTCTGTTTCACTGACGCTTCTGTGAGAGAGAGAGAGAGAGAGT 547  
 181 GTCCTGTAACAGTATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
 548 GTCCTGTAACAGTATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 607  
 241 AATTGACAGCCCACTCTTCCCAATCACTGAGAGAGAGAGAGAGAGAGATC 300  
 608 AATTGACAGCCCACTCTTCCCAATCACTGAGAGAGAGAGAGAGAGAGATC 667  
 301 TGGCATTCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 360  
 668 TGGCATTCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 727  
 361 TCGAAGATC 420  
 728 TCGAAGATC 787  
 421 AAGAAGCCCATAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 480  
 788 AAGAAGCCCATAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 847  
 481 AATTGCTCAGCTTTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 540  
 848 AATTGCTCAGCTTTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 907  
 541 AGTACAGATC 600  
 908 AGTACAGATC 967  
 601 AGGTTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 660  
 968 AGGGCCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1027

Qy 661 GAAGCA 667  
 Db 1028 GAAGCA 1034

## RESULT 2

CA449274 710 bp mRNA linear EST 08-NOV-2002  
 LOCUS CA449274/c  
 DEFINITION UI-H-E11-ayc-a-07-0-UI-51 NCI CGAP E11 Homo sapiens cDNA clone

## ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bcm.tmc.edu  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 Seq primer: M13 FORWARD  
 POLVA=yes.

## FEATURES

source

Location/Qualifiers  
 1. 710  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-E11-ayc-a-07-0-UI"  
 /cissue\_type="Chondrosarcoma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_id="NCI CGAP E11"  
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGCGAC.  
 TAG\_LTB=UI-H-E11  
 TAG\_TTSUB=Chondrosarcoma  
 TAG\_SEQ=AACTGCGAC"

BASE COUNT 214 a 138 c 152 g 206 t

ORIGIN

Query Match 34.5%; Score 628.8; DB 14; Length 710;

Best Local Similarity 93.5%; Pred. No. 6.5e-61;

Matches 666; Conservative 1; Mismatches 43; Indels 2; Gaps 1;

1101 CAGGCTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1160  
 710 CAGGCTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 651  
 1161 CTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1220  
 650 CTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 591

QY 1221 TATCACTGCAACCTACAGTCTTCTTGAGGGGCTCAGACTTTCACCTGGCAA 1280  
 DB 590 TATCACTGCAACCTACAGTCTTCTTGAGGGGCTCAGACTTTCACCTGGCAA 531  
 QY 1281 GTATTAATCGGAGGATCCATGCTGGGGGACTCTTGGAATTTGGGCTTTCGGTGTGTATTA 1340  
 DB 530 ATATTATCGGAGGATCCATGCTGGGGGACTCTTGGAATTTGGGCTTTCGGTGTGTATTA 471  
 QY 1341 GTATCGAAAGGAGAGATCAAGATGCAATATATATGAGAGAGGAGACTCTTACTCT 1400  
 DB 470 GTATCGAAAGGAGAGATCAAGATGCAATATATATGAGAGAGGAGACTCTTACTCT 411  
 QY 1401 TGGGATTTGTAAGAAGACATGAGTCACTCTTACCACTCCCACTTACACTGCA 1460  
 DB 410 TGGATGTTGTAAGAAGACATGAGTCACTCTTACCACTCCCACTTACACTGCA 351  
 QY 1461 GTATGTCCTCAAGACCTACCAACATGAGATTAATTCCTGGAATTTGAGACTGTA 1520  
 DB 350 ATATTATCCCAAGACCTACCAACATGAGATTAATTCCTGGAATTTGAGACTGTA 1293  
 QY 1521 GAGCTTGTGATGTTATGTAAGCTCCCTATATACCAATCCCTAATTCCTCTCTC 1580  
 DB 292 GAGCTTGTGATGTTATGTAAGCTCCCTATATACCAATCCCTAATTCCTCTCTC 233  
 QY 1581 ACCTCCCTCAAGGCTATCTTTGCTGATTCATCTCTGACAGAGCAATGAGAAATG 1640  
 DB 232 ACCTCCCTCAAGGCTATCTTTGCTGATTCATCTCTGACAGAGCAATGAGAAATG 173  
 QY 1641 TGTATATCTGCTGGGAGACCCCTTATCCCAATTAAGCCCTCTTCTGCTTATCA 1700  
 DB 172 TGTATATCTGCTGGGAGATCCCTTATTCAGAGAGCCCTCTTCTGCTTATCA 113  
 QY 1701 ACAGCAATAGGTTCTGTTTATGCTTGAATTCGATTCATGTTATTAATCACTCAT 1760  
 DB 112 ACAGCAATAGGTTCTGTTTATGCTTGAATTCGATTCATGTTATTAATCACTCAT 53  
 QY 1761 TTTATGCTACTATTAATGTTGTAAMCAGCAATTAATTAATTAATTAATTAATTA 1812  
 DB 52 TTTATGCTACTATTAATGTTGTAAMCAGCAATTAATTAATTAATTAATTAATTA 1

RESULT 3  
 BX280403/c 515 bp mRNA linear EST 04-MAR-2003  
 LOCUS BX280403 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166 ;  
 DEFINITION IMAGE:3281166, mRNA sequence.  
 ACCESSION BX280403  
 VERSION BX280403.1 GI:28612394  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCES  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 1 (bases 1 to 515) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Patzsch, E., Peters, M.,  
 Radehof, U., Schneider, D. and Korn, B.  
 TITLE Human Unigeneset - RZPD3  
 JOURNAL Unpublished  
 COMMENT Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGE:3281166  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi?response=libno=972 Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTGACACAGGAAACAGCATAC.  
 Location/Qualifiers  
 1. 515  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE3281166"  
 /feature\_type="carnicoid"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Lu24"  
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu24 was prepared, and as circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (clonides  
 141920-141791 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 137 a 138 c 105 g 133 t 2 others  
 ORIGIN  
 Query Match 28.1%; Score 511.4; DB 13; Length 515;  
 Best Local Similarity 99.4%; Pred. No. 7.9e-48;  
 Matches 512; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 856 GGTCTGCTAGGCGCATGAGGCGCTGGGCTTATGAGGAGATTTCTCTTGGGCAAG 915  
 DB 515 GGTCTGCTAGGCGCATGAGGCGCTGGGCTTATGAGGAGATTTCTCTTGGGCAAG 456  
 QY 916 GAACCAAGTCCATTTTATGATCTCAAGAGACATCTATGGGAGAGAGAG 975  
 DB 455 GAACCAAGTCCATTTTATGATCTCAAGAGACATCTATGGGAGAGAGAGAG 396  
 QY 976 AATGCAAGTGGCTTCTTCAAGGTTTGGAGATATTACAGAGATGAGTCCG 1035  
 DB 395 AATGCAAGTGGCTTCTTCAAGGTTTGGAGATATTACAGAGATGAGTCCG 336  
 QY 1036 CTGCTGCAATGCGCCAGGCTCTGAATCTAGAGCTCAAGGCTCAAGGCTCACTGAC 1095  
 DB 335 CTGCTGCAATGCGCCAGGCTCTGAATCTAGAGCTCAAGGCTCAAGGCTCACTGAC 276  
 QY 1096 AGGAGACGCTCATTAATTTGAGAGATTAATCTGATTAATTAATTAATTAATTA 1155  
 DB 275 AGGAGACGCTCATTAATTTGAGAGATTAATCTGATTAATTAATTAATTAATTA 216  
 QY 1156 CATATCTTCTGATGAGAGATTTGAGAGATTTGATTGATGATGACCGTCAAAATGCG 1215  
 DB 215 CATATCTTCTGATGAGAGATTTGAGAGATTTGATTGATGATGACCGTCAAAATGCG 156  
 QY 1216 CCCCATATCACTGCAACCTACAGATTTTCTGATGGGCTGCACTTACCTCT 1275  
 DB 155 CCCCATATCACTGCAACCTACAGATTTTCTGATGGGCTGCACTTACCTCT 96  
 QY 1276 GCGAATATTACTGAGAGTCCATGAGGAGATCTTGAATTTGGGCTTTCGGTGTGT 1335  
 DB 95 GCGAATATTACTGAGAGTCCATGAGGAGATCTTGAATTTGGGCTTTCGGTGTGT 36  
 QY 1336 AATAGTACTGAGAGAGAGAGATGAGATGAGCA 1370  
 DB 35 AATAGTACTGAGAGAGAGAGATGAGATGAGCA 1

RESULT 4  
 BE674422 519 bp mRNA linear EST 08-SEP-2000  
 LOCUS BE674422  
 DEFINITION 7E01804.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166.3;  
 similar to SW:MG8\_HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 PRECURSOR. ; mRNA sequence.  
 ACCESSION BE674422  
 VERSION BE674422.1 GI:10034963  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 519)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rewall.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 499.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:3281166"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_id="NCI CGAP Lu24"  
 /note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI-CGAP Lu5 was prepared, and 88 circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 141920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 143 a 114 c 143 g 119 t  
 ORIGIN  
 Query Match 28.0%; Score 509.8; DB 10; Length 519;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-47;  
 Matches 511; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 487 CTCGAGCTTTTCAACATCTCAGATTGCTTACTGACCAACCATCATGATCTGATGAC 546  
 DB 7 CGCAGAGCTTTTCAACATCTCAGATTGCTTACTGACCAACCATCATGATCTGATGAC 66  
 QY 547 AAGAGCTGTTCAAAATTTTCATGAGGGTGTGCTTCAATGCTCAGAGCAAGGCTCC 606  
 DB 67 AAGAGCTGTTCAAAATTTTCATGAGGGTGTGCTTCAATGCTCAGAGCAAGGCTCC 126  
 QY 607 ATGGTGACATAGTGAAGAGGTACCACTGACCTATGATGACCGCTACACAGAAGGC 666  
 DB 127 ATGGTGACATAGTGAAGAGGTACCACTGACCTATGATGACCGCTACACAGAAGGC 186  
 QY 667 AACTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGGAAGAGGATTTGC 726  
 DB 187 AACTATGAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGGAAGAGGATTTGC 246  
 QY 727 ATGGCCCACTTTCACAAATCTACAGTATGCAAGGAGGAGCAAGCTTGTATAGCTCTG 786  
 DB 247 ATGGCCCACTTTCACAAATCTACAGTATGCAAGGAGGAGCAAGCTTGTATAGCTCTG 306  
 QY 787 AAGAAGCTCAAGTCACTTGCCCAAGGCCGGGTGGTGGCTTCTCTGTGAGGGCATG 846  
 DB 307 AAGAAGCTCAAGTCACTTGCCCAAGGCCGGGTGGTGGCTTCTCTGTGAGGGCATG 366  
 QY 847 ACGGTGAGAGTGTGCTGATGCGCATGAGGCGCTGTGCTGTAGTGGAGATTTCTGCTT 906  
 DB 367 ACGGTGAGAGTGTGCTGATGCGCATGAGGCGCTGTGCTGTAGTGGAGATTTCTGCTT 426

QY 907 CTGGGACGGGACACAGATGCCATCTTTATAGATCTCAAGAGACATCTATGGGA 966  
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 VERSION BE467477  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 499)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rewall.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 493.  
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 library NCI-CGAP Lu5 was prepared, and 88 circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 141920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
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 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 500 ACATACCTCAGATGCTTACTCAGAACCATCATGATCTGATGACAGACTCTGTCA 559  
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QY 620 TGAAGAGTACAACTGACCTATGTATGACCCGTACACAGAAAGCAATATGAGAAA 679  
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 DB 241 ACAAATCTACAGTATGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 800 GTCACTTCCCAAGAGCCCGGAGTGTGCTACTTCTGTAGAGGAGATGAGGAGAGAGAG 859  
 DB 301 GTCACTTCCCAAGAGCCCGGAGTGTGCTACTTCTGTAGAGGAGATGAGGAGAGAGAG 360  
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 LOCUS RST12477 Atherysa RAGE Library Homo sapiens cDNA, mRNA sequence.  
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 ACCESSION BG193349  
 VERSION BG193349.1 GI:13715036  
 KEYWORDS EST.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
 Lerner, L., Costanzo, D., Thornton, M., Ramachandran, R., Whittington, J.,  
 'E., Veloso, N., Kikla, A., Hesse, J., Cothren, K., Lo, K., Offenbacher,  
 'J., Danzig, J. and Ducar, M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Scott J. Cain  
 Atherysa, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9300  
 Fax: 216 361 9596  
 Email: scain@atherysa.com  
 High quality sequence stop: 551.  
 Location/Qualifiers  
 1. 690  
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 /db\_xref="taxon:9606"  
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 /clone\_idb="Atherysa RAGE Library"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

FEATURES  
 source  
 BASE COUNT  
 ORIGIN  
 190 a 142 c 150 g 207 t 1 others

Query Match 26.0%; Score 473.2; DB 10; Length 690;  
 Best Local Similarity 82.1%; Pred. No. 1.1e-43;  
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 QY 1119 AGTGATTTTCTCTGCTATTAATGAAGCCACAGTCATATCTTGATGTGAGATTT 1178  
 DB 3 AGTGATTTTCTCTGCTATTAATGAAGCCACAGTCATATCTTGATGTGAGATTT 61  
 QY 1179 GAGAAAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1238  
 DB 62 GAGAAAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 121  
 QY 1239 AAGTTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1298  
 DB 122 AAGTTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 181  
 QY 1299 TGT-GGGGAGCTCTGGAATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 1357  
 DB 182 CGTGGGGAGCTCTGGAATTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 241  
 QY 1358 ATGAGATGCAAT 1417  
 DB 242 GACAGATATCAAGAT 301  
 QY 1418 ACATTGAGTCAAGTCTTTTACCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1477  
 DB 302 GCACTCACTGCAAGTCTTTTACCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 361  
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 DB 362 CCAGACATATGAT 421  
 QY 1538 ATCAAAGCTCCCTTATATACCAATCCCTTATGCTCTCTTCACTCTCTCAAGGCTTA 1597  
 DB 422 ATCAAAGTCCCTTATATACCAATCCCTTATGCTCTCTTCACTCTCTCAAGGCTTA 481  
 QY 1598 TCTTTTGTCTATATATCTCTGACAGAGCAATGCAAGATGCTTATCTCTGAGG 1657  
 DB 482 TCTTTTGTCTATATCTCTGACAGAGCAATGCAAGATGCTTATCTCTGAGG 541  
 QY 1658 AACCCCTTATCCCATTAAGCCCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1717  
 DB 542 AACCGTTTATCCCATTAAGCCCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 601  
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 DB 602 CATTATATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661  
 QY 1778 AATGTGTAAACACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAA 1806  
 DB 662 AATATGCGAAGAACGAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAA 690

RESULT 7  
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 ACCESSION EX116917.1 GI:27840301  
 VERSION EX116917.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Ebert, L., Hell, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,  
 Radloff, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 Unpublished  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGP98A225727.  
 RZPDLib; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLib No.972)  
 http://www.rzpd.de/Clonecards/cgi-  
 bin/showlib.pl.cgi?response/libNo=972 Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTACACAGGAAGACGATGAC.

## FEATURES

source

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 from the normalized library NCI CGAP GC4 was prepared, and  
 as circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneids  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

118 a 118 c 105 g 153 t

## ORIGIN

Query Match 25.4%; Score 463.6; DB 13; Length 494;  
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 1 TTTTCTGCAGTGGGCTGCTGAGCTTACCTCGGCAAGATTAATCTGAGGCTCATGT 60  
 1302 GGGGGAATCTTGGATTTGGCTTGGCTTGGATTAATGATGAGGAGGAGATCA 1361  
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 1362 GAATGGCAATATATATGAGAGAGAGGAGCTCTTGAATGTTTAAAGACGAT 1421  
 121 GAATGGCAATATATATGAGAGAGAGGAGCTCTTGAATGTTTAAAGATGACAT 180  
 1422 TCGATGAGCTCTTTCACACCTCCAGTTACATGAGATGATGCCAAGACCTACAA 1481  
 181 TCGATGAGCTCTTTCACACCTCCAGTTACATGAGATGATGCCAAGACCTACAA 240  
 1482 CCATGTAGATTAATCTCGATTTGTGAAGCTAGAACTGTAGCTCTGTATGTTATCA 1541  
 241 CCATGTAGATTAATCTCGATTTGTGAAGCTAGAACTGTAGCTCTGTATGTTATCA 300  
 1542 AAGTCCCTATATATACCAATCCCTAATGCTCTTTCACCTCTTCAGGCTATCTT 1601  
 301 AAGTCCCTATATATACCAATCCCTAATGCTCTTTCACCTCTTCAGGCTATCTT 360  
 1602 TTGCTGATTCATCTCGACAGAGAGCAATTCGAATGTTTATCTGCTGGAGAAC 1661  
 361 TTGCTGATTCATCTCGACAGAGAGCAATTCGAATGTTTATCTGCTGGAGAAC 420  
 1662 CCTTATCCCATTAAGGCTCTTCTTCTGCTCTTATCAAGAGCAATAGGTTCTGT 1721  
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Db 481 TTATGCTTGAATT 494

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 DEFINITION  
 CB153433  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)

## REFERENCE

AUTHORS

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.krdb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
 Location/Qualifiers

## FEATURES

source

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 site\_2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then deacapped  
 with tabacco acid pyrophosphatase (TAP). The deacapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## BASE COUNT

106 a 112 c 112 g 119 t

## ORIGIN

Query Match 24.5%; Score 445.8; DB 14; Length 449;  
 Best Local Similarity 99.6%; Pred. No. 1.6e-40;  
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123 CTTTCTGTTCAATCAGCAGCTACTGTGAGCGAAGTTCAATGAGAGAGATGTGGGCACT 182  
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 61 CCGTGAACAGTATGCAATTCAGAGAGGCGCATGTCATACCTGGAAGATCAA 120  
 243 TTGAGACCCGACACTTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTG 302  
 121 TTGAGACCCGACACTTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTG 180



QY	303	GCATTGCGCTGTGGCCCTTAGAGCAGAGACATTGATGTTCAATTAAGATTCCTCATATTTCTTC	362
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QY	363	GGAAGAGAGAAAGGCGCTTGGTATGCTCTGTGAGATGCTCTCTCTCTTCCGCTCCAA	422
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QY	423	GAAGCCCATAGTAGAGGGGTCA TTGGGCGCTGGTTCACGTTCTTTAGCCATTGAGGTCCAGAA	482
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QY	483	TTTGCTCCAGCTTTTTCACACATACCTCAGATTTGCTTACTCAGCAACCAATCATGATCTGAG	542
Db	361	TTTGCTCCAGCTTTTTCACACATACCTCAGATTTGCTTACTCAGCAACCAATCATGATCTGAG	420
QY	543	TGACACAGCTCTGTTCAATATATTTTCATGA	571
Db	421	TGACACAGCTCTGTTCAATATATTTTCATGA	449

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (pages 10 to 729)	Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Jenner, L., Costanzo, D., McGilligot, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danti, J., and Ducar, M.	Creation of genome-wide protein expression libraries using random activation of gene expression	Nat. Biotechnol. 19 (5), 440-445 (2001)

COMMENT

Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scj@atersys.com  
High quality sequence stop: 445.

FEATURES	Location/Qualifiers
source	1. . 729

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/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology', in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

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Db	61	CGATATACATGCGAAATCTGAATGTTTTCTGTATGGGGGGGCTCCGGCTTTCACATCTGG	120
Qy	1278	CAAGTATTTACTGGAGGTCCATGT-GGGAGACTTTTGAATTTGGGCTTTCGGTGTGTGA	1336
Db	121	CAATATATTAATGGAGGTTCACTGGGGGGACTTTGGAAATTTGGGCTTTTGGTGTGTGA	180
Qy	1337	ATAAGTACTGGAAGGAGAGATCAGATGAGCAATATATATGAGAGAGGGACTTTTGA	1396
Db	181	ACAATATCCGAAAGAGAGACAGATGACAAGATAGATGAGAGAGGGACTTTTC	240
Qy	1397	GCTTTGGGATTTGTTAAGAAGCAATTAGTGCAGTCTTTACACACTCCCACTTACAC	1456
Db	241	ATCTTGATGTGTTAAGAGAGGCACTACATGCACTCTCTTACACACTCCCACTTGTGG	300
Qy	1457	TGCAGTATGTCCCAAGACTACCAACCATGAGATTATTCGTGATTTGTGATGACTGAA	1518
Db	301	TGCAATATGTTCCAAAGCACTACGACGACAGATAGATTATTCGTGATTTGTGATGAGAA	360
Qy	1517	CTGTGAGCTTGTTGATGATTAAATCAAAAGCTCCCTATATACACATCCCTAATTGCTCT	1576
Db	361	CCATGACTTGTGTTGGTGTGTA-CAAACTCCCTGATATACACATCCCTAATTGCTCT	419
Qy	1577	TTCACCTCCCTCAGGCTATCTTTTGTGATATCAATCTGACGAGACAATCAGA	1636
Db	420	TCTCACCCTCTCAGGCTATCTTTTGTGATGATCACTTGTGACGAGAAAAGTCAGA	479
Qy	1637	AATGTGTTTATCTGCTGTGGAAGCCCTTTATCCCAATAAGCCCTCTTGTGCTTGA	1696
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Qy	1697	TCAACAGGACAAATAGGTTCTGTTTATGTCTTGAAATTGCAATCTATATGTTAATAAC	1756
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Qy	1757	TCATTTATTTGTACTATTAATAATGTGTAAACACAAAAAATAAAAAA	1805
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VERSION	AM015382
KEYWORDS	AM015382.1 GI:5864139
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 442)	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
		Tumor Gene Index		
		Unpublished		
		Contact: Robert Strausberg, Ph.D.		
		Email: <a href="mailto:cgaps-remail.nih.gov">cgaps-remail.nih.gov</a>		
		Oligo-dT track not found. Not 1 site shown in beginning of sequence		
		is likely internal to the message. cDNA library Preparation: M.B.		
		Soares Lab Clone distribution: NCI-CGAP clone distribution		
		information can be found through the I.M.A.G.E. Consortium/LLNL at:		
		<a href="http://www-bio.llnl.gov/bdrip/image/image.html">www-bio.llnl.gov/bdrip/image/image.html</a>		
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NCI CGAP Sub1 library is a subtracted library derived from
B1. B1 constitutes a mixture of 21 normalized or
subtracted NCI CGAP libraries: NCI CGAP C04,
NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP C010, NCI CGAP C016
, NCI CGAP K1d5, NCI CGAP K1d12, NCI CGAP K1d3,
NCI CGAP K1d11, NCI CGAP Lym2, NCI CGAP B12, NCI CGAP C08,
NCI CGAP C1L1, NCI CGAP Lc2, NCI CGAP Brn23, NCI CGAP L1u5
, NCI CGAP L1u24, NCI CGAP L1u19, NCI CGAP GC4, NCI CGAP GC6
, NCI CGAP Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with a
driver whose composition is detailed below: NCI CGAP K1d3
pool 1 L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE
cloneids 132376-132391, 145608-145675, 150055-150285)
) NCI CGAP K1d5 pool 1 L1AM 3338-3342, 3722-3725,
3776-3778 (IMAGE cloneids 1323912-132831,
1471368-1472903, 1492104-1493255) NCI CGAP L1u5 pool 1 L1AM
3575-3582, 3851-3854 (IMAGE cloneids 141920-1417991,
1520904-1522439) NCI CGAP GC4 pool 1 L1AM 3164-3167,
3716-3720, 3733-3735 (IMAGE cloneids 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1
L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE cloneids
985608-986759, 1101192-1101959, 1217928-1220615)
NCI CGAP C010 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE
cloneids 1057416-1061255, 1144584-1145351) The resulting
subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldo
, Lemon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
Tag LIB=NCI CGAP Lc12
TAG TISSUE=leiomysarcoma
TAG_SRP=ATCG"

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BASE COUNT 118 a 97 c 127 g 100 t

ORIGIN

Query Match 23.3%; Score 424.4; DB 9; Length 442;  
 Best Local Similarity 99.5%; Pred. No. 3,7e-38;  
 Matches 436; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

487 CTCGAGCTTTTCAACATCACTGAGATTGCTTACTGACCAACCATGATCTGAGTGAC 546  
 5 CGCCAGCTTTTCAACATCACTGAGATTGCTTACTGACCAACCATGATCTGAGTGAC 64  
 547 AAGACTCTGTTCAAAATTTTCATGAGGGTGTGCTTCAGATGTCGACGGAAGTCC 606  
 65 AAGACTCTGTTCAAAATTTTCATGAGGGTGTGCTTCAGATGTCGACGGAAGTCC 124  
 607 ATGGTGACATAGTGAAGAGTGAACAATGACCTATATCAGCCGTACACAGAGGC 666  
 125 ATGGTGACATAGTGAAGAGTGAACAATGACCTATATCAGCCGTACACAGAGGC 184  
 667 AACTATGAGAGAAAGTGGATGAGAGCTTCAAGATATGTCAAGGAAGAGGATTTGC 726  
 185 AACTATGAGAGAAAGTGGATGAGAGCTTCAAGATATGTCAAGGAAGAGGATTTGC 244  
 727 ATGGCCCACTTTTCAAAATTTTCATGAGGGGATGAGAGGAGCTTTGATTAAGCTCG 786  
 245 ATGGCCCACTTTTCAAAATTTTCATGAGGGGATGAGAGGAGCTTTGATTAAGCTCG 304  
 787 AAGAAGCTCAAGAGTCACTTGCCCAAGGCCCGGGTGTGGCTTACTGTGAGGGCAG 846  
 305 AAGAAGCTCAAGAGTCACTTGCCCAAGGCCCGGGTGTGGCTTACTGTGAGGGCAG 364  
 847 ACGGTGAGAGGTCTGTGATGGCCATGAGCGCGCTGGGTCTAGTGGAGAA-TTTCGCT 905  
 365 ACGGTGAGAGGTCTGTGATGGCCATGAGCGCGCTGGGTCTAGTGGAGAA-TTTCGCT 424

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QY 906 TCTGGGCAAGGACACAGA 923
DB 425 TCTGGGCAAGGACACAGA 442

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RESULT 11  
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 LOCUS  
 DEFINITION  
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 AGENCOUNT\_7931447 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6151700  
 5', mRNA sequence.  
 BU154755  
 BU154755.1 GI:22668287  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 888)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 UNPUBLISHED  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DP  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 plate: L1AM13488 row: f column: 21  
 High quality sequence stop: 570.  
 Location/Qualifiers  
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 /clone="IMAGE:6151700"  
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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 2 kb. Library constructed by Life  
 Technologies."

BASE COUNT 235 a 215 c 206 g 232 t

ORIGIN

Query Match 23.2%; Score 423.8; DB 13; Length 888;  
 Best Local Similarity 80.2%; Pred. No. 2.8e-38;  
 Matches 548; Conservative 0; Mismatches 127; Indels 8; Gaps 4;

998 AGGGTTTGGAGACATATTACAGAGAGTGAAGTCCGTGCTGTCACATGCCCCAGCCTC 1057  
 206 AGGGTTTGGAGACATATTACAGAGAGTGAAGTCCGTGCTGTCACATGCCCCAGCCTC 265  
 1058 TGAATCTAAGCTCACTTGAAGGCCCATCACTGAGCTGAGGAGCAGGCTCATTAATCT 1117  
 266 TGAATCTAAGCTCACTTGAAGGCCCATCACTGAGCTGAGGAGCAGGCTCATTAATCT 325  
 1118 GAGTGAATTAATCTGCACTTAATTAAGAGCCCAAGAGTATCTTCATGAGGAGATT 1177  
 326 GAGTGAATTAATCTGCACTTAATTAAGAGCCCAAGAGTATCTTCATGAGGAGATT 385  
 1178 TGAAGACATTTTGTATTGATGTGACCGTCAAAATGCGGCCCATATCACTGCAACACTTA 1237  
 386 TGAAGACATTTTGTATTGATGTGACCGTCAAAATGCGGCCCATATCACTGCAACACTTA 445  
 1238 CAAGTTTCTTGATGGGGTCTCAGACTTTTCACTCTGCGCAAGTATTACTGGGAGGTC 1297  
 446 CAAGTTTCTTGATGGGGTCTCAGACTTTTCACTCTGCGCAAGTATTACTGGGAGGTC 505

QY 1298 ATGTGGGGAGCTTGTGGAATGGGCTTTCGTTGTTGTATTAAGTACTGAGAAAGGAGA 1357  
 DB 506 ATGTGGGGAGCTTGTGGAATGGGCTTTCGTTGTTGTATTAAGTACTGAGAAAGGAGA 565  
 QY 1358 ATCAAGATGGCAATATATATGAGAGAGGAGACT-CTTATGCTTGGGATTTTAAAGAC 1416  
 DB 566 ATCAAGATGGCAATATATATGAGAGAGGAGACTCTTATGCTTGGGATTTTAAAGAC 625  
 QY 1417 GACATTCAGTGGAG--TCTCTTACCACTCCCAAGTATACAGCAAGTAT-GTCCCAAGA 1473  
 DB 626 GACATTCAGTGGAGCTTCTTACCACTCCCAAGTATACAGCAAGTATGCCCCAAGA 685  
 QY 1474 CTTACCAACCATGATGAGATTTCC---TGATTTGTAAGTGAAGTGAAGTCTGCT 1529  
 DB 686 CTTACCAACCATGATGAGATTTCCCTGGGATTTGTAAGTGAAGTGAAGTCTGCT 745  
 QY 1530 TGAATTTATCAAGCTCCCTTATATACACATCCCTAATGCTCTTCACTCTCT 1589  
 DB 746 TCCCGTGTAGTGTAGTGTCCAAAGCTCCCTCTAATATACCCCAATCCCTTAAAT 805  
 QY 1590 CAGGCGCATTTTGTGATATATCATCTCTGACAGAGCAAGCAATGATGTTATCT 1649  
 DB 806 TTGGGTTCTCTTCTCAAACTTTCCCTTTTAAAGAAACCCCAAACTTTTCTT 865  
 QY 1650 GCTGTGGGAACCCCTTATCCCA 1672  
 DB 866 CCGGGGAATTTCTCTCCCA 888

RESULT 12 452 bp mRNA linear EST 08-MAR-2000  
 AI950429/c WQ35601.x1 NCI CGAP GC6 Homo sapiens CDNA clone IMAGE:2473249.3  
 LOCUS similar to SW:BUZY\_HUMAN Q13410 BUTYROPHILIN PRECURSOR ;, mRNA  
 DEFINITION sequence.

ACCESSION AI950429 GI:5742739  
 VERSION AI950429  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 452)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-romell.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldi, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL ac:  
 www-bio.1lm.gov/dbtrp/image/image.html  
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 Location/Qualifiers

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 from the normalized library NCI CGAP GC6 was prepared, and  
 as circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonids  
 1257086-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldi.  
 BASE COUNT 139 a 81 c 109 g 122 t 1 others  
 ORIGIN

Query Match 23 0%; Score 420.2; DB 9; Length 452;  
 Best Local Similarity 95.4%; Pred. No. 1.1e-37;  
 Matches 431; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

QY 1348 AAGGGAAGATGAGATGAGATATATATGAGAGAGGAGCTTTAGTCTTGGAT 1407  
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 QY 1408 GTTAAAGACATTCAGTGCAGTCTCTTTACCACTCCCAAGTACATGAGATGTC 1467  
 DB 392 GTTAAAGACATTCAGTGCAGTCTCTTTACCACTCCCAAGTACATGAGATGTC 333  
 QY 1468 CCAAGCTTACCAACATGAGATATATTCCTGAGATTTGAGACTGAGAGCTTTC 1527  
 DB 332 CCAAGCTTACCAACATGAGATATATTCCTGAGATTTGAGACTGAGAGCTTTC 273  
 QY 1528 GTTAAAGTAAATCAAGTCCCTATATACACCATCCCTAATGCTCTTCACTCTCT 1587  
 DB 272 GTTAAAGTAAATCAAGTCCCTATATACACCATCCCTAATGCTCTTCACTCTCT 213  
 QY 1588 CTCAGGCTATCTTTTGTGATATTCATCTCTGACAGAGCAATGAGATGTTAT 1647  
 DB 212 CTCAGGCTATCTTTTGTGATATTCATCTCTGACAGAGCAATGAGATGTTAT 153  
 QY 1648 CTGCTGTGGGAACCCCTTATCCCAAAAGCCCTCTTCTGCTTATCAAAAGAGAC 1707  
 DB 152 CTGCTGTGGGAACCCCTTATCCCAAAAGCCCTCTTCTGCTTATCAAAAGAGAC 93  
 QY 1708 AATAGTCTCTGTTTATGCTTGAATTCATCTTATGTTATTAACCTATTATGT 1767  
 DB 92 AATAGTCTCTGTTTATGCTTGAATTCATCTTATGTTATTAACCTATTATGT 33  
 QY 1768 GTTACTATTAAATGTGTAAGTCAAAAGAA 1799  
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RESULT 13 667 bp DNA linear GSS 02-NOV-2001  
 AG046849 Pan troglodytes DNA, clone: PTB-026D03.F, genomic survey sequence.  
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 DEFINITION AG046849.1 GI:16583741  
 ACCESSION  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (Chimpanzee)  
 ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 1 (bases 1 to 667)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE Unpublished

JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-romell.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldi, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL ac:  
 www-bio.1lm.gov/dbtrp/image/image.html  
 Insert length: 607 Std Error: 0.00  
 Seg primer: -40UP from Gibco.  
 Location/Qualifiers

source 1..452  
 /organism="Homo sapiens"  
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 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI CGAP GC6 was prepared, and  
 as circles were made in vitro. Following HAP purification,

## COMMENT

clone tracking errors.

PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
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1. .667  
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BASE COUNT 156 a 142 c 158 g 210 t 1 others  
ORIGIN

Query Match 22.9%; Score 417.4; DB 29; Length 667;  
Best Local Similarity 82.6%; Pred. No. 1.7e-37;  
Matches 489; Conservative 0; Mismatches 102; Indels 1; Gaps 1;

115 GAGAGCTCTCTTCTGTTTCATACACGCTACTGTGACGAAGTTTCATGAGAGAGTGT 174  
66 GAGAGCTCTCTTCTGTTTCATACACGCTACTGTGACGAAGTTTCATGAGAGAGTGT 125  
175 GGGGCAATCCGTGAACGATATGAGATTCAGAGAGTGAAGGCAATGCTGCAATCCCTGGA 234  
126 GGGGCGGTCGGTGAACGATATGAGATTCAGAGAGTGAAGGCAATGCTGCAATCCCTGGA 185  
235 AGGATCAATTCAGACCCCACTCTGCCCCCACTCACTGAGGCTGTGAGATTAAGGAT 294  
186 AGGATCAATTCATACCCCACTCTGCCCCCACTCACTGAGGCTGTGAGATTAAGGAT 245  
295 TCTGCTGCAATTCAGGCTGTGAGGCTTGAAGAGCAATGAGTTCATTAAGATTCCTTC 354  
246 TACTGCTGCAATTCAGGCTGTGAGGCTTGAAGAGCAATGAGTTCATTAAGATTCCTTC 305  
355 ATTCTTGGAGAGAGGAGGCTGTGAGGCTTGAAGAGCAATGAGTTCATTAAGATTCCTTC 414  
306 ATTCTTGGAGAGAGGAGGCTGTGAGGCTTGAAGAGCAATGAGTTCATTAAGATTCCTTC 365  
415 CGCTCCAGAGAGCCATATGAGGAGTCAATGAGGCTGTGAGGCTTGAAGATTCATTCAG 474  
366 CGCTCCAGAGAGCCATATGAGGAGTCAATGAGGCTGTGAGGCTTGAAGATTCATTCAG 425  
475 GTCCAGAAATTTCTCCAGCTTTTCAACATACCTGAGTTGCTTACAGAACCATCATG 534  
426 GCGCAGATGTGGTGCAGTTTTCATCATACCTGAGTTGCTTACAGAACCATCATG 485  
535 GATCTGATGACAGAGATCTCTGTTCAATATTTTCATGAGGCTGTGAGGCTTGAAGATTC 594  
486 GATCTGATGACAGAGATCTCTGTTCAATATTTTCATGAGGCTGTGAGGCTTGAAGATTC 544  
595 CAGGCAAGTTCATGAGTGAATATGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 654  
545 TTGCTTATGATTAATGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 604  
655 CACACAGAGGCAATGATGAGAGAGGAGTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 706  
605 CTCACATTAAGGATTTTATTTCTTTGTTAATCTCCCTGTAATGTTAATGT 656

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ACCESSION AI655261  
VERSION AI655261.1 GI:4739240  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 455)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldi, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
[www-bio.illn.gov/biopr/image/image.html](http://www-bio.illn.gov/biopr/image/image.html)  
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Seq primer: -40UP from G1bco.

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/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI CGAP G64 was prepared, and  
86 circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subcloning hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subcloning by Bento Soares and M. Fatima Bonaldi."

BASE COUNT 138 a 82 c 111 g 124 t  
ORIGIN

Query Match 22.7%; Score 413.8; DB 9; Length 455;  
Best Local Similarity 95.6%; Pred. No. 5.5e-37;  
Matches 435; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

1346 GAAAGGAGAGGATGCAATGCAATATATGAGAGAGAGGAGCTTTAGTCTTGGA 1405  
455 GAAAGGAGAGGATGCAATGCAATATATGAGAGAGAGGAGCTTTAGTCTTGGA 396  
1406 TTGTTAAGAGAGGATGCAATGCAATATATGAGAGAGAGGAGCTTTAGTCTTGGA 1465  
395 GTGTTAAGAGAGGATGCAATGCAATATATGAGAGAGAGGAGCTTTAGTCTTGGA 336  
1466 TCCCAAGACCTACCAACATGATGATTAATCTCGATTTGTAAGCTAGAACTGTAGCT 1525  
335 TCCCAAGACCTACCAACATGATGATTAATCTCGATTTGTAAGCTAGAACTGTAGCT 276  
1526 TCGTTATGTTAATCAAGGCTCCCTAATATACCAATCCCTAATGCTCTTCACTC 1585  
275 TCGTTATGTTAATCAAGGCTCCCTAATATACCAATCCCTAATGCTCTTCACTC 216  
1586 CTCTCAGGCTAATCTTTGCTGATTCATCTGACCAAGAGAAATGCAATATGTTT 1645  
215 CTCTCAGGCTAATCTTTGCTGATTCATCTGACCAAGAGAAATGCAATATGTTT 156  
1646 ATCTGCTGAGGAGAGCCCTTATCCATTAAGGCTCTTCTGCTGCTTATCAACAGG 1705  
155 ATCTGCTGAGGAGAGCCCTTATCCATTAAGGCTCTTCTGCTGCTTATCAACAGG 96  
1706 ACAATATGCTTCTGTTATATGCTTGAATGCAATTAAT-GTTAATTAATCAATTAAT 1764  
95 ACAATATGCTTCTGTTATATGCTTGAATGCAATTAATCAATTAATCAATTAAT 36

QY 1765 TGGTACTATTAAATGTGTAAACACAAAAA 1799  
 DB 35 TGTGTTACTATTAAATGTGTAAACACCTAAAAA 1

RESULT 15  
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 ACCESSION BQ277274  
 VERSION BQ277274.1 GI:20487482  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1400)  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: NCI

CDNA Library Preparation: Michael Brownstein Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM2057 row: n column: 09  
 High quality sequence stop: 410.  
 Location/Qualifiers

FEATURES  
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 Site 2: SfiI (ggccgcctcgcc); Double-stranded cDNA;  
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 ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary  
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 5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)NN-3'. Full-length  
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 Creator SMART kit and size-selected to contain the 1-2 kb  
 size fraction (other fractions present in NIH\_MGC\_126 and  
 NIH\_MGC\_128). Library created in the laboratory of T.  
 Udell, M.D., Ph.D. (NIH, NIH). Note: this is a NIH\_MGC  
 library."

BASE COUNT 360 a 429 c 267 g 342 t 2 others  
 ORIGIN

Query Match 22.0%; Score 401.6; DB 13; Length 1400;  
 Best Local Similarity 90.7%; Pred. No. 6e-36;  
 Matches 439; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

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 QY 1313 GGAATTGGGCTTGGTGTGTTGTAATAGTACTGGAAGGAGATCGAATGGCAAT 1372  
 DB 63 GGAATTGGGCTTGGTGTGTTGTAATAGTACTGGAAGGAGATCGAATGGCAAT 122

QY 1372 TATATGAGAGAGGAGACTCTTAAGTCTTGGATTGTAAAGACATTCAGTGCAGTC 1432  
 DB 123 TATATGAGAGAGGAGACTCTTAAGTCTTGGATTGTAAAGACATTCAGTGCAGTC 182  
 QY 1433 TCTTACCACTCCCACTTACCTGACAGTATGTCCCAAGACCTACCACTGATGAT 1492  
 DB 183 CCTTACCACTCCCACTTACCTGACAGTATGTCCCAAGACCTACCACTGATGAT 242  
 QY 1493 TATTCCTGATGTGAGCTAGACTGAGCTTGTGATGTATCAAAAGTCCCTTA 1552  
 DB 243 TATTCCTGATGTGAGCTAGACTGAGCTTGTGATGTATCAAAAGTCCCTTA 302  
 QY 1553 TATACACCACTCCCTAATGCTCTCTCACTCCCTCAGGCTATCTTTCGTGATTC 1612  
 DB 303 TATACACCACTCCCTAATGCTCTCTCTCACTCCCTCAGGCTATCTTTCGTGATTC 362  
 QY 1613 ATCTGACACAGACCAATCAGAAATGTATCTGCTGTGGAAACCTTTATCCCA 1672  
 DB 363 ACTCTGACACAGATTAATCAGAAATGTATCTGCTGTGGAAACCTTTATCCCA 422  
 QY 1673 TAAAGCCCTTCTCTTGTGCTTATCAACAGACAAATAGTT-CTGTTTATGCTTG 1731  
 DB 423 GGAAGCCCTTCTCTTGTGCTTATCAACAGAAATAGGTTCTGTTTATGCTTG 482  
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 DB 483 AAT 486

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 14, 2003, 23:45:56 ; Search time 4626 Seconds  
(without alignments)  
3263.219 Million cell updates/sec

Title: US-10-027-923-2  
Perfect score: 1873  
Sequence: 1 MWLLILSLTLKEDVRGSA.....QPLNLELSSGPITGLDRLL 369

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
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35: em\_hcg\_rod:  
36: em\_hcg\_mam:  
37: em\_hcg\_vrt:  
38: em\_sy:  
39: em\_hcgo\_hum:  
40: em\_hcgo\_mus:  
41: em\_hcgo\_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1873	100.0	1110	6 AX709349	AX709349 Sequence
2	1873	100.0	1823	6 AX709347	AX709347 Sequence
3	1870	99.8	2172	6 AX068372	AX068372 Sequence
4	1830.5	97.7	2349	6 AX068368	AX068368 Sequence
5	1794	95.8	2149	6 AX068374	AX068374 Sequence
6	1780	95.0	2551	6 AX068366	AX068366 Sequence
7	1754.5	93.7	2326	6 AX068370	AX068370 Sequence
8	1648	88.0	2064	6 AX068376	AX068376 Sequence
9	1608.5	85.9	2241	6 AX068371	AX068371 Sequence
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13	1484.5	79.3	4303	6 AR145366	AR145366 Sequence
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15	1484.5	79.3	4518	6 AX548892	AX548892 Sequence
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18	1470.5	78.5	3282	6 AR038828	AR038828 Sequence
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RESULT 1

## ALIGNMENTS



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 LOCUS AX709349 1110 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 3 from Patent WO02070708.  
 ACCESSION AX709349  
 VERSION AX709349.1 GI:29564891  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
 Glutamate receptor modulatory proteins and nucleic acids encoding them  
 JOURNAL Patent: WO 02070708-A 3 12-SEP-2002;  
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 Score: 1873.00 Matches: 369  
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 Gaps: 0  
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 LOCUS AX709347 1823 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 1 from Patent WO02070708.  
 ACCESSION AX709347  
 VERSION AX709347.1 GI:29564889  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.E.  
 Glutamate receptor modulatory proteins and nucleic acids encoding them  
 JOURNAL Patent: WO 02070708-A 1 12-SEP-2002;  
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Best Local Similarity: 100.00%      Mismatches: 0
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DEFINITION      AX068372
ACCESSION      AX068372
VERSION      AX068372.1 GI:12578537
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 Schwarz, D.A. and Maki, R.A.
AUTHORS      Metabotropic glutamate receptors and methods of use therefor
TITLES      Patent: WO 0102566-A 7 11-JAN-2001;
JOURNAL      Neurocrine Biosciences, Inc. (US)
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Percent Similarity: 100.00%      Conservative: 1
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Qy      101 HisSerAlaValAlaLeuGluGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120
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DEFINITION Sequence 3 from Patent WO0102566.
ACCESSION  AX068368
VERSION     AX068368.1  GI:12578534
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS   Schwarz,D.A. and Maki,R.A.
TITLE      Metabotropic glutamate receptors and methods of use therefor
JOURNAL    Patent: WO 0102566-A 3 11-JAN-2001;
           Neurocrine Biosciences, Inc. (US)
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Best Local Similarity: 85.98%      Mismatches: 0
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DB:          Gaps:      1

US-10-027-923-2 (1-369) x AX068368 (1-2349)
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Qy      41 PheSerValHisIleGlnProThrValAspGluValHisGluLysArgCysGlyValAla 60
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Db      725 GAAGAGAAAGAGGCTTGGCTGTGCTGTGCTGTGAGATGGCTCTCTCTCTCCGCTCAAG 784
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Qy      201 SerMetValAspIleValIleValArgTyrAsnIleThrTyrValSerAlaValIleThrGlu 220
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QY	Db	262	LYLybLeuThrSerIbLeuPbLYbAlaArgValValAlaTYrPheCysGtGtYmet	281
QY	Db	1325	AAAGAGTCAACAGTCACTTGCCCAAGGCCGGGGTGGTGGCCCTACTTGTGTAAGGCATG	138
QY	Db	282	ThrValArgSgLYleuLeuMetAlaMetArgArgLYleuValGtYglUphLeuLeu	301
QY	Db	1385	ACGGTAGAGGTCTGCTGATGGCAAGAGCGCTGGGCTGTAGTGGAGAAATTTCTGGCT	144
QY	Db	302	LeuGtLYArgGtUProApAlaIlePheIleGtIleSerLYsAsnSerIleUtrGtU	321
QY	Db	1445	CTGGGCAAGGAAACCAATGCCATCTTTATTTGAGATCTCAAAACACGATCTTAAGGAA	1504
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QY	Db	1505	GACAGAGAAATATCCCAAGGTGCTCTTCAAGGGTGTGGAGACATTTTACACAGAAGT	1564
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LOCUS	AX068374	2149 bp	DNA	linear
DEFINITION	Sequence 9 from Patent WO0102566.			PAT 25-JAN-2001
ACCESSION	AX068374			
VERSION	AX068374.1	GI:12578538		
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE				
AUTHORS	Schwarz, D.A. and Maki, R.A.			
TITLE	Metabotropic glutamate receptors and methods of use therefor.			
JOURNAL	Patent: WO 0102566-A 9 11-JAN-2001;			
	Neurocrine Biosciences, Inc. (US)			
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Sequence 1 from Patent WO0102566.
AX068366
VERSION AX068366.1 GI:12578533
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ORGANISM Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Schwarz, D.A. and Maki, R.A.
  Metabotropic glutamate receptors and methods of use therefor
  Patent: WO 0102566-A 11-JAN-2001;
  Neurocrine Biosciences, Inc. (US)
  location/Qualifiers
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AX068370
VERSION AX068370.1 GI:12578535
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 Schwarz, D.A. and Makl, R.A.  
 Metabotropic glutamate receptors and methods of use therefor  
 Patent: WO 0102566-A 5 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)  
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 ACCESSION AX068376  
 VERSION AX068376.1 GI:12578539  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 Schwarz, D.A. and Makl, R.A.  
 Metabotropic glutamate receptors and methods of use therefor  
 Patent: WO 0102566-A 11 11-JAN-2001;  
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 DB 1025 GGTTCAAGCTATTTCATGCTCAGCCTCCAGAGAGCTAGGCTGCTTCAACTTTGG 1084  
 QY 220 ----- 220  
 DB 1085 CCTCAAGTATCTGCTGCTTTGGCCTTCCAAATTGCTGGATTATGGGCAATGAGCCACC 1144  
 QY 221 -----Gly 221  
 DB 1145 ACAGCAACCGGCGCAGTGGCCGATCTTAGAACACTGTTGAGGTGCTTTCTGATTTTAAAGC 1204  
 QY 222 AenTyrGlyGluSerGlyMetGlyAlaPheLysAspMetSerAlaLysGlyGlyIleCys 241  
 DB 1205 AACTATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAAGCAAGAGGAGATTGTC 1264  
 QY 242 IleAlaHisSerTyrLysIleTyrSerAspAlaGlyGluGlnSerPheAspLysLeu 261  
 DB 1265 ATGCGCCACTCTTACAAATCTACAGTATGACAGGAGGAGAGCTTTGATTAAGCTGCTG 1324  
 QY 262 LysLysLeuThrSerHisLeuProLysAlaArgValAlaIleTyrPheCysGluGlyMet 281  
 DB 1325 AAGAAGCTACAAAGTCACTTGCCCAAGGCGCGGTGGTGGCTTCTGTGTGAGGGCAGT 1384  
 QY 282 ThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyIlePheLeu 301  
 DB 1385 ACGGTAGAGGTCTGTGATGAGGCGCATGAGGCGCTGCTGCTAGTGGAGAAATTTGCTT 1444  
 QY 302 LeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyrGlu 321  
 DB 1445 CTGGGC----- 1450  
 QY 322 AspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArgSer 341  
 DB 1451 -----AspArg 1456  
 QY 342 GluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGlyProIle 361  
 DB 1457 GAGTCCGTGCTGCTGCACATGCCCCAGCCTCTGAATCTAGAGCTCAGTTCAAGGGCCATC 1516  
 QY 362 ThrGlyLeuArgAspArgLeuIle 369  
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 AR270570 4078 bp DNA linear PART 10-APR-2003  
 LOCUS AR270570 Sequence 1133 from patent US 6500938.  
 DEFINITION AR270570  
 ACCESSION AR270570.1 GI:29701804  
 VERSION AR270570.1  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 4078)  
 AUTHORS Au-Young,J. and Seilhamer,J.J.  
 TITLE Composition for the detection of signaling pathway gene expression  
 JOURNAL Patent: US 6500938-A 1133 31-DEC-2002;  
 FEATURES Location/Qualifiers  
 source 1..4078  
 BASE COUNT 994 a 1074 c 1076 g 934 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 1,01e-134 Length: 4078  
 Score: 1484.50 Matches: 306  
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 Best Local Similarity: 85.00% Indels: 22  
 Query Match: 79.26% Gaps: 2  
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US-10-027-923-2 (1-369) x AR270570 (1-4078)

QY 1 MetValLeuLeuLeuIleLeuSerValLeuLeuLeuLysGluAspValArgLysSerAla 20  
 DB 151 ATGCTCTTCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTG 210  
 QY 21 GlnSerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 211 CAGTCCAGAGAGAGAGGGGTGGTGGTGCATCATCCGGGTGACATCTTAATGAGCTCTC 270  
 QY 41 PheSerValHisGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60  
 DB 271 TTTTCTTCTCATCACAGCCTTACTGTGACAAAGTTCAAGAGAGAGTGGGGCGGTC 330  
 QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgLys 80  
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 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
 DB 391 TCAGACCCCACTCTTGCCCAACATCACATCGGGCTGTGAGATTAAGGAGCTCCTGCTG 450  
 QY 101 HisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
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 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerLys 140  
 DB 511 GAAGAGAAAGAGGCTTGGTACGCTGTGTGATGGTCCCTCTTCTCTCCCTCCAG 570  
 QY 141 LysProIleValGlyValIleGlyProGlyLysSerSerSerLeuAlaIleGlnValGlnAsn 160  
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 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 DB 631 TTGCTCAGCTTTTCAACATCACTCAGATTGCTACTCAGCAACGACAGATCTGAGT 690  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValIleProSerAspAlaGlnIleAlaArg 200  
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 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
 DB 1051 CTTTGGGAGTATGATGC-----TGG 1071

QY 321 GUAAPARGARGYSCYS-GLNGLYARGPHELEUGLNGLYPHEGLYASPILEUHTISAR 340  
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 DB 1102 CACGAGAGCTGTTGGTGGCATCACATCAAGCTCCATCTCCCATGTCAGTGGT 1159  
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 LOCUS Sequence 1 from patent US 6211353.  
 DEFINITION ARI45364  
 ACCESSION ARI45364 GI:15107231  
 VERSION ARI45364.1 GI:15107231  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4207)  
 AUTHORS Burnett,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
 TITLE Isolated nucleic acid encoding a human mglurs  
 JOURNAL Patent: US 6211353-A 1 03-APR-2001;  
 FEATURES location/Qualifiers  
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 BASE COUNT 1011 a 1120 c 1112 g 964 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.06e-134 Length: 4207  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
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 US-10-027-923-2 (1-369) x ARI45364 (1-4207)

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 QY 181 ASPLYSTHLEUPHELYSTYRPHMETARGVALAIPROSERASPLAINGINALAARG 200  
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 DB 1060 GCCATGTGACATTAATGAAAGAGTACACTGACCTTAATGATACACCGCTGCACACGAA 1119  
 QY 221 GLYASNTYRGJLYUUSERGJLYMETGUALAPHELYASPMESERALALYSGLUGLYLE 240  
 DB 1120 GGCACCTAAGGAGAAAGTGGATGGAAGCCTTCAAGATATATGTCAGCAGGAAGGAGATT 1179  
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 QY 281 METTHRVALARGJLYLEUHEUETALAMETARGARGLEUGLYLEUVALGLYUHPHELEU 300  
 DB 1300 ATGACGCTGAGAGCTCTGCTGATGCGCATGAGGCGCTGGCTTACCGGAGAAATTTCTG 1359  
 QY 301 LEULEUGLYARGGLUPROBAPALALIEPHELLLEGLULSERLYASNSERILLEUTTP 320  
 DB 1360 CTTCTGGGACAGTATGCG-----TGG 1380  
 QY 321 GUAAPARGARGYSCYS-GLNGLYARGPHELEUGLNGLYPHEGLYASPILEUHTISAR 340  
 DB 1381 GCTGACAGGATGATGTGACAG-----ATGATAT 1410  
 QY 340 GSERGJUSERVALLEUHTISMETPCROGINPROLEUASNULEUGLUSEUSERGJLY 359  
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 RESULT 12  
 ARI45365 4207 bp DNA linear PAT 08-AUG-2001  
 LOCUS Sequence 3 from patent US 6211353.  
 DEFINITION ARI45365  
 ACCESSION ARI45365 GI:15107232  
 VERSION ARI45365.1 GI:15107232  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 4207)  
 AUTHORS Burnett,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
 TITLE Isolated nucleic acid encoding a human mglurs  
 JOURNAL Patent: US 6211353-A 3 03-APR-2001;  
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 US-10-027-923-2 (1-369) x ARI45365 (1-4207)

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VERSION	ARI45366.1
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SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified, 1 (bases 1 to 4303)
AUTHORS	Burnett,J.Paul., Jr., Mayne,N.Gall., Sharp,R.Leon., and Shnyder,Y.Marie. Isolated nucleic acid encoding a human mglURS Patent: US 6211353-A 4 03-APR-2001; Location/Qualifiers 1..4303
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Db	520 CAGTCAGTAGAGAGAGGAGGTGGTGCCTCACACCAGGAGATCATTAATTTAGAGCTTC 575
QY	41 PheSerValHisHisGlnProThrValAspGluValHisGluArgLysCysGlyAlaVal 60
Db	580 TTTCTGTTCATCCACCGCTTACTGTGGACAAGATTCAAGAGAACTGGGGCCGTC 639
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QY	81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100
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Db	760 CATTCGGCTGTGGCCTTAAGCAGAGCAATGATGTCATAAAGATTCCTCATTTCTTCA 819
QY	121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140
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QY	141 LysProGlyValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160
Db	880 AACCCATATGATGGGCTCATTTGGGCTGGCTCCAGTTCCTATACCAATTCAGGCTCCAGAT 939
QY	161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaIleSerAlaThrIleMetAspLeuSer 180
Db	940 TTGCTCCAGCTTTCAACATACCTCAAGTTCCTTACTACCAACCAAGCATGGATCTAGAT 999
QY	181 AspLysThrLeuPheLysTrpPheMetArgValValProSerAspAlaGlnGlnAlaArg 200
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 Db 151 ATGGTCTCTGTGATCTCTGTCAGTCTTATGAAGAAGATGCGGGAGTGCA 210  
 QY 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 Db 211 CAGTCAGTAGAGAGAGGGGTGGGCTCAATCCGGGTGACATCTTATGGAGCTCTC 270  
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 Db 271 TTTTCTGTTCAATCAGCAGCTACTGTGCAAAAGTTCAATGAGAGAAATGTGGGCGGTC 330  
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 Db 331 CGTGAACAGATGAGCATTCAGAGAGTGAGGCCATGCTGCATACCTGGAAGAAGATCAAT 390  
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 Db 631 TTGCTCAGCTTTTCAACATTACTCAGATTGCTTACTCAGCAACAGCATGTGATCGAG 690  
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 Db 691 GACMAAGACTGTTCAAAATATTTCATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG 750  
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 Db 751 GCCATGTGACATAGTAGAGAGGTACACTGACCTATGTATCAGCCGTGCACACAGAA 810  
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Db 931 CTGAAGAACTCACAAGTCACTTGGCCCAAGGCCGGGGTGTGGCTGTCTTCTGTGAGGCG 990  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1484.5	79.3	4078	4	US-09-016-434-1133
4	1484.5	79.3	4207	3	US-08-660-148-1
5	1484.5	79.3	4207	3	US-08-660-148-3
6	1484.5	79.3	4303	3	US-08-660-148-4
7	1484.5	79.3	4303	3	US-08-660-148-6
8	1470.5	78.5	3282	1	US-08-072-574-11
9	1470.5	78.5	3282	1	US-08-486-270-11
10	1470.5	78.5	3282	3	US-08-367-264-11
11	1470.5	78.5	3282	4	US-09-153-757-11
12	1470.5	78.5	3282	4	US-09-459-715-11

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36	1117.5	59.7	4300	1	US-08-463-642-1	Sequence 1, Appl1
37	1117.5	59.7	4300	1	US-08-455-602-1	Sequence 1, Appl1
38	1117.5	59.7	4300	2	US-08-465-157-1	Sequence 1, Appl1
39	1117.5	59.7	4300	5	PCT-US91-09422-1	Sequence 1, Appl1
40	1117.5	59.7	5336	5	PCT-US91-09422-16	Sequence 16, Appl1
41	1061.5	56.7	3330	1	US-08-072-574-1	Sequence 1, Appl1
42	548	29.3	2724	3	US-08-823-110-5	Sequence 5, Appl1
43	548	29.3	2724	3	US-08-604-298-5	Sequence 5, Appl1
44	548	29.3	3321	3	US-08-855-146-1	Sequence 1, Appl1
45	548	29.3	3321	3	US-08-855-146-3	Sequence 3, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-695-481-1  
/ Sequence 1, Application US/09695481  
/ Patent No. 6534287  
/ GENERAL INFORMATION:  
/ APPLICANT: STORMAN, THOMAS M.  
/ APPLICANT: LEVINTHAL, CYNTHIA  
/ APPLICANT: STOROHAN, LAURA  
/ APPLICANT: HAMMERLAND, LANCE G.  
/ APPLICANT: KRAPCHO, KAREN J.  
/ APPLICANT: NPS PHARMACEUTICALS, INC.  
/ TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
/ FILE REFERENCE: 1094.2.6  
/ CURRENT APPLICATION NUMBER: US/09/695,481  
/ PRIOR FILING DATE: 2000-10-24  
/ PRIOR APPLICATION NUMBER: 60/161,481  
/ PRIOR FILING DATE: 1999-10-25  
/ NUMBER OF SEQ ID NOS: 7  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 1  
/ LENGTH: 2826  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ NAME/KEY: CDS  
/ LOCATION: (1)..(2826)  
/ US-09-695-481-1

#### Alignment Scores:

Pred. No.: 5,35e-175  
Score: 1484.50  
Percent Similarity: 87.22%  
Best Local Similarity: 85.00%  
Query Match: 79.26%  
Gaps: 4  
Length: 2826  
Matches: 306  
Conservative: 8  
Mismatch: 22  
Indels: 24  
Gaps: 2





QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 Db 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACGACGATGATGAGT 540  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 Db 541 GACAAAGACTCTGTTCAATATTTTCATGAGAGGTTGTGCTTCAATGATGTCAGCGAAG 600  
 QY 201 SerMetValAspIleValLysArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 Db 601 GCATGTGTGACATTAAGTGAAGAGTCACTGACCTATGATACAGCCGTGCACACAGAA 660  
 QY 221 GlyAsnTyrGlyLysSerGlyMetGluAlaPheLysAspMetSerAlaLysGlnGlyLe 240  
 Db 661 GGCACATATGAGAAAGTGGAGTGAAGCCTTCAAGATATGTCAAGCAAGAAAGGAT 720  
 QY 241 CysIleAlaHisSerTyrLysIleTyrSerAsnAlaGlyGlnGlnSerPheAspLysLeu 260  
 Db 721 TGCATGCCCACTCTTACAAATCTACAGTAATGACAGGAGAGAGCTTGTATAGCTG 780  
 QY 261 LeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaAlaTyrPheCysGlyGly 280  
 Db 781 CTGAAGAAGCTCAAGTCACTTGCCCAAGCCCGGGTGGCTGCTTCTGTGAGGCG 840  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgLysGlnGlyLeuValGlyGlnPheLeu 300  
 Db 841 ATACAGGTGAGAGGTCTGCTGATGAGCCATAGCGCTGAGCTTACGCGAAGATTTCTG 900  
 QY 301 LeuLeuGlyArgGlnProAspAlaIlePheIleGlnLysSerLysAsnSerIleLeuTrp 320  
 Db 901 CTTCTGGCGCATATGCG-----TGG 921  
 QY 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 Db 922 GCTGACAGGATGATGATGACAG-----ATGATAT 951  
 QY 340 GSerGlySerValLeuLeuHisMetProGlnProLeuAsnLeuGlnLeuSerGly 359  
 Db 952 CAGCGAAGACTGTGTGGCATCAATCAATCAAGCTCCCAATCTCCGATGCAAGTGT 1009  
 Db  
 RESULT 3  
 US-09-016-434-1133  
 ; Sequence 1133 Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Sellhammer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016.434  
 ; FILING DATE: HEREMITH  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1133:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4078 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: 91408051  
 ; US-09-016-434-1133  
 ;  
 ; Alignment Scores:  
 ; Pred. No.: 9,8e-175 Length: 4078  
 ; Score: 1484.50 Matches: 306  
 ; Percent Similarity: 87.22% Conservative: 8  
 ; Best Local Similarity: 85.00% Mismatches: 22  
 ; Query Match: 79.26% Indels: 24  
 ; Gaps: 2  
 ; US-10-027-923-2 (1-369) x US-09-016-434-1133 (1-4078)  
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 QY 1 MetValLeuLeuLeuLeuLeuSerValLeuLeuLeuLysGlnAspValArgGlySerAla 20  
 Db 151 ATGTGCTTCTGTGTATCTGTGATCTGATCTTAATTTGAAAGAAATATCCGTGGAGTGC 210  
 QY 21 GlnSerSerGluArgArgValAlaAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 Db 211 CAGTCCAGTGAAGAGAGGTGTGTGCTCAATCCGGGTGACATCTTATGAGCTCTC 270  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGlnLysArgGlyAlaVal 60  
 Db 271 TTTTCTGTTCAATCAGCAGCTACTGTGCAAAAGTTCAATGAGGAAGTGTGGCGGTC 330  
 QY 61 ArgGlnGlnTyrGlyLysIleGlnArgValGlnAlaMetLeuHisThrLeuGlnLysIleAsn 80  
 Db 331 CGTGAACAGTATGCGCATTCAGAGAGTGAAGCCATGCTCATCCCTGGAAAGATCAAT 390  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGlnLysLeuArgAspSerCysTrp 100  
 Db 391 TCAACCCCACTCTTCCCAATCAATCAATCGGCTGTGAGTAAGGACTCTGCTGG 450  
 QY 101 HisSerAlaValAlaLeuGlnSerIleGlnPheIleArgAspSerLeuIleSerSer 120  
 Db 451 CATTGGCTGTGGCCCTTAGAGGAGGACATTTGATTCAAGATTCCTCATTTCTTCA 510  
 QY 121 GlnGlnGlnGlnGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
 Db 511 GAAGAGAAAGAGGCTTGTAACCTGTGTGAAGGTCTCTCTCTTCCCTCCAG 570  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValAsn 160  
 Db 571 AAGCCCATGATAGGGGTCATTTGGCTGCTCAGTTCTGTACCAATTCAGTCCAGAT 630  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
 Db 631 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTATCAGCAACGACATGATGATGAGT 690  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArg 200  
 Db 691 GACAAAGACTCTGTTCAATATTTTCATGAGAGGTTGTGCTTCAATGATGTCAGCGAAG 750  
 QY 201 SerMetValAspIleValLysArgTyrAsnTrpThrTyrValSerAlaValHisThrGlu 220  
 Db 751 GCCATGTGTGACATTAAGTGAAGAGTCACTGACCTATGATACCCGTGCACACAGAA 810  
 QY 221 GlyAsnTyrGlyLysSerGlyMetGluAlaPheLysAspMetSerAlaLysGlnGlyLe 240  
 Db 811 GGCACATATGAGAAAGTGGAGTGAAGCCTTCAAGATATGTCAAGCAAGAAAGGAT 870

QY 241 CyeIIleAlaHisSerTyrIleTyrSerAsnAlaGluGlnSerPheAspLeu 260.  
 DB 871 TGCATGCCCACTTTCAAAATCTACAGTATCAGGAGGAGAGCTTTGATTAAGCTG 930  
 QY 261 LeuIleValSerThrSerHisLeuProIleValAlaArgValAlaTyrPheCysGluGly 280  
 DB 931 CTGAAGAAGCTCAACAATCTCACTTCCCAAGGCCGGGGTGGCTGCTCTGTAAGGCGC 990  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 991 ATGACGGTGAAGAGTCTGCTGATGGCCATGAGGCGCTGGCTCAAGCGGAGAAATTTCTG 1050  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTyr 320  
 DB 1051 CTCTGGGCACTATGAGC-----TGG 1071  
 QY 321 GluAspArgArgIleCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
 DB 1072 GCTGACAGTATGATGTGACAG-----ATGATAT 1101  
 QY 340 gSergIleValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
 DB 1102 CAGGAGAACTGTGTGGCATCAACAATCAAGCTCCAAATCTCCGATGTCAAGTGTG 1159  
 RESULT 4  
 US-08-660-148-1  
 / Sequence 1, Application US/08660148  
 / Patent No. 6211353  
 / GENERAL INFORMATION:  
 / APPLICANT: Burnette, J. P.  
 / APPLICANT: Mayne, Nancy G.  
 / APPLICANT: Sharp, Robert L.  
 / APPLICANT: Snyder, Yvonne M.  
 / TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
 / NUMBER OF SEQUENCES: 6  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSER: Eli Lilly and Company  
 / STREET: Lilly Corporate Center  
 / CITY: Indianapolis  
 / STATE: Indiana  
 / COUNTRY: United States of America  
 / ZIP: 46285  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/660,148  
 / FILING DATE:  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/282,853  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Gaylo, Paul J.  
 / REGISTRATION NUMBER: 36,808  
 / REFERENCE/DOCKET NUMBER: X-9419  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (317) 276-0756  
 / TELEFAX: (317) 276-3861  
 / INFORMATION FOR SEQ ID NO: 1:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4207 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: 460..3999

US-08-660-148-1  
 Alignment Scores:  
 Pred. No.: 1,03e-174 Length: 4207  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: 3 Gaps: 2  
 US-10-027-923-2 (1-369) x US-08-660-148-1 (1-4207)  
 QY 1 MetValLeuLeuLeuIleLeuSerValIleuLeuLeuGlyLeuValArgGlySerAla 20  
 DB 460 ATGGTCTTCTGTGATTCCTGTGATCTTACTTTTAAAGAAGATTCCTGGAGATGCA 519  
 QY 21 GlnSerSerGluArgArgValAlaHisMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 520 CAGTCCAGTGAAGAGAGGGTGGCTGCATGCCCGGTGACATCTATATTGAGGCTCTC 579  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgIleCysGlyAlaVal 60  
 DB 580 TTTTCTGTTCATCACAGCCTTACTGTGACAAAGTTCATGAGAGAGTGTGGGGGCTC 639  
 QY 61 ArgGluGlnIleGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
 DB 640 CGTGAACAGTATGGCATTCAGAGAGTGAAGGCCATCTCCATACCTCGAAGAGATCAAT 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
 DB 700 TCAGACCCCACTCTTGGCCAAACATCACATGGGCTGAGATTAAGGAGATCTCTGCTG 759  
 QY 101 HisSerAlaValAlaLeuGlnIleSerIleGluPheIleArgAspSerIleSerSer 120  
 DB 760 CATTGCGCTGTGGCCCTTAAGCAGAGCATTTGATTAAAGATTCCTCATTTCTTCA 819  
 QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerPheArgSerIle 140  
 DB 820 GAAGAGAGAGAGGCTTGGTACCGTGTGTGATGGCTCTCTCTTCCCTCCGCTCAAG 879  
 QY 141 LysProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
 DB 880 AAGCCCATGATGAGGGGTCAATGGGCTGCGCTCAGATTCTGAGCCATTACAGTCCAGAA 939  
 QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleThrAspLeuSer 180  
 DB 940 TTGCTCAGCTTTTCAACATACCTCAAGATTGCTTACTGCAACCAAGCATGATCTGAG 999  
 QY 181 AspLysThrLeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnIleAsnArg 200  
 DB 1000 GACAAACTCTGTCAAAATATTTCATGAGGCTTGGCTTCAAGATGCTCAGCAGCGCAAG 1059  
 QY 201 SerMetValAspIleValIleValArgTyrAsnTyrThrTyrValSerAlaValHisThrGlu 220  
 DB 1060 GCCATGTGACATGATGTAAGAGGTACCACTGACCTATGATACGCTTGACACAGAA 1119  
 QY 221 GlyAsnTyrGlyGlnSerIleMetGluAlaPheLysAspMetSerAlaIleGluGlyIle 240  
 DB 1120 GGCACCTATGAGAAAGTGGAGTGAAGGCTTCAAGATATGTCAAGCAAGAGAGGAGATT 1179  
 QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGluGlnIleSerPheAspLysLeu 260  
 DB 1180 TGCATGCCCACTTTCAAAATCTACAGTATGACAGGGAGACAGCTTATATAAGCTG 1239  
 QY 261 LeuIleValSerThrSerHisLeuProIleValAlaArgValAlaIleTyrPheCysGluGly 280  
 DB 1240 CTGAAGAAGCTCAACAATCTCACTTCCCAAGGCCGGGGTGGCTGCTCTGTAAGGCGC 1299  
 QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
 DB 1300 ATGACGGTGAAGAGTCTGCTGATGGCCATGAGGCGCTGGCTTACGCGGAGAAATTTCTG 1359  
 QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerIleAsnSerIleLeuTyr 320



APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: X-9419  
REFERENCE/DOCKET NUMBER: 36,808  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..4095  
US-08-660-148-4

Alignment Scores:  
Pred. No.: 1.07e-174 Length: 4303  
Score: 1484.50 Matches: 306  
Percent Similarity: 87.22% Conservative: 8  
Best Local Similarity: 85.00% Mismatches: 22  
Query Match: 79.26% Indels: 24  
DB: 3 Gaps: 2

US-10-027-923-2 (1-369) x US-08-660-148-4 (1-4303)

QY 1 MetValIeuLeuLeuIleuSerValIeuLeuLeuValAlaArgIleSerAla 20  
DB 460 ATGCTCTTCTGTGATCCCTGACGCTTCTTTGAAAGAAGTGCCTGGAGGCA 519  
QY 21 GluSerSerGluArgValAlaAlaHisMetLeuGluAspIleIleIleGlyAlaLeu 40  
DB 520 CAGTCCAGTAGAGGAGGGGTGGCTGCACATGCCGGGTACATCATTTAGAGCTCTC 579  
QY 41 PhsSerValHisIleGlnProThrValAspGluValHisGluArgValGlyAlaVal 60  
DB 580 TTTTCGTATATACCAAGCTTACTGTGACAAAGTTATATAGAGAAAGTGTGGGCGGTC 639  
QY 61 ArgGluGlnTyrGlyIleGlnArgValGluAlaMetLeuHisThrLeuGluArgIleAsn 80  
DB 640 CGTGAACAGATGGCATTCAGAGAGTGGAGCCATGCTGATCCCTCGAAGAGATCAAT 639  
QY 81 SerAspProThrIeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTyr 100  
DB 700 TCAGACCCCACTCTTGCCCAATCATCACTGGGCTGTGATGATTAAGGAGACTCCTGCTGG 759

QY 101 HisSerAlaValAlaIeuGluInserIleGluPheIleArgAspSerIleIleSerSer 120  
DB 760 CATTGGCTGTGGCCCTTAGAGAGAGCATTTAGATTCATTAAGATTCCTCATTTCTTCA 819  
QY 121 GluGluGluGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140  
DB 820 GAAGAGAAAGAGCTTGGTACCTGTGATGGCTGCTCTCTTCTCCCTCCAG 879  
QY 141 LysProIleValIleGlyValIleGlyProGlySerSerSerSerIleuAlaIleGlnValGlnAsn 160  
DB 880 AACCCCATAGTAGGGGTGATTTGGCCCTGCTCAGTTCTGATCCATTCAGGTCCGAAT 939  
QY 161 LeuLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIleMetAspLeuSer 180  
DB 940 TTGCTCAGCTTTTCAACACTGATGCTTACTTACAGCAACAGCATGATGTGAGT 999  
QY 181 AspLysThrIeuPheLysTyrPheMetArgValAlaProSerAspAlaGlnAlaArg 200  
DB 1000 GACAAGACTGTCTCAAAATATTCATGAGGGTGTGCTTCAGATGCTCAGCAGGCAAG 1059  
QY 201 SerMetValAspIleValIleValysArgTyrAsnTyrThrTyrValSerAlaValHisThrGlu 220  
DB 1060 GCCATGTGACATAGTGAAGAGTACACTGACCTATGTATACGCCGTGCACACAGAA 1119  
QY 221 GlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAspMetSerAlaLysGluGlyIle 240  
DB 1120 GGCACATAGAGAAAGTGGATGGAAGCTTCAAGATATGTACAGCAAGAGGATTT 1179  
QY 241 CysIleAlaHisSerTyrIleTyrSerAsnAlaGlyGluInserPheAspLysLeu 260  
DB 1180 TGCATGCGCCACTTACAAATCTACATAGTACAGGAGGAGCAGACTTGTATAGCTG 1239  
QY 261 LeuLysLysLeuPheSerHisLeuProLysAlaArgValAlaTyrPheCysGluGly 280  
DB 1240 CTGAAGAAGCTCAAGTCACTGCCCAAGGCCCGGGTGGCTGCTTCTGTGAGGC 1299  
QY 281 MetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuValGlyGluPheLeu 300  
DB 1300 ATGACGCTAGAGGTCTGCTGATGCGCATGAGCCGCTGGGTCTTACCGGAGAAATTTCTG 1359  
QY 301 LeuLeuGlyArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTyr 320  
DB 1360 CTTCTGGGCGAGTATGAC-----TGG 1380  
QY 321 GluAspArgArgLysCysGlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisArg 340  
DB 1381 GCTGACAGGTATGATGTGACAG-----ATGATAT 1410  
QY 340 gSerGluSerValIeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerSerGly 359  
DB 1411 CAGCGAAGCTGTGTGTGATCAATCAATCAAGCTCCATCTCCCATGTCAAGTGT 1468

RESULT 7  
US-08-660-148-6  
; Sequence 6, Application US/08660148  
; Patent No. 6211353  
; GENERAL INFORMATION:  
; APPLICANT: Burnette, J. P.  
; APPLICANT: Mayne, Nancy G.  
; APPLICANT: Sharp, Robert L.  
; APPLICANT: Snyder, Yvonne M.  
; TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
; TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/660,148  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/282,853  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gaylo, Paul J.  
 REGISTRATION NUMBER: 36,808  
 REFERENCE/DOCKET NUMBER: X-9419  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 276-0756  
 TELEFAX: (317) 276-3861  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4303 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: mRNA  
 US-08-660-148-6

Alignment Scores:  
 Pred. No.: 1.07e-174 Length: 4303  
 Score: 1484.50 Matches: 306  
 Percent Similarity: 87.22% Conservative: 8  
 Best Local Similarity: 85.00% Mismatches: 22  
 Query Match: 79.26% Indels: 24  
 DB: Gaps: 2

US-10-027-923-2 (1-369) x US-08-660-148-6 (1-4303)

QY 1 MetValLeuLeuLeuLeuSerValLeuLeuLeuLeuGluAspValArgGlySerAla 20  
 DB 460 AUGGUCUCCUUGUGAGUCCUGUCAGUCUUCUUAAGAAAGAGUGCCUGGAGAGUGCA 519  
 QY 21 GlnSerSerGluArgArgValAlaAlaMetLeuGlyAspIleIleIleGlyAlaLeu 40  
 DB 520 CAGUCAGAGAGAGAGGAGGUGGUGGUCUACAUCCCGGUGACAUUUAUGAGCUCUC 579  
 QY 41 PheSerValHisIleGlnProThrValAspGluValHisGluArgGlySerGlyAlaVal 60  
 DB 580 UUUUCUGUACUACAGCCUACUGAGCAAGUUCUUAUGAGAGAGAGUGGCGGUC 639  
 QY 61 ArgGluGlnIleGlnIleGlnArgValGluAlaMetLeuHisThrLeuGluValGluLeu 80  
 DB 640 CGGAAACAGAUUGGCAUUCAGAGAGGAGGCAUUCUGUACCCUGGAAAGAGUCAAU 699  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuGlyCysGluIleArgAspSerCysTrp 100  
 DB 700 UCGAGACCCACACUCCUGCCCAUACACUUGGCUUGAGUAAAGGACUCCUGCUG 759  
 QY 101 HisSerAlaValAlaLeuGlnGlnSerIleGluPheIleArgAspSerLeuIleSerSer 120  
 DB 760 CAUUCGCGUGGCGCCUAGAGAGAGAGAUUGAGUUAAGAUUCCUCAAUUCUUA 819  
 QY 121 GlnGluGlnGlnGlnLeuValCysSerValAspGlySerSerSerPheArgSerGly 140  
 DB 820 GAAGAGAGAGAGAGAGGAGUAGCCUGUGAGUAGGCGCCUCCUCCUCCUCCUCCAG 879  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerLeuAlaIleGlnValGlnAsn 160  
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# RESULT 8

US-08-072-574-11  
 Sequence 11, Application US/08072574  
 Patent No. 5521297  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: I-law, Chen  
 APPLICANT: Portzler, Aaron  
 TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 00719  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/072,574  
 FILING DATE: 19930604  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen B.  
 REGISTRATION NUMBER: 31,192  
 REFERENCE/DOCKET NUMBER: P41 9383  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 213-622-7700  
 TELEFAX: 213-489-4210  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:



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1 LENGTH: 3282 base pairs
2 TYPE: nucleic acid
3 STRANDEDNESS: both
4 TOPOLOGY: both
5 MOLECULE TYPE: cDNA
6 FEATURE:
7 NAME/KEY: CDS
8 LOCATION: 370..3003
9 OTHER INFORMATION: /product= "HUMAN MGUR5C"
10 OTHER INFORMATION: /note= "Variant of MGUR5A with truncated 3' end."
11 US-08-072-574-11
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13 Alignment Scores:
14 Pred. No.: 3,856-173 Length: 3282
15 Score: 1470.50 Matches: 304
16 Percent Similarity: 86.67% Conservative: 8
17 Best Local Similarity: 84.44% Mismatches: 24
18 Query Match: 78.51% Indels: 24
19 DB: 1 Gaps: 2
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38 QY 101 HisSerAlaValAlaLeuGlnGlnSerileGluPheileArgAspSerLeuileSerSer 120
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41 QY 121 GluGluGlnGluGlyLeuValCysSerValAspGlySerSerSerSerPheArgSerLys 140
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45 Db 790 AAGCCCAATAGAGGGGCTCATTTGGGCGCTGCACATTTCTGTAAGCCATTCAAGTCCAGAT 849
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53 QY 201 SerMetValAspIleValileValysArgTyrAsnTrpThrTyrValileSerAlaValHisThrGlu 220
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56 QY 221 GlyAsnTyrGlyGluSerGlyMetGluLysPheLysAspMetSerAlaLysGluGlyLys 240
57 Db 1030 GGCAACTATGTAGAGAAAGTGGATGGACCTCCCAAGATATGTACGACCAAGAGAGGAGATT 1089
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59 QY 241 CysIleIleHisSerTyrLysIleTyrSerAsnIleGlyGluGlnSerPheAspLysLeu 260
60 Db 1090 TGCATGCGCCACTCTTACAAATCTCAAGTATGTACAGGGAGACAGAGCTTTGATTAAGCTG 1149

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6 Db 1270 CTTCTGGGCGCTGATGGC-----TGG 1290
7 Oy 321 GluAspArgArgLysCys-GlnGlyArgPheLeuGlnGlyPheGlyAspIleLeuHisAr 340
8 Db 1291 GCTGACAGGATATGATGTGACAG-----ATGATAT 1320
9 Oy 340 gSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGluLeuSerGly 359
10 Db 1321 CAGCGAAGAGCTGTGTGGTCATCAACAATCAAGCTCCAAATCTCCGATGTCAAGTGT 1378
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12 RESULT 9
13 US-08-486-270-11
14 ; Sequence 11, Application US/08486270
15 ; Patent No. 5807689
16 ; GENERAL INFORMATION:
17 ; APPLICANT: Daggett, Lorrie
18 ; APPLICANT: Ellis, Steven B.
19 ; APPLICANT: Liaw, Chen
20 ; APPLICANT: Pontstler, Aaron
21 ; APPLICANT: Johnson, Edwin C.
22 ; APPLICANT: Hess, Stephen D.
23 ; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
24 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
25 ; NUMBER OF SEQUENCES: 13
26 ; CORRESPONDENCE ADDRESS:
27 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
28 ; STREET: 444 South Flower Street, Suite 2000
29 ; CITY: Los Angeles
30 ; STATE: CA
31 ; COUNTRY: USA
32 ; ZIP: 90071
33 ; COMPUTER READABLE FORM:
34 ; MEDIUM TYPE: Floppy disk
35 ; COMPUTER: IBM PC compatible
36 ; OPERATING SYSTEM: PC-DOS/MS-DOS
37 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
38 ; CURRENT APPLICATION DATA:
39 ; APPLICATION NUMBER: US/08/486,270
40 ; FILING DATE: 02-JUN-1994
41 ; CLASSIFICATION: 435
42 ; PRIOR APPLICATION DATA:
43 ; APPLICATION NUMBER: US 08/072,574
44 ; FILING DATE: 04-JUN-1993
45 ; ATTORNEY/AGENT INFORMATION:
46 ; NAME: Reiter, Stephen E.
47 ; REGISTRATION NUMBER: 31,192
48 ; REFERENCE/DOCKET NUMBER: PP41 9772
49 ; TELECOMMUNICATION INFORMATION:
50 ; TELEPHONE: 619-546-4737
51 ; TELEFAX: 619-546-9392
52 ; INFORMATION FOR SEQ ID NO: 11:
53 ; SEQUENCE CHARACTERISTICS:
54 ; LENGTH: 3282 base pairs
55 ; TYPE: nucleic acid
56 ; STRANDEDNESS: both
57 ; TOPOLOGY: both
58 ; MOLECULE TYPE: cDNA
59 ; FEATURE:
60 ; NAME/KEY: CDS
61 ; LOCATION: 370..3003
62 ; OTHER INFORMATION: /product= "HUMAN MGUR5C"
63 ; OTHER INFORMATION: /note= "Variant of MGUR5A with truncated 3' end."

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US-08-486-270-11

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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US-10-027-923-2 (1-369) x US-08-486-270-11 (1-3282)

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## RESULT 10

US-08-367-264-11

Sequence 11, Application US/08367264

Patent No. 6001581

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Pontler, Aaron

APPLICANT: Johnson, Edwin C.

APPLICANT: Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

## CORRESPONDENCE ADDRESSES:

ADDRESSER: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/367,264

FILING DATE: 02-JUN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/072,574

FILING DATE: 04-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: FPA1 9772

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3282 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 370..3003

OTHER INFORMATION: /product= "HUMAN MGLUR5C"

OTHER INFORMATION: /note= "variant of MGLUR5A with truncated 3' end."

US-08-367-264-11

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1	3,856-173	1470.50	86.67%	78.51%	3282	304	8	24	24	2



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RESULT 12
US-09-459-715-11
; Sequence 11, Application US/09459715
; Patent No. 6485919
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie

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?      Ellis, Steven B.
?      Liaw, Chen
?      Pontbrier, Aaron
?      Johnson, Edwin C.
?      Hess, Stephen D.
?      TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
?      NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
?      NUMBER OF SEQUENCES: 13
?      CORRESPONDENCE ADDRESS:
?      ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
?      STREET: 444 South Flower Street, Suite 2000
?      CITY: Los Angeles
?      STATE: CA
?      COUNTRY: USA
?      ZIP: 90071
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: Floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: PatentIn Release #1.0, Version #1.25
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/09/459,715
?      FILING DATE: 13-Dec-1999
?      CLASSIFICATION: <Unknown>
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: 08/367,264
?      FILING DATE: <Unknown>
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Reiter, Stephen E.
?      REGISTRATION NUMBER: 31,192
?      REFERENCE/DOCKET NUMBER: PP41 9772
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 619-546-4737
?      TELEFAX: 619-546-9392
?      INFORMATION FOR SEQ ID NO: 11:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 3282 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: both
?      TOPOLOGY: both
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 370..3003
?      OTHER INFORMATION: /product= "HUMAN MGLUR5C"
?      /note= "variant of MGLUR5A with truncated 3' end."
?      SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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?      Pred. No.: 3,85e-173
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?      Percent Similarity: 86.67%
?      Best Local Similarity: 84.44%
?      Query Match: 78.51%
?      Gaps: 2
?      US-10-027-923-2 (1-369) x US-09-459-715-11 (1-3282)
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Db      370  ATGTCCTCTTCTGTATCTGTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 429
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Db 970 GCCATGTGACATGAAAGAGTACACCTGAGCTCATGATGATACGCGTGACACAGAA 1029  
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RESULT 13  
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Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Dagegett, Lortie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontelzer, Aaron  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGUR5A"  
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Best Local Similarity: 84.44% Mismatches: 24  
Query Match: 78.51% Indels: 24  
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 ; Patent No. 5807689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Daggett, Lorrie  
 ; APPLICANT: Ellis, Steven B.  
 ; APPLICANT: Liaw, Chen  
 ; APPLICANT: Pontabier, Aaron  
 ; APPLICANT: Johnson, Edwin C.  
 ; APPLICANT: Hees, Stephen D.  
 ; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Pretty, Schroeder, Brueggemann & Clark  
 ; STREET: 444 South Flower Street, Suite 2000  
 ; CITY: Los Angeles  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486,270  
 ; FILING DATE: 02-JUN-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/072,574  
 ; FILING DATE: 04-JUN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Reiter, Stephen E.  
 ; REGISTRATION NUMBER: 31,192  
 ; REFERENCE/DOCKET NUMBER: FP41 9772  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-546-4737  
 ; TELEFAX: 619-546-9392  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4085 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 370..3912  
 ; OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
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 Alignment Scores:  
 Pred. No.: 5,53e-173 Length: 4085  
 Score: 1470.50 Matches: 304  
 Percent Similarity: 86.67% Conservative: 8  
 Best Local Similarity: 84.44% Mismatches: 24  
 Query Match: 78.51% Indels: 24  
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 Db 370 ATGGTCTTCTGTGTATCTGTCTGATGCTTATGGAAGAAAGATATCCGTGGAGGTGCA 429  
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; Patent No. 6001581  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontabler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hees, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/367,264  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 4085 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 370..3912  
; OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-367-264-7  
Alignment Scores:  
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Score: 1470.50 Matches: 304  
Percent Similarity: 86.67% Conservative: 8  
Best Local Similarity: 84.44% Mismatches: 24  
Query Match: 78.51% Indels: 24  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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20	505	27.0	4209	11 AK053447	AK053447 Mus muscu
21	499	26.6	1065	29 CNG05504	AL352309 Tetradon
22	499	26.6	1238	11 AK020963	AK020963 Mus muscu
23	491	26.2	722	28 A2815421	A2815421 ZMO083H07
24	480.5	25.7	744	29 CNG03KCA	AL247981 Tetradon
25	475	25.4	664	12 B1862234	B1862234 603075928
26	433.5	23.1	392	14 T78107	T78107 YC98a01.r1
27	429	22.9	515	13 BX280403	BX280403 BX280403
28	426.5	22.8	664	14 CD355039	CD355039 UT-M-GMO-
29	391	20.9	916	13 BX410048	BX410048 BX410048
30	390	20.8	657	28 B2164680	B2164680 CH230-388
31	372.5	19.9	485	9 AL134272	AL134272 DKF2P547H
32	362	19.3	681	29 CNG0300B	AL221636 Tetradon
33	360	19.2	770	13 BU283975	BU283975 603864890
34	352	18.8	532	29 B2930457	B2930457 CH240_36M
35	348	18.6	600	14 CA526444	CA526444 8012-19 M
36	340.5	18.2	978	29 CNG0300A	AL221635 Tetradon
37	336	17.9	673	28 B2101647	B2101647 CH230-236
38	333	17.8	589	29 BX191055	BX191055 Danio rer
39	325.5	17.4	608	12 BM701852	BM701852 UT-B-CQ1-
40	318.5	17.0	455	12 B1514260	B1514260 B160014B
41	317.5	17.0	2299	11 AK030224	AK030224 Mus muscu
42	312	16.7	2262	11 AK029734	AK029734 Mus muscu
43	311	16.6	703	10 BB357072	BB357072 BB357072
44	301.5	16.1	902	29 CNG04KXY	AL295243 Tetradon
45	295	15.8	934	13 BU912251	BU912251 AGENCOURT

#### ALIGNMENTS

RESULT 1  
LOCUS BC031602  
DEFINITION Homo sapiens, clone IMAGE:5167902, mRNA.  
ACCESSION BC031602  
VERSION BC031602.1 GI:21594893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 1297)  
Strausberg, R.



## ORIGIN

## Alignment Scores:

Pred. No.:	1,52e-91	Length:	519
Score:	872.00	Matches:	169
Percent Similarity:	99.41%	Conservative:	0
Best Local Similarity:	99.41%	Mismatches:	1
Query Match:	46.56%	Indels:	0
DB:	10	Gaps:	0

US-10-027-923-2 (1-369) x BE674422 (1-519)

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QY 163 GlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMetAspLeuSerAspLys 182
DB 10 CAGCTTTCAACACTACTCATATGCTTACTCAGCAACATCATGATTCGATGCAAG 69
QY 183 ThrLeuPheLysTyRheMetArgValIalProSerAspAlaGlnGlnAlaArgSerMet 202
DB 70 ACTCTGTCAAATATTTCAATGAGGTTGTGCTTCAGATCTCAGCAGGCAAGTCCATG 129
QY 203 ValAspIleValIleArgTyRThrTyRValIleSerAlaValIleThrGluGluAan 222
DB 130 GTGAGACATAGTGAAGAGTACCACTGACCTATGTATCAGCCCTACACACAGAGGCAC 189
QY 223 TYRGIYGLuSerGIYMetGluAlaPheLysAspMetSerAlaLysGluGluIleCysIle 242
DB 190 TATGGAGAAAGTGGATGGAGGCTTCAGAGATATGTCAAGCAAGAGGAGATTGCAATC 249
QY 243 AlaIleSerTyRLeuIleTyRSerAsnAlaGluGluGlnSerPheAspLysLeuLeuLys 262
DB 250 GCCCACTTTACAAATATCTACAGTAATGACGAGGAGACAGCTTTGATTAAGCTGCAAG 309
QY 263 LysLeuThrSerHisLeuProLysAlaArgValIalAlaTyRheCysGluGluMetThr 282
DB 310 AAGCTCAACAGTCACTTCCCAAGGCCCGGCTGTGCTTCTGTGAGGCGCATAGACG 369
QY 283 ValArgGIYLeuLeuMetAlaMetArgArgLeuGIYLeuValGIYGluPheLeuLeu 302
DB 370 GTGAGAGGCTGTGCTGATGCGCATGAGGCGGCTTGGCTTACTGGAGAAATTTCTGCTTCG 429
QY 303 GIYArgGluProAspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrpGluAap 322
DB 430 GGAAGGGAACCAAGATGCCATCTTTATTTGAGATCTCAAGAAAGACGATCCATGGAAGAC 489
QY 323 ArgArgLysCysGlnGluArgPheLeuGln 332
DB 490 AGAAGAAATGCGCAAGTCCCTTCCTTCAG 519

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RESULT 3  
BE67477 499 bp mRNA linear EST 27-JUL-2000  
LOCUS h266d08.x1 NCI CGAP Lu24 Homo sapiens CDNA IMAGE:3212943 3,  
DEFINITION similar to SW-MGR5 HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECURSOR: ; mRNA sequence.  
ACCESSION BE67477 GI:9513252  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapdb-remail.nih.gov  
Tissue Procurement: Christopher Moskajuk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: -40UP from Gibco  
High quality sequence stop: 493.  
Location/Qualifiers

## FEATURES

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/clone\_idb="NCI CGAP Lu24"  
/note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and 88 clones were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 107 c 138 g 113 t

## Alignment Scores:

Pred. No.:	4.11e-89	Length:	499
Score:	851.00	Matches:	165
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.44%	Indels:	0
DB:	10	Gaps:	0

US-10-027-923-2 (1-369) x BE67477 (1-499)

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QY 167 IleProGlnIleAlaTySerAlaThrIleMetAspLeuSerAspLysThrLeuPheLys 186
DB 3 ATACCTCAATGCTTACTCAGCAACATCATGATCTGATGACAAAGACTCTGTCAAA 62
QY 187 TYRPhMetArgValIalProSerAspAlaGlnGlnAlaArgSerMetValAspIleVal 206
DB 63 TATTTCAATAGGGTTGTGCTTCAAGATGCTCAGACGAGGAGGAGGTCATGGTGGACATAGTG 122
QY 207 LysArgTyRAsnTrpThrTyRValSerAlaValIleThrGluGluLysThrGluGluSer 226
DB 123 AAGAGGTACAACTGACCTATGATATCAGCCGTCACACAGAGGCAACTATGGAAGAAAGT 182
QY 227 GlyMetGluAlaPheLysAspMetSerAlaLysGluGluIleCysIleAlaHisSerTyR 246
DB 183 GGAATGGAAGCCTTCAAGATATGTCAAGCAAGAGGAGATTGCAATGCCCACTCTTAC 242
QY 247 LysIleTySerAsnAlaGluGlnGlnSerPheAspLysLeuLeuLysLeuThrSer 266
DB 243 AAAATCTACAGTAATGACGAGGAGCAGACCTTTGATTAAGCTCTGAAAGAACTCAAAAGT 302
QY 267 HisLeuProLysAlaArgValIalAlaTyRheCysGluGluMetThrValArgGIYLeu 286
DB 303 CACTTCCCAAGGCCCGGTGTGCTTCTGTGAGGGCATGACGGTGAAGAGGTCTG 362
QY 287 LeuMetAlaMetArgArgLeuGIYLeuValGIYGluPheLeuLeuGluGluArgGluPro 306
DB 363 CTGATGGCCATAGAGGGCTGTGATGAGGAGAAATTTCTGCTTCTGGGCAAGGAAACA 422
QY 307 AspAlaIlePheIleGluIleSerLysAsnSerIleLeuTrpGluLysArgArgLysCys 326
DB 423 GATGCCATCTTTATTTGAGATCTCAAGAAAGACGATCTTGGGAAGACAGAAAGAAATGC 482
QY 327 GlnGluArgPheLeu 331
DB 483 CAAGGCGCTTCCTT 497

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RESULT 4

CB153433 449 bp mRNA linear EST 29-JAN-2003  
 LOCUS K-EST0210877 BT694954 Homo sapiens cDNA clone BT694954-28-C09 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CB153433  
 VERSION CB153433.1 GI:28138427  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 449)  
 AUTHORS Kim,M.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished  
 COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongjung@mail.kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
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 with tobacco acid pyrophosphatase (TAP). The deapped  
 intrac mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."  
 BASE COUNT 106 a 112 c 112 g 119 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,32e-77 Length: 449  
 Score: 750.00 Matches: 147  
 Percent Similarity: 99.33% Conservative: 1  
 Best Local Similarity: 98.66% Mismatches: 1  
 Query Match: 40.04% Indels: 0  
 Gaps: 0  
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 QY 41 PheserValHshIsgInProThrValAspGluValHsgIuaTgLyCySgIyAlaVal1 60  
 Db 2 TTTTCTTTCATCATCCAGCCCTACTGTGACGACAACTTATGAGAGAGTGTGGCGCAGTC 61  
 QY 61 ArgIuGlnTrpGlyIleGlnAlaValAlaMetLeuHshIthrLeuGluAlaTgAsn 80  
 Db 62 CGTGAACAGATGCGATTCCAGAGAGTGAAGCCATGTGTCGATACCCCTGGAAGATCAAT 121  
 QY 81 SerAspProThrLeuLeuProAsnIleThrLeuLysCysGluIleArgAspSerCysTrp 100

Db 122 TCAGACCCCACTTGGCCCAATCATCACTGGCTGTGATGATGAGGATTCCTGCTGG 181  
 QY 101 HtSerAlaValAlaLeuGlnGlnSerIleGluPhaIleArgAspSerLeuIleSerSer 120  
 Db 182 CATTCGGCTGTGGCCCTTGAAGCAGACCATTTGATTAAGATTCCTCCATTTCTTCG 241  
 QY 121 GluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 140  
 Db 242 GAAG 301  
 QY 141 LysProIleValGlyValIleGlyProGlySerSerSerSerSerSerSerSerSer 160  
 Db 302 AACCCATAGTAGAGGAGTCAATGGCTGGCTGGTTCAGATTCTGTAGCCATTGACATTCAGATCAGAAAT 361  
 QY 161 LeuLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 180  
 Db 362 TTGCTCCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 421  
 QY 181 AspLysThrLeuPheLeuTyrPheMet 189  
 Db 422 GACAAAGCTCTTTCATAATTTTCATG 448  
 RESULT 5  
 AK032422  
 LOCUS  
 DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
 enriched library, clone:6430542K11 product:ME18AOTROPIC GLUTAMATE  
 RECEPTOR MGLUR5 PRECURSOR homolog [Rattus norvegicus], full insert  
 sequence.  
 ACCESSION AK032422  
 VERSION AK032422.1 GI:26082838  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Komno,H., Akiyama,J., Nishi,K., Kitsuai,T., Taishiro,H., Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Keshwagi,K.,  
 Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,K., Tanaka,T., Ohara,E., Matsubara,S.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsubara,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,  
 Arakawa,T., Hara,A., Fukunishi,Y., Komno,H., Adachi,J., Fukuda,S.,  
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,I.,  
 Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,  
 Kadohika,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,C.,  
 Fleischmann,W., Gaasterland,T., Glessl,C., King,B., Kochiwa,H.,  
 Kuehl,P., Lewis,S., Matsuo,Y., Nikido,I., Pesole,G.,  
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Wagner, L., Mashio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Bromberg, M.J., Bul, C., C., Fletcher, C., Fujita, M., Gariboldi, M., Gattolich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Tero-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Haesegawa, Y., Kawaji, H., Kohlschütter, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

6 (bases 1 to 3879)

Adachi, S., Alizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hirozane, T., Hori, F., Imoto, J., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawaji, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takaue, F., Takaku-Akita, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
 Location/Qualifiers

1. 3879

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/tissue\_type="olfactory brain"

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/dev\_stage="adult"

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BASE COUNT 1026 a 975 c 954 g 924 t

ORIGIN

Alignment Scores:

Pred. No.: 3,57e-74 Length: 3879

Score: 735.50 Matches: 147

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Best Local Similarity:	86.47%	Mismatches:	7
Query Match:	39.27%	Indels:	13
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DB	3	GGGCGCATTCAGATTCAGAACTTCCTCCAGCTTTCACACATACCTCGATGCTTACTCT	62
QY	174	AlaThrIleMetAspLeuSerAspLysThrLeuPheLysTyrPheMetArgValPro	193
DB	63	GCAACTGACATGAGATTGAGTGAACAAGCTTATTCAATCACTTCATAGAGGTTGACT	122
QY	194	SezAspAaIeGInGInAlaArgSerMetValAspIleValLysArgTyrAsnTyrThrTyr	213
DB	123	TGGATGCGCCACGACAGCCCGACGATGTGACATGACATGACATGACATGACAT	182
QY	214	ValSerAlaValAlaIleThrGluGlyAsnTyrGlyGluSerGlyMetGluAlaPheLysAsp	233
DB	183	GTCTCAGCTGTGCACACAGAAAGCACTATGAGAAAGTGGAGTGAAGGCTTTCAGAT	242
QY	234	MetSerAlaLysGluGlyIleGlyIleAlaIleAsnTyrLysIleTyrSerAsnAlaGly	253
DB	243	ATGTCACGGAAGGAAGGATTTGATGCGCCACTTACAAATCTACAGAAATGCTGGG	302
QY	254	GluGlnSerPheAspLysLeuLeuLysLeuThrSerHisLeuPheLysArgVal	273
DB	303	GACACAGCTTTGACAAAGCTTTGAAAAAGCTCAGAAATCTTTTACCTTAAAGCCCGAGT	362
QY	274	ValAlaTyrPheCysGluGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeu	293
DB	363	GTACCTGCTCTCTGTGAAGGATGATGACAGTTGAGATGCTGCTCATGCGCATGACGCTTG	422
QY	294	GlyLeuValGlyGluPheLeuLeuLeuGlyArgGluProAspAlaIlePheIleGluIle	313
DB	423	GGTCTACAGAGGGAATTTCTACTTGGGCGAGTATGCG-----	461
QY	314	SerLysAsnSerIleLeuTyrGluAspArg	323
DB	462	-----TGGGCTGACAGG 473	
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DEFINITION	UT-H-B10-aac-d-06-0-UT-s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710331 3', mRNA sequence.		
ACCESSION	AM015382		
VERSION	AM015382.1	GI:5864139	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 442)		
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgaps-remail.nih.gov">cgaps-remail.nih.gov</a> Oligo-dT track not found. Not 1 site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution <a href="http://www-bio.linn.gov/bdrrp/image/image.html">www-bio.linn.gov/bdrrp/image/image.html</a> Seq primer: M13 Forward		
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	/mol_type="mRNA"		

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NCI CGAP Sub1 library is a subtracted library derived from
BI - BI constitutes a mixture of 21 normalised or
subtracted NCI_CGAP libraries: NCI_CGAP_Co4,
NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16,
NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3,
NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8,
NCI_CGAP_Co11, NCI_CGAP_Les2, NCI_CGAP_Br23, NCI_CGAP_Lus5,
NCI_CGAP_Lus24, NCI_CGAP_Lus19, NCI_CGAP_GC4, NCI_CGAP_GG6,
NCI_CGAP_Br25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with a
driver whose composition is detailed below: NCI_CGAP_Kid3
pool 1 LAM 3334-3337, 3682-3683, 3798-3803 (IMAGE
Cloneids 1322376-1323911, 1456008-1456775, 1500552-1502855)
NCI_CGAP_Kid5 pool 1 LAM 3338-3342, 3722-3725,
3776-3778 (IMAGE Cloneids 1323912-1325831,
1471368-1472903, 1492104-1493255) NCI_CGAP_Lus pool 1 LAM
3575-3582, 3851-3854 (IMAGE Cloneids 1414920-1417991,
1520904-1522439) NCI_CGAP_GC4 pool 1 LAM 3164-3167,
3716-3720, 3733-3735 (IMAGE Cloneids 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI_CGAP_Pr22 pool 1
LAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneids
985608-986759, 1101192-1101959, 1217928-1220615)
NCI_CGAP_Co10 pool 1 LAM 2644-2653, 2871-2872 (IMAGE
Cloneids 1057416-1061255, 1144584-1145351) The resulting
subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldo
Lemon & Soares (1996): Normalization and Subtraction:
Two Approaches to Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG LIB=NCI_CGAP_Les2
TAG TISSUE=leiomysarcoma
TAG_SEQ=ATCG"
BASE COUNT 118 a 97 c 127 g 100 t
ORIGIN

```

```

Alignment Scores:
Pred. No.: 1,11e-74 Length: 442
Score: 727.00 Matches: 144
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 38.81% Indels: 1
DB: 9 Gaps: 0

```

US-10-027-923-2 (1-369) x AN015382 (1-442)

```

QY 163 Glnleupheanilleproglinlealalyseralathrillemetaspheuserys 182
DB 8 CAGCTTTTCAACATACCTCAGATTCCTTACTCAGAACATCATCATGAGTGTACAG 67
QY 183 Thrleuphealytyrphemearyvalalproserapalaglnalalargseret 202
DB 68 ACTCGTTCAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGCAGCAGGATCCATG 127
QY 203 Valaplievallyarqlytyrphasanthrlyrvalseralalvalhithgluglyan 222
DB 128 GTGACATAGTGAAGAGGTACACGTGACCTTATGATCAGCCGTACACACGAGAGGCAAC 187
QY 223 TyrglygluserglymetglualaphelyaspmecseralalygluglylyeCyrlle 242
DB 188 TATGAGAAAGTGGGATGGAAGCTTCAAGTATAGTCAGGAGGAGGAGGATTTGCATC 247
QY 243 Alahiserlytyrlylytyrseranallaglygluglyinserphasplysleulelys 262
DB 248 GCCACCTTCAAAATCTTACAGTATGACAGGGGAGGAGGCTTGAATAGGCTGTGAG 307
QY 263 Lysleuthrserhaleuprolysalargvalalalytyrphacygluglymetthr 282

```

```

DB 308 AAGTCACAAAGTCACTTGCCCAAGGCCGGGTGGCTCACTTCTGTGAGGCGCATACG 367
QY 283 ValArglyleulemetalaameryargyleuglyvleuValglyglu-Pheleule 302
DB 368 GTGAGAGGTGTGCTGAGAGGCGCATAGGCGCTGGTCTAGTGAGAGAAATTTGCTTCT 427
QY 302 uGlyArglyupro 306
DB 428 GGGCAGGGAACCA 440

```

```

RESULT 7
BU351729 657 bp mRNA linear EST 28-NOV-2002
603527561F1 CSEQCHN69 Gallus gallus CDNA clone CHEST47616 5', mRNA
sequence.
ACCESSION
BU351729
VERSION
BU351729.1 GI:25859730
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 657)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNA
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
JOURNAL
MEDLINE
PUBMED
12445392

```

```

COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

```

```

FEATURES
source
location/Qualifiers
1..657
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST47616"
/sex="Female"
/tissue_type="cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN69"

```

```

/Note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded CDNA
was blunt-ended, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

```

```

BASE COUNT 161 a 168 c 178 g 150 t
ORIGIN

```

```

Alignment Scores:
Pred. No.: 2.07e-73 Length: 657
Score: 718.50 Matches: 141
Percent Similarity: 78.90% Conservative: 31
Best Local Similarity: 64.68% Mismatches: 29

```



Query Match: 38.36% Indels: 17  
 DB: 13 Gaps: 2  
 US-10-027-923-2 (1-369) x BU351729 (1-657)

QY 138 ArgSerlybProlleValIleGlyProGlySerSerSerLeuAlaIleGln 157  
 DB 11 CGCTGAGGAAGCCATTGGCGGAGTCATTGGCCCTGCTCCAGTCCAGTCCAG 70  
 QY 158 ValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMet 177  
 DB 71 GTCAGAACTCTGTCGAGCTCTTGACATCCCAAAATTCCTCACTGCCACAGCATC 130  
 QY 178 AspLeuSerAspLyThrLeuPheLyThrPheMetArgValAlaProSerAspAlaGln 137  
 DB 131 GACTGAGTACAAAGACTCTCTCAAGATATTTCTCCGTGTGTCCTGACACATC 150  
 QY 198 GlnAlaArgSerMetValAspIleValIleArgTyAsnThrTyValIleSerAlaVal 217  
 DB 191 CAAGCCCGGCGCATGCTCGATATTGTCAAGCGTTACAACTGACTTACGTGCGCGCTG 250  
 QY 218 HisThrGlnGlyAsnTyArgIlyGlySerGlyMetGlnAlaPheLyAspMetSerAlaLyS 237  
 DB 251 CACACTGAAGAAATTAACGGGGAAGTGAATGAGGCTTCAAGAGCTGCGTCCCAA 310  
 QY 238 GlnGlyIleCyAlleAlaHisSerTyArgIleTySerAsnAlaGlyGlnSerPhe 257  
 DB 311 GAGGCGCTCTGCACTTGTCTCATCTTGCACAAATCTATAGCAATGTGGGGAAGAAAGCTTT 370  
 QY 258 AspLyLeuLeuLybLybLeuThrSerHisLeuProLybAlaArgValAlaTyPhe 277  
 DB 371 GATCGCTGCTCGCAAGCTCGCGAAGATTAACCAAGCTGAGGTGCTTGTCTTC 430  
 QY 278 CyeGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgIleGlyLeuValGly 297  
 DB 431 TGTGAGGCGATGACGCTGAGGAGGATCTCTATGACAGTCTGAGAGTGGCTGGG 490  
 QY 298 GlnPheLeuLeuLeuGlyArgGlnProAspAlaIlePheIleGlyLeuSerLybAsnSer 317  
 DB 491 GAGTCTCTGCTAATGGAAGTGAACGCT----- 517  
 QY 318 IleLeuTrpGlnAspArgArgLybCyGlnGlyArgPheLeuGlnGlyPheGlyAspIle 337  
 DB 518 -----TGGGCAGACAG-----GATGAATCATTTGAAGTTTGAACAGAA 559  
 QY 338 LeuHisArgSerGlySerValLeuLeuHisMetProGlnProLeuAsnLeuGln 355  
 DB 560 GCAAAATGAGGATCATCTATCAATGCAATCTCAGAGGTCTGTGATTTGAT 613

RESULT 8  
 BU393781 669 bp mRNA linear EST 27-NOV-2002  
 LOCUS 603803380F1 CSEBCHN57 Gallus gallus cDNA clone CHEST778020 5', mRNA  
 DEFINITION  
 ACCESSION BU393781  
 VERSION BU393781.1 GI:25762820  
 KEYWORDS EST  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 669)  
 Boardman, P.E., Sanz-Esguerra, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,  
 A Comprehensive Collection of Chicken CDNAS  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335514  
 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers

## FEATURES

## source

1..669  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="white Leghorn, Hiseer"  
 /db\_xref="taxon:9031"  
 /clone="CHEST778020"  
 /dev\_stage="16 day embryo"  
 /lab\_host="DH10B"  
 /clone\_1lb="CSEBCHN57"

/note="Organ: Brain; Vector: pBluescript II KS(+); Site: 1:  
 EcoRI; Site: 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with EcoRI  
 , size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

## BASE COUNT

165 a 174 c 179 g 151 t

## ORIGIN

## Alignment Scores:

Pred. No.: 2,136-73 Length: 669  
 Score: 718.50 Matches: 141  
 Percent Similarity: 78.90% Conservative: 31  
 Best Local Similarity: 64.68% Mismatches: 29  
 Query Match: 38.36% Indels: 17  
 DB: 13 Gaps: 2

US-10-027-923-2 (1-369) x BU393781 (1-669)

QY 138 ArgSerlybProlleValIleGlyProGlySerSerSerLeuAlaIleGln 157  
 DB 23 CGCTGAGGAAGCCATTGGCGGAGTCATTGGCCCTGCTCCAGTCCAGTCCAG 82  
 QY 158 ValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIleMet 177  
 DB 83 GTCAGAACTCTGTCGAGCTCTTGACATCCCAAAATTCCTCACTGCCACAGCATC 142  
 QY 178 AspLeuSerAspLyThrLeuPheLyThrPheMetArgValAlaProSerAspAlaGln 137  
 DB 143 GACTGAGTACAAAGACTCTCTCAAGATATTTCTCCGTGTGTCCTGACACATC 202  
 QY 198 GlnAlaArgSerMetValAspIleValIleArgTyAsnThrTyValIleSerAlaVal 217  
 DB 203 CAAGCCCGGCGCATGCTCGATATTGTCAAGCGTTACAACTGACTTACGTGCGCGCTG 262  
 QY 218 HisThrGlnGlyAsnTyArgIlyGlySerGlyMetGlnAlaPheLyAspMetSerAlaLyS 237  
 DB 263 CACACTGAAGAAATTAACGGGGAAGTGAATGAGGCTTCAAGAGCTGCGTCCCAA 332  
 QY 238 GlnGlyIleCyAlleAlaHisSerTyArgIleTySerAsnAlaGlyGlnSerPhe 257  
 DB 323 GAGGCGCTCTGCACTTGTCTCATCTTGCACAAATCTATAGCAATGTGGGGAAGAAAGCTTT 382  
 QY 258 AspLyLeuLeuLybLybLeuThrSerHisLeuProLybAlaArgValAlaTyPhe 277  
 DB 383 GATCGCTGCTCGCAAGCTCGCGAAGATTAACCAAGCTGAGGTGCTTGTCTTC 442  
 QY 278 CyeGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgIleGlyLeuValGly 297  
 DB 443 TGTGAGGCGATGACGCTGAGGAGGATCTCTATGACAGTCTGAGAGTGGAGTGGG 502

QY 298 GluPheLeuLeuLeuGluArgGluProAspAlaIlePheIleGluIleSerLyAsnSer 317  
 DB 503 GAGTTCCTGCTAATTGAGAGTACGGT----- 529  
 QY 318 IleLeuTrpGluAspArgLyAsGlnGlyArgPheLeuGlnGlyPheGlyAspIle 337  
 DB 530 -----TGGGACAGACAG-----GATGAGTCATTTGAGGTTTGAACAGGAA 571  
 QY 338 LeuHisArgSerGluSerValLeuLeuHisMetProGlnProLeuAsnLeuGlu 355  
 DB 572 GCAAATGAGAGCATCACTATCAACTGCATCTCAGAGGCTTGTCAATTGAT 625  
 RESULT 9  
 BG150163  
 LOCUS 414 bp mRNA linear EST 05-FEB-2001  
 DEFINITION nadd4603.x1 NCI CGAP Lu24 Homo sapiens cDNA IMAGE:3368404 3  
 similar to SW:MRS HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 PRECURSOR. [1] ; mRNA sequence.  
 BG150163  
 ACCESSION BG150163.1 GI:12662193  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 414)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E.B. Consortium/LMW, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 354.  
 Location/Qualifiers  
 1. 414  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3368404"  
 /tissue\_type="carcinoid"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP Lu24"  
 /note="Organ: Lung; Vector: pT7TD-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI CGAP Lu5 was prepared, and ss circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneIDs  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bernaldo."  
 BASE COUNT 110 a 91 c 118 g 95 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 9.59e-71 Length: 414  
 Score: 693.00 Matches: 134  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.26% Mismatches: 0  
 Query Match: 37.00% Indels: 0  
 DB: 10 Gaps: 0  
 US-10-027-923-2 (1-369) x BG150163 (1-414)

QY 163 GluLeuPheAsnIleProGlnIleAlaIleArgSerAlaThrIleMetAspLeuSerAspLyS 182  
 DB 10 CACCTTTCAACATTCCTCAGATTGCTTACTGACGACATCATGATTCGATGACGAC 69  
 QY 183 ThrLeuPheLeuTrpPheMetArgValValProSerAspAlaGlnGlnAlaArgSerMet 202  
 DB 70 ACTGCTTCAAATATTTCAATGAGGGTGTGTCCTTCGATGATTCACGACGACGATCATG 129  
 QY 203 ValAspIleValLeuAspArgTrpAsnTrpThrTrpValSerAlaValHisThrGluGlyAsn 222  
 DB 130 GTGACATGATGAGAGGTGACACTGACCTATGTAATCAGCCCTACACAGAGGAC 189  
 QY 223 TyrGlyGluSerGlyMetGluAlaPheLyAspMetSerAlaLyGluGlyIleCysIle 242  
 DB 190 TATGAGAAAGTGGATGAGAGGAGCTTCGAAAGATATATCAGCGAAGAGGATTCATC 249  
 QY 243 AlHisSerTrpLySileTrpSerAlaAlaGlyGlnGlnSerPheAspLySleLeuLyS 262  
 DB 250 GCCCAGCTTACAAATCACTACACTAATGCGAGGACAGAGCTTTGATTAAGCTGTCGAG 309  
 QY 263 lyeLeuThrSerHisLeuProLySAlaArgValAlaIleTyrPheCysGluGlyMetThr 282  
 DB 310 AACCTCAAGATCACTGCTCCAGAGCCGGGTGTGACCTACTTCTGTGAGGACATGACG 369  
 QY 283 ValArgGlyLeuLeuMetAlaMetArgLyGlyLeuValGly 297  
 DB 370 GTGAGAGTGTGCTGATGGCCATGAGGCGGCTGTGATTTGG 414  
 RESULT 10  
 BU390603 673 bp mRNA linear EST 27-NOV-2002  
 LOCUS 603801605F1 CSEQCHN57 Gallus gallus cDNA clone CHEST77411 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BU390603.1 GI:25759641  
 VERSION EST.  
 KEYWORDS Gallus gallus (chicken)  
 SOURCE Gallus gallus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 REFERENCE 1 (bases 1 to 673)  
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 CURT. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1. 673  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="CHEST77411"  
 /dev\_stage="16 day embryo"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN57"  
 /note="Organ: brain; Vector: pBluescript II KS(+); Site\_1:  
 EcoRI; Site\_2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer. Using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was blunted, ligated to NotI adapters, digested with EcoRI

, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 165 a 173 c 180 g 155 t  
ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 671.00	673	144	31	30	25	3
Best Local Similarity: 62.09%						
Query Match: 35.82%						

US-10-027-923-2 (1-369) x BU930603 (1-673)

```

Qy 138 ArgSerLysPProIleVal-GlyValIle-GlyProGlySerSerSerLeuAlaIleG 157
Db 23 GCGCTGAGAGAGCCATTGCGGAGTCATTCGCCCTGCTCCAGCTCAGTGCATCC 82
Qy 157 InValGln-AsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerAlaThrIle 176
Db 83 AGGTCAGAGAACCTCTCGAGCTCTTGACATCCCAATTCCTCTGCTGACACAGC 142
Qy 177 MetAspLeuSerAspLysThrLeuPheLysThrPheMetArgValValProSerAspAla 186
Db 143 ATCGACCTGAGTGCAGAGACTCTCTACAGATATTTCTCCGTGCGTCCCTCGACACA 202
Qy 197 GlnGlnAlaArgSerMetValAspIleValIleValArgThrAspThrThrValSerAla 216
Db 203 CTCAGAGCCCGCGCATGCTCGATATGTCAGAGCTTACCACTGAGCTTACGTCGCC 262
Qy 217 ValHisThrGlnGlnAsnTyrgLysGlnSerGlyMetGlnAlaPheLysAspMetSerAla 236
Db 263 GTGCACACTAGAGAAATTACGGGAAAGTGGAATGAGAGCTTCAAGAGCTGCGTCC 322
Qy 237 LysGlnGlyTLeuCyAlaAlaHisSerTyrgLysIleTySerAsnAlaGlyGlnGlnSer 256
Db 323 CAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 382
Qy 257 PheAspLysLeuLeuLysLysLeuThrSerHisLeuProLysAlaArgValAlaTyrg 276
Db 383 TTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 442
Qy 277 PheCyGlnGlyMetThrValArgGlyLeuLeuMetAlaMetArgArgLeuGlyLeuVal 296
Db 443 TTCTGTAGAGGCGATGACGCTGAGGGAGATCTCTCTCTGATGACGCTGAGGATCTT 502
Qy 297 GlyLysLeuLeuLeuGlyArgGlnProAspAlaIlePheIleGlnIleSerLysAsn 316
Db 503 GGGAGATTCCTGCTAATTGAGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532
Qy 317 SerIleLeuThrGlnLysAspArgLysCyGlnGlnIleArgPheLeuGlnIleGlyAsp 336
Db 533 -----TGGCAGACGACA-----GATGAGTCATTTAGAGCTTATGACAG 571
Qy 337 IleLeuHisArgSerGlnSerValLeuLeuHisMetProGlnProLeuAsn----- 353
Db 572 GAAGCAATGAGGAGCATCATCAATGCAATCTCAAGAGCTTGTGCTTTGATGAC 631
Qy 354 -----LeuGlnLeuSerSerGly 359
Db 632 TACTATCTGAGAGCTGCTTCTGGA 655

```

## RESULT 11

LOCUS AG046849 667 bp DNA linear GSS 02-NOV-2001  
DEFINITION Pan troglodytes DNA, clone: PTB-026D03.F, genomic survey sequence.  
ACCESSION AG046849

## VERSION

AG046849.1 GI:16583741

## KEYWORDS

GSS.  
Pan troglodytes (chimpanzee)

## SOURCE

Pan troglodytes

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

## REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

## TITLE

BAC end sequences of library PTB

## JOURNAL

Unpublished

## AUTHORS

2 (bases 1 to 667)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

## TITLE

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenro-chou, Tsukuba, Ibaraki, Japan, 305-8565, Japan (E-mail: chimpes@gs.c.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

## COMMENT

Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1. 667

## FEATURES

/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-026D03.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_11b="PTB Chimpanzee Male BAC library"

## BASE COUNT

156 a 142 c 158 g 210 t

## ORIGIN

1 others

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 637.00	667	132	11	33	1	0
Percent Similarity: 81.25%						
Best Local Similarity: 75.00%						
Query Match: 34.01%						

US-10-027-923-2 (1-369) x AG046849 (1-667)

```

Qy 38 GlyAlaLeuPheSerValHisGlnProThrValAspGlnValHisGlnArgLysCyG 57
Db 66 GAGAGCTCTCTTTCTGTTATGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 125
Qy 58 GlyAlaValArgGlnGlnTyrgLysIleGlnArgValGlnAlaMetLeuHisThrLeuGln 77
Db 126 GGGGCGGCTCGTAAAGATGCAATGCAAGAGTGAGAGCCATGCTGCTACCTCGAA 185
Qy 78 ArgIleAsnSerAspProThrLeuLeuProAsnIleThrLeuGlyCyGlnIleArgAsp 97
Db 186 AGGATCAATTCATACCCACACCTCTTCCCAATCACTGAGGCTGTGAGATGAGGAC 245
Qy 98 SerCySerTrpHisSerAlaValAlaLeuGlnGlnSerIleGlnIleArgAspSerLeu 117
Db 246 TACTGCTGGCATTCGGTTGGTCTTGAAGCATAGCATTTGTTCTATTAAGATTCCTT 305
Qy 118 IleSerSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 137
Db 306 ATTCTTTTAAAGAGAAAGGCTGTGACCTGTGTGATGCTGCTGCTTCTTCTTCTT 365
Qy 138 ArgSerLysPProIleValIleGlyValIleGlyProGlySerSerSerLeuAlaIleGln 157

```

Db	366	CGGTCGAAGAAGCCATATATTAGGGGTTATGTGATCGATTCAGTTCTGCTCATTCGAC	425
Qy	158	ValGlnAsnLeuLeuGlnLeuPheAsnIleProGlnIleAlaTySerIaThrIleMet	177
Db	426	GCGCGAATGTGCTCAGTTTTCACACATCTGACATTGGTTTACGATGAACACCATG	485
Qy	178	AspLeuSerArgPheThrLeuPheLeuTyThrPheMetArgValValProSerAspAlaGln	197
Db	486	GATCGAATGACAAAGACTGTGTTCAATTAATTCATAGAGATGTGCTTTAAT-GCTTAA	544
Qy	198	GlnAlaArgSerMetValAspIleValIysArgTyArgThrPheThrTyR	213
Db	545	TTTGTTATGATTATGTGTGACATACGTATAGGCTCAATTGTGTCAT	592
RESULT 12			
LOCUS	CB730684	471 bp	mRNA linear EST 11-APR-2000
DEFINITION	AMGNNUC:NRHY7-00025-C6-A nrhy7 (10850) Rattus norvegicus cDNA clone		
ACCESSION	CB730684		
VERSION	CB730684.1	GI:29797818	
KEYWORDS	EST.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Amgen, Inc		
AUTHORS	Amgen EST Program.		
TITLE	Amgen Rat EST Program		
JOURNAL	Unpublished		
COMMENT	Contact: Dan Fitzpatrick Amgen, Inc One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881 Plate: 00025 row: c column: 6.		
FEATURES			
Source	1. 471 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /clone_nrhy7-00025-C6" /clone_1db="nrhy7 (10850)" /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat hypochthalmus adult female Wistar rat avg. insert size 2.3 kb fraction 6 and 7"		
BASE COUNT	113 a 134 c 120 g 104 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	3,136-61	Length:	471
Score:	612.50	Matches:	123
Percent Similarity:	89.10%	Conservative:	16
Best Local Similarity:	78.85%	Mismatches:	14
Query Match:	32.70%	Indels:	3
DB:	14	Gaps:	3
US-10-027-923-2 (1-369) x CB730684 (1-471)			
Qy	82	AspProThrLeuLeuProAsnIleThrLeuGlyCysGlnIleIleArgAspSerCysThrPis	101
Db	3	GACCCGGTGCCTCTGCCCAACATCATCTGGGGCAGTGAATCCGGGACCTCTCTGGCAC	62
Qy	102	SerAlaValAlaLeuGlnGlnSerIleGlnPheIleArgAspSerLeuIleSer---Ser	120
Db	63	TCTTCAGTGGCTCTCGAACAAGACATCGAATTCATCAGAGACTCCCTGATTTCACATCCA	122
Qy	121	GlnGlnGlnGlnGlyLeu---ValCysSerValAspGlySerSer---SerSerPheArg	138
Db	123	GATGAGAAGAGATGGGCTGAACGATCTCGCTCATGGCCAGACCCCTGCGACAG	182
Qy	139	SerIysIysProIleValGlyValIleGlyProGlySerSerSerIleuAlaIleGlnVal	158

Db	183	ACTAAGAAGCCATTATTCGAGATGATCGGCGCTCGGCTCCAGCTCTGGGCAATTCAGT	242
Qy	159	GlAbnntleuenglntleupheanllleproglntllalaTyrsSerlAaThrIleMetAsp	178
Db	243	CAGAAATCTTCACAGCTGTTGCACATCCACAGATGCCATATTCGTGCACAGCATGAC	302
Qy	179	leuSerAspTyrsThrleupheleTyrsPheMetArgAlaValProSerAspAlaGln	198
Db	303	CTGAGTACCAAACTTTGTACAAATACTTCTGAGSGTGGTCCCTTGTGACACTTGGAC	362
Qy	199	AlaArgSerMetValAspIleValIleAspArgTyrsAntpThrTyrsAlaSerAlaValHis	218
Db	363	GCAAGGCGCATGCTGCACATATGCAACGCTTACACATGACCACTATGCTCAGCAGTCCAC	422
Qy	219	ThrlGlnIlyAsnTyrglygyluSerGlyMetGlnAlaIleAspMet	234
Db	423	ACGAAAGGAATTAAGGAGAGTGAATGATGCTTCAAGAAGACTG	470
RESULT 13			
LOCUS	BG695213	682 bp	RNA linear EST 04-MAY-2001
DEFINITION	NISC.Iv191g09.w1 Soares NMBP2 pituitary Mus musculus cDNA clone		
ACCESSION	BG695213		
VERSION	BG695213.1		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.		
AUTHORS	1 (bases 1 to 682)		
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Unpublished		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	cDNA Library Preparation: M. Bento Soares Laboratory		
	DNA Sequencing by: National Institutes of Health Intramural		
	Sequencing Center (NISC)		
	clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LINL at:		
	<a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a>		
	MGI:1596648		
	Plate: L1AM9922		
	Seq primer: T7 primer.		
FEATURES	Location/Qualifiers		
SOURCE	1..682		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:4317880"		
	/tissue_type="pituitary gland"		
	/dev_stage="embryo, 14 dpc"		
	/lab_host="DH108 (phage-resistant)"		
	/note="Organ: brain; Vector: pT73D-Pac; Site: 1: NotI;		
	Site 2: EcoRI; 1st strand cDNA was primed with a NotI -		
	oligo(dT) primer		
	5'-AAGTCGAAGAATTCGGCGCGCGCGCTTTTTTTTTTTTTTTT-3';		
	double-stranded cDNA was ligated to EcoRI adaptors		
	5'-AATTCGACGAGG-3' AND 5'-CTCTGTCGG-3' (Pharmacia)		
	, digested with NotI and cloned into the NotI and EcoRI		
	sites of the pT73D-PacI vector. Library went through one		
	round of normalization, and was constructed in the		
	laboratory of M. Bento Soares (University of Iowa)."		
BASE COUNT	190 a	121 c	162 g
ORIGIN			209 t
Alignment Scores:	1,42e-58	Length:	682
Prod. No.:	592.00	Matches:	115
Score:			

Percent Similarity: 97.48%  
 Best Local Similarity: 96.64%  
 Query Match: 31.61%  
 DB: 10  
 Gaps: 0

US-10-027-923-2 (1-369) x BG695213 (1-682)

QY 186 LyeTyrPheMetArgValAlaProSerAspAlaGlnGlnAlaArgSerMetValAspIle 205  
 Db 7 AAGTACTTCAATGAGGCTTGTACCTTCGGATGCCAGACGCCAGCATGTGACATA 66  
 QY 206 VallyaArgTyrAsnTPtrTyrValSerAlaValHisThrGlnGlnGlnGlnGln 225  
 Db 67 GTGAGAGATACACACTGACTTATGTCTCAGCTGTGACACAGAGCAACTATGAGAA 126  
 QY 226 SerGlyMetGlnAlaPheLeuAspMetSerAlaValGlnGlnGlnGlnGlnGln 245  
 Db 127 AGTGGAGTGGAGGCTTTCAAAGATATGTCAAGCAAGAGGATTTCCATCGCCACTCT 186  
 QY 246 TyrValIleTyrSerAsnAlaGlnGlnGlnSerPheAspLeuLeuLeuLeuLeuThr 265  
 Db 187 TACAAATCTACACCAATGCTGGGGAACAGACTTTGACAGCTGTGAAAAGCTCAGA 246  
 QY 266 SerHisLeuProIyValAlaArgValAlaAlaTyrPheCysGlnGlnGlnGlnGlnGln 285  
 Db 247 AGTCATTACTTAAAGCCCGGCTGTAGCTGTCTTCTGTGAAGCATGACAGTTGAGGT 306  
 QY 286 LeuLeuMetAlaMetArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 304  
 Db 307 CTGCTCATGGCCATGAGACCGCTTGGGTCTAGCAGAGGGAATTTCTACTTGGGCGA 363

RESULT 14  
 B2181748 837 bp DNA linear GSS 11-OCT-2002  
 LOCUS B2181748  
 DEFINITION CH230-388J12.TU CHORI-230 Segment 2 Rattus norvegicus genomic clone  
 B2181748  
 ACCESSION B2181748.1 GI:23827927  
 VERSION GSS.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus (Norway rat)  
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 837)  
 Zhao,S., Shetty,J., Shatman,S., Tsegaye,G., Geer,K., Shvartsbeyn  
 'A., Gebregziabher,B., Overton,L., Russell,D., Chen,D., Riggs,P., de  
 Jong,P. and Fraser,C.M.  
 Rat BAC End Sequences from Library CHORI-230 MboI segment  
 Unpublished  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the rat BAC library CHORI-230  
 (http://www.chori.org/bacpac/rat230.htm). For BAC library  
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/orering/information.htm). BAC end  
 page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
 Plate: 388 row: J column: 12  
 Seq primer: SP6  
 Class: BAC ends.

## FEATURES

## source

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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10116"  
 /clone="CH230-388J12"

/sex="Female"  
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 /clone\_id="CHORI-230 Segment 2"  
 /note="Vector: PTARPA1.3; Site 1: MboI, Site 2: MboI;  
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 Pieter de Jong"

BASE COUNT 186 a 224 c 256 g 171 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 8.64e-58 Length: 837  
 Score: 586.50 Matches: 121  
 Percent Similarity: 83.73% Conserved: 18  
 Best Local Similarity: 72.89% Mismatches: 24  
 Query Match: 31.31% Indels: 3  
 DB: 28 Gaps: 3

US-10-027-923-2 (1-369) x B2181748 (1-837)

QY 20 AlaGlnSerSerGlnArgValAlaAlaHisMetLeuGlnAspIleIleGlyAla 39  
 Db 336 GCGAGTGCCTGTCGCCAGCCCTCGTGGCGAATGAGCAGAGTGCATCATCGAGCC 395  
 QY 40 LeuPheSerValHisIleGlnProThrValAspGluValHisGluArgLysCysGlyAla 59  
 Db 396 CTCTTCAGTCCATACACAGCCTCCAGCCGAGAGAGTACCAGAAAGAGTGGGAG 455  
 QY 60 ValArgGlnGlnTyrGlyIleGlnArgValGlnAlaMetLeuHisThrLeuGlnArgIle 79  
 Db 456 ATCAGGAGACAGATAGGTATCCAGAGGGTGGAGGCCATGTTCACACAGTTGATTAAGATT 515  
 QY 80 AsnSerAspProThrLeuLeuProAsnIleThrLeuGlnGlnGlnGlnGlnGlnGlnGln 99  
 Db 516 AACGGGACCCGGGTGCTCCGCCCAATCATCTGTGGCGAGTACATCCGGACTCTGC 575  
 QY 100 TrpHisSerAlaValAlaLeuGlnGlnSerIleGlnPheIleArgAspSerLeuIleSer 119  
 Db 576 TGCGACTCTTCATGCTGCTCGAAGAGATGGAATTCATCAGAGACTCCCTGATTCC 635  
 QY 120 --SerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 136  
 Db 636 ATCCGAGATAGAGAAGATGGGCTGAACCGATGCTGCTGATGCGCAGACCTGCCCCCT 695  
 QY 137 PheArgSerIleValProIleValAlaGlyValIleGlyProGlySerSerSerLeuAlaIle 156  
 Db 696 GCGAGAGCTAAGAAGCTATGTCTGAGTGTATGGCCCTGCTCAGCTGTGGCCATT 755  
 QY 157 GlnValGlnAsnLeuGlnLeuPheAsnIleProGlnIleAlaTyrSerAlaThrIle 176  
 Db 756 TCAGTCCAGATTTCTTCAGCTGTGTCAGATCCACAGATCCGCTTATGTGCCACAGC 815  
 QY 177 MetAspLeuSerAspIys 182  
 Db 816 ATGACCTGAGTGACAA 833

RESULT 15  
 CB750802 439 bp mRNA linear, EST 11-APR-2003  
 LOCUS CB750802  
 DEFINITION AMGNNUC.NRHYS-00030-G10-A W Rat hypothalamus (10471) Rattus  
 norvegicus cDNA clone nrhys-00030-g10 5', mRNA sequence.  
 CB750802  
 ACCESSION CB750802.1 GI:29818104  
 VERSION  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 439)  
 Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished  
 Contact: Dan Fitzpatrick

Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881  
Plate: 00030 row: 9 column: 10.

FEATURES  
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Location/Qualifiers  
/organism="Rattus norvegicus"  
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kb fraction 6 and 7"

BASE COUNT 104 a 127 c 110 g 98 t  
ORIGIN

## Alignment Scores:

Pred. No.:	5,19e-56	Length:	439
Score:	567.50	Matches:	116
Percent Similarity:	88.97%	Conservative:	13
Best Local Similarity:	80.00%	Mismatches:	13
Query Match:	30.30%	Indels:	3
DB:	14	Gaps:	3

US-10-027-923-2 (1-369) x CB750802 (1-439)

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OY      85  LeuLeuProaenliethrLeuGlyCyseGluileAargaspSerCyETPHiSerAlaVal 104
Db      4  CTCTCGAACACATCACTCTGGGCGAGTGCAGATCCGGACTCTGCTGGCACTCTTCACTG 63
OY      105 AlaleuGluInSerileGluPheileAargaspSerleuileSer---SerGluGluGlu 123
Db      64  GCTCTCGAACAGAGATGAATTCATCAAGACTCTGATTTCCATCCGAGATGAGAG 123
OY      124 GluGlyLeu---ValCyseSerValaspGlySerSer---SerSerPheArgSerIlyls 141
Db      124  GATGGGCTGAACCGATGCTGCTGATGCGCAGACCCCTCGCGAGAGACTAAGAG 183
OY      142 ProileValGlyValileGlyProGlySerSerSerleuAlileGlnValGlnaspLeu 161
Db      184  CCTATTGCTGAGATGATCGCCCTGGCTCCAGCTCTGTGGCCATTCAAGTCCAGATCTT 243
OY      162 LeuGlnLeuPheAenliethrProGlnleAlaTySerAlaThrileMetAspLeuSerasp 181
Db      244  CTCAGCTGTTCGACATCCACAGATCGCTAATTCGACACAGCATAGACCTGATGAC 303
OY      182 LysThrLeuPheIlyTyPheMetArgValValProSerAspAlaGlnGlnAlaArgSer 201
Db      304  AAAACTTTGTACAAATACTTCTCTGAGGGTGGTCCCTTCTGACACTTTCAGGCAAGGCG 363
OY      202 MetValAspIleValIleValArgTyTrasnTPThrTyValSerAlaValHisThrGluGly 221
Db      364  ATGCTCGACATAGTCAAGCGTTTCACTGACCTATGTCTCAGCAGTCCACACAGAAAGG 423
OY      222 AsnTyTrGlyGluSer 226
Db      424  AATTACGGCGAGAGT 438
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Search completed: December 15, 2003, 03:10:07  
Job time : 2639 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 15:19:23 / Search time 4194.38 seconds  
(without alignments)  
10826.305 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110

Sequence: 1 atgagccttcgttgatcct.....tgagggacagcgtcatctaa 1110

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

GeneBml:\*  
1: gb\_ba:\*  
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7: gb\_ph:\*  
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31: em\_hgt\_inv:\*  
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40: em\_hgt\_inv:\*  
41: em\_hgt\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1110	6	AX709349
2	1110	100.0	1823	6	AX709347
3	1008	90.8	2172	6	AX068372
4	894	80.5	2149	6	AX068374
5	809	72.9	2064	6	AX068376
6	560	50.5	2241	6	AX068371
7	560	50.5	2326	6	AX068370
8	560	50.5	2349	6	AX068368
9	559	50.4	2551	6	AX068366
10	507	45.7	152269	9	AC136759
11	378	34.1	182701	2	AC026078
12	253	22.8	58560	2	AC131048
13	253	22.8	146921	2	AC130357
14	253	22.8	173032	9	AC130364
15	253	22.8	173795	2	AC130356
16	222	20.0	4078	6	AR270570
17	222	20.0	4207	6	AR145364
18	222	20.0	4207	6	AR145365
19	222	20.0	4303	6	AR145366
20	222	20.0	4303	6	AR145367
21	222	20.0	4518	6	AX548892
22	222	20.0	4518	6	AX548892
23	222	20.0	4614	9	HUMKGR55B
24	176	15.9	133278	2	AC034188
25	176	15.9	137384	2	AP001828
26	176	15.9	145299	2	AP000653
27	176	15.9	196373	2	AC022004
28	176	15.9	202218	9	AC026201
29	176	15.9	202864	2	AP003178
30	171	15.4	3282	6	AR038828
31	171	15.4	3282	6	AR038845
32	171	15.4	3282	6	AR256861
33	171	15.4	3282	6	121438
34	171	15.4	4085	6	AR038826
35	171	15.4	4085	6	AR038843
36	171	15.4	4085	6	AR256859
37	171	15.4	4085	6	121436
38	171	15.4	4181	6	AR038827
39	171	15.4	4181	6	AR038844
40	171	15.4	4181	6	AR256860
41	171	15.4	4181	6	121437
42	155	14.0	106316	9	AP000626
43	94	8.5	79253	9	AC107937
44	88	7.9	71127	2	AC131278
45	88	7.9	152537	9	AC055731

#### ALIGNMENTS

RESULT 1  
AX709349  
LOCUS AX709349 1110 bp DNA linear PAT 04-APR-2003  
DEFINITION Sequence 3 from Patent WO02070708.  
ACCESSION AX709349  
VERSION AX709349.1 GI:29564891  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Bates, B.G., Xie, Y., Gulukota, K. and Paulsen, J.E.  
Glutamate receptor modulatory proteins and nucleic acids encoding  
them





Db 4 ATGGTCCTTGTGATCCTGTCAGTCTTATTTTGAAGAAGATGTCGGTGGAGTGA 63  
 QY 61 CAGTCCAGTGAAGAGGGGTGTGGCTCACAATGTGGGTACATATTAATGAGCTCTC 120  
 Db 64 CAGTCCAGTGAAGAGGGGTGTGGCTCACAATGTGGGTACATATTAATGAGCTCTC 123  
 QY 121 TTTTCTGTCATGACCAAGCTTCTGTGAGCAAGATTGATGAGAGAGTGTGGGCAATC 180  
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 Db 184 CGTGAACAGTATGAGCTTCAAGAGGTGAGAGCCATGCTGCAATCCCTGGAAGATCAAT 243  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAGGAAATTCCTGTGG 300  
 Db 244 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAGGAAATTCCTGTGG 303  
 QY 301 CATTCGGCTGTGGCCCTAGAGAGCAAGCAATGATTCATAAGAGATTCCCTCATTTCTTCG 360  
 Db 304 CATTCGGCTGTGGCCCTAGAGAGCAAGCAATGATTCATAAGAGATTCCCTCATTTCTTCG 363  
 QY 361 GAAAGAGAGAGGGCTGTGATGCTGTGAGATGGCTCTTCTCTTCCCTCCGCTCAAG 420  
 Db 364 GAAAGAGAGAGGGCTGTGATGCTGTGAGATGGCTCTTCTCTTCCCTCCGCTCAAG 423  
 QY 421 AAGCCCATATAGGGGTCTTGGGCTGTGGCTTCCAGTCTTATGAGCATTCAGTCCAAAT 480  
 Db 424 AAGCCCATATAGGGGTCTTGGGCTGTGGCTTCCAGTCTTATGAGCATTCAGTCCAAAT 483  
 QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAT 540  
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 QY 541 GACAGAAGCTGTTCAAATATTTTCATGAGAGGTGTGTGCTTCAGATGCTCAGCAGCAAG 600  
 Db 544 GACAGAAGCTGTTCAAATATTTTCATGAGAGGTGTGTGCTTCAGATGCTCAGCAGCAAG 603  
 QY 601 TCCATGCTGACATATGTAAGAGGTACACTGAGCCTATGATATGATCCGTCACACAGAA 660  
 Db 604 TCCATGCTGACATATGTAAGAGGTACACTGAGCCTATGATATGATCCGTCACACAGAA 663  
 QY 661 GGCAACATGAGAGAGGTGAGAGGCTTCAAGATATGTCAGGAGAAAGAGGAT 720  
 Db 664 GGCAACATGAGAGAGGTGAGAGGCTTCAAGATATGTCAGGAGAAAGAGGAT 723  
 QY 721 TGATGCCCCACTTTTCAAAATCTACATATGTCAGGAGAGCAAGCTTGTATAGCTG 780  
 Db 724 TGATGCCCCACTTTTCAAAATCTACATATGTCAGGAGAGCAAGCTTGTATAGCTG 783  
 QY 781 CTGAAAGAGCTCACAATGCTACTTGGCCAGAGCCCGGGTGTGGCTTCTGTGAGGGC 840  
 Db 784 CTGAAAGAGCTCACAATGCTACTTGGCCAGAGCCCGGGTGTGGCTTCTGTGAGGGC 843  
 QY 841 ATGACGGTGAAGAGGTGTGATGAGGAGGAGGCTGAGGCTTATGAGGAGAAATTTCTG 900  
 Db 844 ATGACGGTGAAGAGGTGTGATGAGGAGGAGGCTGAGGCTTATGAGGAGAAATTTCTG 903  
 QY 901 CTTCCTGGGAGGAGAACAGATGTCATCTTATGAGATCTCAAGAGACAGATCTATAG 960  
 Db 904 CTTCCTGGGAGGAGAACAGATGTCATCTTATGAGATCTCAAGAGACAGATCTATAG 963  
 QY 961 GAAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGCTTTTGAAGACATATTCACAGA 1020  
 Db 964 GAAAGACAGAAAGAAATGCAAGGTGCTTCTTCAAGGCTTTTGAAGACATATTCACAGA 1023  
 QY 1021 AGTAGAGCCGTCGTCGACATGCCCCAGGCTTGAATCTAGAGCTCAAGTTCAGGGCCC 1080  
 Db 1024 AGTAGAGCCGTCGTCGACATGCCCCAGGCTTGAATCTAGAGCTCAAGTTCAGGGCCC 1083  
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RESULT 3  
 AX068372  
 LOCUS 2172 bp DNA linear PAT 25-JAN-2001  
 DEFINITION Sequence 7 from Patent WO0102566.  
 AX068372  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 FEATURES  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT 554 a 488 c 544 g 586 t  
 ORIGIN  
 Query Match 90.8%; Score 1008; DB 6; Length 2172;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 QY 61 CAGTCCAGTGAAGAGGGGTGTGGCTCACAATGTGGGTACATATTAATGAGCTCTC 120  
 Db 425 CAGTCCAGTGAAGAGGGGTGTGGCTCACAATGTGGGTACATATTAATGAGCTCTC 484  
 QY 121 TTTTCTGTCATGACCAAGCTTCTGTGAGCAAGATTGATGAGAGAGTGTGGGCAATC 180  
 Db 485 TTTTCTGTCATGACCAAGCTTCTGTGAGCAAGATTGATGAGAGAGTGTGGGCAATC 544  
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 Db 605 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATGAGGAAATTCCTGTGG 664  
 QY 301 CATTCGGCTGTGGCCCTAGAGAGCAAGCAATGATTCATAAGAGATTCCCTCATTTCTTCG 360  
 Db 665 CATTCGGCTGTGGCCCTAGAGAGCAAGCAATGATTCATAAGAGATTCCCTCATTTCTTCG 724  
 QY 361 GAAAGAGAGAGGGCTGTGATGCTGTGAGAGGAGGCTTCTTCTTCCCTCCGCTCAAG 420  
 Db 725 GAAAGAGAGAGGGCTGTGATGCTGTGAGAGGAGGCTTCTTCTTCCCTCCGCTCAAG 784  
 QY 421 AAGCCCATATAGGGGTCTTGGGCTGTGATGCTTATGAGATCTCAAGAGACAGATCTATAG 480  
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QY 721 TGCATCGCCCACTCTTCAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAGCTG 780  
DB 1085 TGCATCGCCCACTCTTCAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAGCTG 1144  
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QY 841 ATGACGGGTGAGAGGTCTGTATGGCCCATGAGGGCCCTGGGTCTAGTGGAGAAATTTCTG 900  
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DB 1385 AGTAGTCCGTGCTGTGCAATGCGCCGCTCGAATCTAGAGCTCAAGTTCAAGGGCC 1444  
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DB 1445 ATCACTGAGACTGAGGAGCAGGCTCATCTAA 1474

RESULT 4  
AX068374 2149 bp DNA linear PAT 25-JAN-2001  
LOCUS Sequence 9 from Patent WO0102566.  
DEFINITION AX068374  
ACCESSION AX068374.1 GI:12578538  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 9 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES  
Source Location/Qualifiers  
1..2149  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 547 a 485 c 538 g 579 t  
ORIGIN

Query Match 80.5%; Score 894; DB 6; Length 2149;  
Best local similarity 99.8%; Pred. No. 0;  
Matches 994; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 61 CAGTCCAGTGAAGAGAGGTGGTGGCTCAATGCTGGGTGACATCATTTATGAGCTCTC 120  
DB 425 CAGTCCAGTGAAGAGAGGTGGTGGCTCAATGCTGGGTGACATCATTTATGAGCTCTC 484  
QY 121 TTTTCTGTTCATCAACAGCTTACTGTGACGAAGTTCAATGAGAGAAAGTGTGGGCAATC 180  
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QY 181 CGTGAACAGTATGGCATTTCAGAGAGTGGAGGCCATGCTGCATACCCCTGAAAGGATCAAT 240  
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QY 241 TCAGACCCCACTACTTGGCCCAATCACTGAGCTGTGTAGATTAAGGATTTCTGTCTG 300  
DB 605 TCAGACCCCACTACTTGGCCCAATCACTGAGCTGTGTAGATTAAGGATTTCTGTCTG 664  
QY 301 CATTCGGCTGTGGCCCTTGAAGCAGAGCATTTGATTAAGAGATTTCCCTCATTTCTTGG 360  
DB 665 CATTCGGCTGTGGCCCTTGAAGCAGAGCATTTGATTAAGAGATTTCCCTCATTTCTTGG 724  
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DB 725 GAAGAGAGAGAGGCTTGTATGCTGTGTGATGGCTCTCTTCTTCCGCTCCAG 784  
QY 421 AAGCCCATATGAGGGGTCAATTTGGCTGTTCAGATTCTTTAGCCATTCAAGTCCAGAAAT 480  
DB 785 AAGCCCATATGAGGGGTCAATTTGGCTGTTCAGATTCTTTAGCCATTCAAGTCCAGAAAT 844  
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DB 905 GACAAGACTCTGTTCAAAATATTTATGATGAGGGTGTGCTTCAAGTCTCAGAGGCAAG 964  
QY 601 TCCATGTTGACATATGTAAGAGGTAACAATGACCTATGATCAAGCCGTACACAGAA 660  
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QY 721 TGCATCGCCCACTCTTCAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAGCTG 780  
DB 1085 TGCATCGCCCACTCTTCAAAATCTACATATGACAGGGAGAGAGCTTTGATTAAGCTG 1144  
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QY 901 CTTCCTGGGCAAGGAAACAGATGCGATCTTTATTTAGATCTCAAGAAACAGCATCTATGG 960  
DB 1265 CTTCCTGGGCAAGGAAACAGATGCGATCTTTATTTAGATCTCAAGAAACAGCATCTATGG 1324  
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DB 1325 GAAGACAGAGAAATATGCGAAGTGGCTTCTTCAAG 1360

RESULT 5  
AX068376 2064 bp DNA linear PAT 25-JAN-2001  
LOCUS Sequence 11 from Patent WO0102566.  
DEFINITION AX068376  
ACCESSION AX068376.1 GI:12578539  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Schwarz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 11 11-JAN-2001;

Neurocrine Biosciences, Inc. (US)  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

BASE COUNT 518 a 466 c 519 g 561 t

ORIGIN

Query Match 72.9%; Score 809; DB 6; Length 2064;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 909; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 425 CAGTCCAGTGAAGAGGGTGGTCACTGCTGGGTGACATATTATTTGAGCTTC 484  
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 485 TTTTCTGTTATCACTCAAGCTTCTGTGAGCAAGTTTCAAGAGAAAGTGTGGGCACTC 544  
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 665 CATTCGGCTGTGGCCCTTAAGAGAGCAATTAAGATTCCTCATTTCTTCG 724  
 361 GAAGAGAGAGGGCTTGGATGCTGTGAGATGGCTCTCTTCCTTCCTGCTCAAG 420  
 725 GAAGAGAGAGGGCTTGGATGCTGTGAGATGGCTCTCTTCCTTCCTGCTCAAG 784  
 421 AAGCCCAATAGAGGGCTCATTTGGCTGTGCTTCAAGTTCTTACGATTCAGTCCAGAA 480  
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 1205 ATGACGGTGAAGGCTGTGCTGATGCGCATGAGCGCTGTGGTCTTATGGAGAAATTTCTG 1264

901 CTTCTGGGAG 911  
 1265 CTTCTGGGAG 1275

RESULT 6  
 AX068371  
 LOCUS  
 DEFINITION Sequence 6 from Patent WO0102566.  
 ACCESSION AX068371  
 VERSION AX068371.1 GI:12578536  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Schwarz, D.A. and Maki, R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 6 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

BASE COUNT 552 a 516 c 561 g 612 t

ORIGIN

Query Match 50.5%; Score 560; DB 6; Length 2241;  
 Best Local Similarity 99.7%; Pred. No. 4.6e-312;  
 Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGTCCCTCTGATCTGTCACTCTTACTTTGAAGAAGATCCGAGGAGTCA 60  
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 725 GAAGAGAGAGGGCTTGGATGCTGTGAGATGGCTCTCTTCTTCCTGCTCAAG 784  
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 905 GACAAGACTCTGTTCAAAATTTTCAATAGAGGGTGTGCTTCAAGATTCCTTCAAGAAC 964

Query 601 TCAGTGTGACATAGTGAAGAGGTACCACTGACCTATGATGAGCCGTACACAGAA 660  
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Qy 661 GG 662  
Db 1025 GG 1026

RESULT 7  
AX068370 2326 bp DNA linear PAT 25-JAN-2001  
LOCUS AX068370  
DEFINITION Sequence 5 from Patent WO0102566.  
ACCESSION AX068370  
VERSION AX068370.1 GI:12578535  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Schwartz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 5 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES location/Qualifiers  
source 1.2326  
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/mol\_type="genomic DNA"  
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BASE COUNT 581 a 535 c 580 g 630 t  
ORIGIN

Query Match 50.5%; Score 560; DB 6; Length 2326;  
Best Local Similarity 99.7%; Pred. No. 4.6e-312;  
Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGTCCTTGTGATCTGTCAGTCTTACTTTTGAAGAAGATGTCGAGAGTGA 60  
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Qy 61 CAGTCCAGTGAAGAGAGGTGGTGTCAATGCTGGGTGACATCATTTATGAGCTCTC 120  
Db 425 CAGTCCAGTGAAGAGAGGTGGTGTCAATGCTGGGTGACATCATTTATGAGCTCTC 484  
Qy 121 TTTTCTGTTCAACACAGCTTACTGTGACCAAGTTCAATGAGAGAGTGGGGCAGTC 180  
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Qy 301 CATTCGGCTGTGGCCCTTAAGAGACATTAAGTTCAATAGAGATTCCTCATTTCTTCG 360  
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Qy 361 GAAGAGAGAGAGGCTGTGATGCTGTGATGAGGCTCTCTCTCCCTCCGCTCCAG 420  
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Qy 421 AAGCCATAGTAGGGGTCAATGGGCTGTGATTCAGATTCCTTAGCCATTCAGATTCAGAT 480  
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Query 541 GACAAGACTCTGTTCAATATTTTCATGAGGGTGTGCTTCAGATGCTCAGACGCAAG 600  
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Qy 601 TCAGTGTGACATAGTGAAGAGGTACCACTGACCTATGATGAGCCGTACACAGAA 660  
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Qy 661 GG 662  
Db 1025 GG 1026

RESULT 8  
AX068368 2349 bp DNA linear PAT 25-JAN-2001  
LOCUS AX068368  
DEFINITION Sequence 3 from Patent WO0102566.  
ACCESSION AX068368  
VERSION AX068368.1 GI:12578534  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Schwartz, D.A. and Maki, R.A.  
TITLE Metabotropic glutamate receptors and methods of use therefor  
JOURNAL Patent: WO 0102566-A 3 11-JAN-2001;  
Neurocrine Biosciences, Inc. (US)  
FEATURES location/Qualifiers  
source 1.2349  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 588 a 538 c 586 g 637 t  
ORIGIN

Query Match 50.5%; Score 560; DB 6; Length 2349;  
Best Local Similarity 99.7%; Pred. No. 4.6e-312;  
Matches 660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGTCCTTGTGATCTGTCAGTCTTACTTTTGAAGAAGATGTCGAGAGTGA 60  
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Qy 61 CAGTCCAGTGAAGAGAGGTGGTGTCAATGCTGGGTGACATCATTTATGAGCTCTC 120  
Db 425 CAGTCCAGTGAAGAGAGGTGGTGTCAATGCTGGGTGACATCATTTATGAGCTCTC 484  
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Db 665 CATTCGGCTGTGGCCCTTAAGAGACATTAAGTTCAATAGAGATTCCTCATTTCTTCG 724  
Qy 361 GAAGAGAGAGAGGCTGTGATGCTGTGATGAGGCTCTCTCTCCCTCCGCTCCAG 420  
Db 725 GAAGAGAGAGAGGCTGTGATGCTGTGATGAGGCTCTCTCTCCCTCCGCTCCAG 784  
Qy 421 AAGCCATAGTAGGGGTCAATGGGCTGTGATTCAGATTCCTTAGCCATTCAGATTCAGAT 480  
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 RESULT 9  
 AX068366 2551 bp DNA linear PAT 25-JAN-2001  
 LOCUS Sequence 1 from Patent WO0102566.  
 AX068366  
 AX068366 GI:12578533  
 DEFINITION  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Schwarz, D.A. and Maki, R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 1 11-JAN-2001;  
 Neurocrine Biosciences, Inc. (US)  
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 DB 485 TTTTCTGTATCATCAGCCTACTGTCGACGAAGTTTATGAGAGAGTGTGGGCGAGTC 544  
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 DB 545 CGTGAACATGATGATTCATGAGAGTGAAGGCCATGCTGATACCTCGAAGAGATCAAT 604  
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 AC136759  
 AC136759 GI:27777598  
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 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barrera, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A.,  
 Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Faro, S., Ferreira, P., Flitzgerald, M., Gage, D., Galagan, J.,  
 Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karakas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,  
 Matthews, C., McCarthy, M., Melidrim, J., Menus, L., Mihova, T.,  
 Mienna, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., North, C.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunhang, P., Pierre, N., Raymond, C., Retta, R.,  
 Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,  
 Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,  
 Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (07-NOV-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 152269)  
 REFERENCE  
 AUTHORS Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barrera, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A.,  
 Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Faro, S., Ferreira, P., Flitzgerald, M., Gage, D., Galagan, J.,  
 Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karakas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,  
 Matthews, C., McCarthy, M., Melidrim, J., Menus, L., Mihova, T.,  
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TITLE
JOURNAL
REFERENCE
AUTHORS
Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-DEC-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 152269)
Britten, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
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Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A.,
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Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karacas, A., Kellis, C., Lander, T., Levine, R.,
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 17, 2003 this sequence version replaced gi:27151430.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L28531
Center clone name: L14_J_20
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Only the first 152.3 kilobases of this clone are being submitted.
The remainder overlaps accession number AC130364 [WIGR project
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DEFINITION SEQUENCE, 27 unordered pieces.
ACCESSION AC026078
VERSION AC026078.3 GI:9958231
KEYWORDS HTG, HTGS_PHASE1, HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE 1. (bases 1 to 182701)
AUTHORS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL The sequence of Homo sapiens clone
REFERENCE 2 (bases 1 to 182701)
AUTHORS Waterston,R.H.
TITLE Direct Submission

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## JOURNAL COMMENT

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Submitted (19-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7534279.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center project name: H NH0335L17
----- Project Information -----
Sequencing vector: Summary Statistics
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
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Assembly program: Phrap; version 0.990319
Consensus quality: 172513 bases at least Q40
Consensus quality: 175496 bases at least Q30
Consensus quality: 177269 bases at least Q20
Insert size: 181000; agarose-fp
Insert size: 180101; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.04 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 133639 148404: contig of 14766 bp in length
* 148405 148504: gap of unknown length

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JOURNAL  
 Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE  
 3 (bases 1 to 58560)  
 AUTHORS  
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
 Barrera, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boulanger, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
 Cook, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J., S., Dodge, S.,  
 Fardo, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,  
 Gardy, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
 Karst, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,  
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 McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mlenga, V.,  
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,  
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
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 Zembek, L., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## COMMENT

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Sep 4, 2002 this sequence version replaced gi:22267776.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L27942

Center clone name: 995\_C\_20

\* NOTE: This record contains 74 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
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 23684 24370: contig of 688 bp in length  
 24371 24470: gap of 100 bp  
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 25161 25260: gap of 100 bp  
 25261 25969: contig of 709 bp in length  
 25970 26069: gap of 100 bp  
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 27563 27662: gap of 100 bp  
 27663 28372: contig of 710 bp in length  
 28373 28472: gap of 100 bp  
 28473 29170: contig of 698 bp in length  
 29171 29270: gap of 100 bp  
 29271 29949: contig of 679 bp in length  
 29950 30049: gap of 100 bp  
 30050 30750: contig of 701 bp in length  
 30751 30850: gap of 100 bp  
 30851 31531: contig of 681 bp in length  
 31532 31631: gap of 100 bp  
 31632 32395: contig of 764 bp in length  
 32396 32495: gap of 100 bp  
 32496 33183: contig of 688 bp in length  
 33184 33283: gap of 100 bp  
 33284 33985: contig of 702 bp in length  
 33986 34085: gap of 100 bp  
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 34762 34861: gap of 100 bp  
 34862 35574: contig of 713 bp in length  
 35575 35674: gap of 100 bp  
 35675 36383: contig of 709 bp in length  
 36384 36483: gap of 100 bp  
 36484 37178: contig of 695 bp in length  
 37179 37278: gap of 100 bp  
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* 38836 39519: contig of 684 bp in length
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* 39620 40308: contig of 689 bp in length
* 40309 40408: gap of 100 bp in length
* 40409 41107: contig of 699 bp in length
* 41108 41207: gap of 100 bp in length
* 41208 41905: contig of 698 bp in length
* 41906 42005: gap of 100 bp in length
* 42006 42687: contig of 682 bp in length
* 42688 42787: gap of 100 bp in length
* 42788 43499: contig of 712 bp in length
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* 43600 44307: contig of 708 bp in length
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* 44408 45087: contig of 680 bp in length
* 45088 45187: gap of 100 bp in length
* 45188 45872: contig of 685 bp in length
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Query Match 22.8%; Score 253; DB 2; Length 58560;
Best Local Similarity 100.0%; Pred. No. 2.4e-134;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 660 AGGCAATATGAGGAAGTGGAGTGGAGGCTTCAAGATATGTCAGCGAAGAGGAT 719
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DEFINITION AC130357.2 GI:22857687
SEQUENCE, 3 unordered pieces.
AC130357
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VERSION HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 146921)
Birtren,B., Nusbbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-208A14
Unpublished
2 (bases 1 to 146921)
Birtren,B., Nusbbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 146921)
Birtren,B., Nusbbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
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O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunthang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schnupack,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,J.,
Tefaye,S., Theodore,J., Topham,K., Travers,M., Vasilev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 14, 2002 this sequence version replaced gi:22165292.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center Project name: L27963
Center clone name: 208 A.14
----- Summary Statistics
Sequencing vector: Plasmid, n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145664 bases at least Q40
Consensus quality: 145764 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 146721; sum-of-contigs
Quality coverage: 18.2 in Q20 bases; agarose-fp
Quality coverage: 18.7 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 11413: contig of 11413 bp in length
* 11414 11513: gap of 100 bp
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* 12217 12316: gap of 100 bp
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FEATURES
Source

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Best Local Similarity 100.0% Pred. No. 2.2e-134
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 660 AGGCACTATGGAAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAGAGGAT 719
DB 77486 AGGCACTATGGAAGAAAGTGGATGGAAGCTTCAAGATATGTCAGCGAAGAGAGGAT 77427
QY 720 TTGCATCGCCCACTTCAAAATCTACAGTAATGCAAGGAGAGAGGCTTGTATAGCT 779
DB 77426 TTGCATCGCCCACTTCAAAATCTACAGTAATGCAAGGAGAGAGGCTTGTATAGCT 77367
QY 780 GCTGAAGAAAGCTCAAGTCACTTGCACAGCCCGGCTGCTGCTTCTGTAGAGG 839
DB 77366 GCTGAAGAAAGCTCAAGTCACTTGCACAGCCCGGCTGCTGCTTCTGTAGAGG 77307
QY 840 CATGACGGTGAAGAGTCTGCTGATGCGCATAGAGCCCTGGGCTCTGTGAGAGATTTC 899
DB 77306 CATGACGGTGAAGAGTCTGCTGATGCGCATAGAGCCCTGGGCTCTGTGAGAGATTTC 77247
QY 900 GCTTCTGGGACAG 912
DB 77246 GCTTCTGGGACAG 77234

RESULT 14
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LOCUS Homo sapiens chromosome 11, clone RP11-707M1, complete sequence.
DEFINITION AC130364
AC130364 GI:23683265
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 173032)
Birren, B., Nuebaum, C. and Lander, B.
Homo sapiens chromosome 11, clone RP11-707M1
Unpublished
2 (bases 1 to 173032)
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camara, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

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Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 173032)
REFERENCE
AUTHORS
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camara, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 173032)
REFERENCE
AUTHORS
Birren, B., Nuebaum, C., Lander, B., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camara, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (10-OCT-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 10, 2002 this sequence version RepeatMasker:
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/BW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: 707_M_1
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/chromosome="11"
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/clone="RP11-707M1"
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## TITLE

## JOURNAL

REFERENCE  
AUTHORS

Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Punthang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teste, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
(bases 1 to 173795)

Barren, B., Bastien, V., Bloom, T., Boguslavsky, L., Boulghalter, B., Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A., Cook, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J., Dodge, S., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Punthang, P., Piere, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teste, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 10, 2002 this sequence version replaced gi:23477886.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIRB

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information

Center project name: L27938

Center clone name: 871\_G\_20

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 3810: contig of 3810 bp in length  
\* 3811 3910: gap of 100 bp  
\* 3911 47222: contig of 43312 bp in length  
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## FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2e-134;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: December 14, 2003, 21:51:55  
Job time: 4199.38 secs







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; Patent No. 6534287  
; GENERAL INFORMATION:  
; APPLICANT: STORMANN, THOMAS M.  
; APPLICANT: LEVINTHAL, CYNTHIA  
; APPLICANT: STORJOHANN, LAURA  
; APPLICANT: HAMMERLAND, LANCE G.  
; APPLICANT: KRAPCHO, KAREN J.  
; APPLICANT: NPS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; FILE REFERENCE: 1094.2.6  
; CURRENT APPLICATION NUMBER: US/09/695,481  
; CURRENT FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 60/161,481  
; PRIOR FILING DATE: 1998-10-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent In Ver. 2.1  
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; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
; OTHER INFORMATION: molecule comprising portions of human mGluR2 and  
; OTHER INFORMATION: the human calcium receptor.  
; NAME/KEY: CDS  
; LOCATION: (1)...(3129)  
US-09-695-481-5

Query Match 20.0%; Score 222; DB 4; Length 3129;  
Best Local Similarity 99.1%; Pred. No. 2.9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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QY 641 TATCAGCCGTGACACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 700  
Db 641 TATCAGCCGTGACACACAGAAAGGCACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 700  
QY 701 TGTGAGGAGGAAGGATTTGATGCGCCACTCTTACAAATCTACAGTAATGACGGG 760  
Db 701 TGTGAGGAGGAAGGATTTGATGCGCCACTCTTACAAATCTACAGTAATGACGGG 760  
QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAAGCTCACAACTCACTTGCCCAAGCCCGGCTGG 820  
Db 761 AGCAGAGCTTTGATAGCTGCTGAAGAAGCTCACAACTCACTTGCCCAAGCCCGGCTGG 820

QY 821 TGGCCTACTCTGTGAGGAGGATGACGGGTGAGAGGCTGTGATGAGGCCATGAGGCGCTGG 880  
Db 821 TGGCCTACTCTGTGAGGAGGATGACGGGTGAGAGGCTGTGATGAGGCCATGAGGCGCTGG 880  
QY 881 GTCTAG 886  
Db 881 GTCTAG 886

RESULT 3  
US-09-016-434-1133  
; Sequence 1133, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 845-4166  
; TELEFAX: (650) 855-0555  
; INFORMATION FOR SEQ ID NO: 1133:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4078 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1408051  
US-09-016-434-1133

Query Match 20.0%; Score 222; DB 4; Length 4078;  
Best Local Similarity 99.1%; Pred. No. 2.9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 461 TAGCCATTGAGTTCAGAAATTTGCTCAGCTTTTCAACATCACTCAGATTGCTTACTGAG 520  
Db 611 TAGCCATTGAGTTCAGAAATTTGCTCAGCTTTTCAACATCACTCAGATTGCTTACTGAG 670  
QY 521 CAACCATCATGATGATGAGTGAAGAGCTGTGTTCAATATTTTCAGAGGGTGTGCTT 580  
Db 671 CAACCATCATGATGATGAGTGAAGAGCTGTGTTCAATATTTTCAGAGGGTGTGCTT 730  
QY 581 CAGATGCTCAGCAGCAGAGGCTCATGCTGATGAGCATAGTGAAGAGGTAACAATGACCTATG 640  
Db 731 CAGATGCTCAGCAGCAGAGGCTCATGCTGATGAGCATAGTGAAGAGGTAACAATGACCTATG 790

QY 641 TATCAGCCCTGACACACAGAGGCACTATGAGAAAAGTGGATGGAAGCTTCAAGATA 700  
DB 791 TATCAGCCCTGACACAGAGGCACTATGAGAAAAGTGGATGGAAGCTTCAAGATA 850  
QY 701 TGTCAAGCAGAGAGGAGATTGTCATGCCCACTCTTACAAATCTACAGTAATGACGGGG 760  
DB 851 TGTCAAGCAGAGAGGAGATTGTCATGCCCACTCTTACAAATCTACAGTAATGACGGGG 910  
QY 761 AACAGAGCTTTGATAGCTGCTGAGAAAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 820  
DB 911 AACAGAGCTTTGATAGCTGCTGAGAAAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 970  
QY 821 TGGCCCTACTTGTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGGCCATGAGGCGCTGG 880  
DB 971 TGGCCCTACTTGTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGGCCATGAGGCGCTGG 1030  
QY 881 GTCTAG 886  
DB 1031 GTCTAG 1036

## RESULT 4

US-08-660-148-1  
Sequence 1, Application US/08660148  
Patent No. 6211353

## GENERAL INFORMATION:

APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..3999  
US-08-660-148-1

Query Match 20.0%; Score 222; DB 3; Length 4207;

Best Local Similarity 99.1%; Pred. No. 2,9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TGGCATTTCAGTCCAGATTTGCTCCAGCTTTTCAACCTACCTGAGATTGCTTACTGAG 520  
DB 920 TGGCATTTCAGTCCAGATTTGCTCCAGCTTTTCAACCTACCTGAGATTGCTTACTGAG 979  
QY 521 CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAAAATATTTCATGAGGGTTGTGCTT 580  
DB 980 CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAAAATATTTCATGAGGGTTGTGCTT 1039  
QY 581 CAGATGCTCAGCAGGCAAGTCCATGCTGAGCATGATGTAAGAGTCAACCTGACCTATG 640  
DB 1040 CAGATGCTCAGCAGGCAAGTCCATGCTGAGCATGATGTAAGAGTCAACCTGACCTATG 1099  
QY 641 TATCAGCCCTGACACACAGAGGCACTATGAGAAAAGTGGATGGAAGCTTCAAGATA 700  
DB 1100 TATCAGCCCTGACACACAGAGGCACTATGAGAAAAGTGGATGGAAGCTTCAAGATA 1159  
QY 701 TGTCAAGCAGAGAGGAGATTGTCATGCCCACTCTTACAAATCTACAGTAATGACGGGG 760  
DB 1160 TGTCAAGCAGAGAGGAGATTGTCATGCCCACTCTTACAAATCTACAGTAATGACGGGG 1219  
QY 761 AACAGAGCTTTGATAGCTGCTGAGAAAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 820  
DB 1220 AACAGAGCTTTGATAGCTGCTGAGAAAGCTCAAGTCACTTGCCCAAGGCCCGGGTGG 1279  
QY 821 TGGCCCTACTTGTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGGCCATGAGGCGCTGG 880  
DB 1280 TGGCCCTACTTGTGTGAGGCGATGACGGTGAAGAGTCTGCTGATGGCCATGAGGCGCTGG 1339  
QY 881 GTCTAG 886  
DB 1340 GTCTAG 1345

## RESULT 5

US-08-660-148-3  
Sequence 3, Application US/08660148  
Patent No. 6211353

## GENERAL INFORMATION:

APPLICANT: Burnett, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756

TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-3

Query Match 20.0%; Score 222; DB 3; Length 4207;  
Best Local Similarity 76.3%; Pred. No. 2.9e-102;  
Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 520  
DB 920 UACCCAUUCAGGCGCCAGAAUUGUCUCCAUUUCACACACUCCAGAUUGUCUACAG 979  
QY 521 CAACCATCATGATCTGATGACAGAGCTGTTCAATATTTTCATGAGGGTGTGCTT 580  
DB 980 CAACCATCATGATCTGATGACAGAGCTGTTCAATATTTTCATGAGGGTGTGCTT 1039  
QY 581 CAGATGCTCAGCAGCAGAGGTCATGATGATGATGATGATGATGATGATGATGATGATG 640  
DB 1040 CAGATGCTCAGCAGCAGAGGTCATGATGATGATGATGATGATGATGATGATGATGATG 1099  
QY 641 TATCAGCCGTCACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
DB 1100 UATCAGCCGTCACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 1159  
QY 701 TGTCAAGGAGAGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 760  
DB 1160 UGTCAAGGAGAGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1219  
QY 761 AGCAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 820  
DB 1220 AGCAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1279  
QY 821 TGCCCTACTTCTGTGAGGCGCATGACGCTGATGATGATGATGATGATGATGATGATG 880  
DB 1280 TGCCCTACTTCTGTGAGGCGCATGACGCTGATGATGATGATGATGATGATGATGATG 1339  
QY 881 GTCTAG 886  
DB 1340 GTCUAG 1345

## RESULT 6

US-08-660-148-4  
Sequence 4, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..4095  
US-08-660-148-4

Query Match 20.0%; Score 222; DB 3; Length 4303;  
Best Local Similarity 99.1%; Pred. No. 2.9e-102;  
Matches 422; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 520  
DB 920 TAGCCATTGAGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATTGCTTACTCAG 979  
QY 521 CAACCATCATGATCTGATGACAGAGCTGTTCAATATTTTCATGAGGGTGTGCTT 580  
DB 980 CAACCATCATGATCTGATGACAGAGCTGTTCAATATTTTCATGAGGGTGTGCTT 1039  
QY 581 CAGATGCTCAGCAGCAGAGGTCATGATGATGATGATGATGATGATGATGATGATGATG 640  
DB 1040 CAGATGCTCAGCAGCAGAGGTCATGATGATGATGATGATGATGATGATGATGATGATG 1099  
QY 641 TATCAGCCGTCACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 700  
DB 1100 TATCAGCCGTCACACAGAGGCACTATGAGAAAGTGGAGTGAAGCTTCAAGATA 1159  
QY 701 TGTCAAGGAGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 760  
DB 1160 TGTCAAGGAGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1219  
QY 761 AGCAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 820  
DB 1220 AGCAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1279  
QY 821 TGCCCTACTTCTGTGAGGCGCATGACGCTGATGATGATGATGATGATGATGATGATG 880  
DB 1280 TGCCCTACTTCTGTGAGGCGCATGACGCTGATGATGATGATGATGATGATGATGATG 1339  
QY 881 GTCTAG 886  
DB 1340 GTCTAG 1345

## RESULT 7

US-08-660-148-6  
Sequence 6, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-6

Query Match 20.0%; Score 222; DB 3; Length 4303;  
Best Local Similarity 76.3%; Pred. No. 2,9e-102;

Matches 325; Conservative 97; Mismatches 4; Indels 0; Gaps 0;

QY 461 TAGCCATTAGGTCGCAAGATTGCTCCAGCTTTTCAACATCACTGAGATTGCTTACTAG 520  
DB 920 UAGCCAUUCAGGUCAGAAUUCUCUCCAGCUUUCACAAACUCCAGAUUCUCUACUCAG 979  
QY 521 CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAATATTTTCAAGAGGTTGCTT 580  
DB 980 CAACGAGCAUGGAGUUCGAGUGACAAAGCUCUCAAUUCUACAGAGGUGUUCU 1039  
QY 581 CAGATCTGAGCAGGAGGATCCATGATGAGCATAGTGAAGAGTCAACTGAGCCTATG 640  
DB 1040 CAGAUUCUCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1099  
QY 641 TATCAGCCGCTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGGCTTCAAGATA 700  
DB 1100 UAUACAGCCGUGACACAGAAAGCACTATGAGAAAGTGGATGAGAGGCTTCAAGATA 1159  
QY 701 TGTCAAGCAGAAAGGAGATTTGATGATGCTTCACTTCAAAATCTTCACTATGCAAGG 760  
DB 1160 UGTCAAGCAGAAAGGAGATTTGATGATGCTTCACTTCAAAATCTTCACTATGCAAGG 1219  
QY 761 AGCAGAGCTTTGATAGCTGCTGAGAGAGCTCAAGTCACTGAGGAGGAGGAGGAGGAGG 820  
DB 1220 AGCAGAGCTTTGATAGCTGCTGAGAGAGCTCAAGTCACTGAGGAGGAGGAGGAGGAGG 1279  
QY 821 TGGCCCTACTTGTGTGAGGAGTACGCTGAGAGAGTGTGATGAGCAGGAGGAGGAGG 880  
DB 1280 UGGCCCTGCTGCTGAGGAGTACGCTGAGAGAGTGTGATGAGCAGGAGGAGGAGGAGG 1339  
QY 881 GTCTAG 886  
DB 1340 GUCUAG 1345

RESULT 8

US-08-072-574-11

Sequence 11, Application US/08072574

Patent No. 5521297

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Portisler, Aaron

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 00719

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/072,574

FILING DATE: 19930604

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9383

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-622-7700

TELEFAX: 213-489-4210

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3282 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 370..3003

OTHER INFORMATION: /note="Variant of MGLUR5A with truncated 3' end."

US-08-072-574-11

Query Match 15.4%; Score 171; DB 1; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;

Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 461 TAGCCATTAGGTCGCAAGATTGCTCCAGCTTTTCAACATCACTGAGATTGCTTACTAG 520  
DB 830 TAGCCATTAGGTCGCAAGATTGCTCCAGCTTTTCAACATCACTGAGATTGCTTACTAG 889  
QY 521 CAACCATCATGATCTGAGTGAACAAGCTCTGTTCAATATTTTCAAGAGGTTGCTT 580  
DB 890 CAACGAGCAUGGAGUUCGAGUGACAAAGCUCUCAAUUCUACAGAGGUGUUCU 949  
QY 581 CAGATCTGAGCAGGAGGATCCATGATGAGCATAGTGAAGAGTCAACTGAGCCTATG 640  
DB 950 CAGATCTGAGCAGGAGGATCCATGATGAGCATAGTGAAGAGTCAACTGAGCCTATG 1009  
QY 641 TATCAGCCGCTGACACAGAAAGCACTATGAGAAAGTGGATGAGAGGCTTCAAGATA 700  
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DB 1070 TGTCAAGCAGAAAGGAGATTTGATGATGCTTCACTTCAAAATCTTCACTATGCAAGG 1129  
QY 761 AGCAGAGCTTTGATAGCTGCTGAGAGAGCTCAAGTCACTGAGGAGGAGGAGGAGGAGG 820

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Db      1130 AGCAGAGCTTGATAGCTGCGTGAAGAAAGCTCACAAGTCACTTGCCCAAGGCCGGGTGG 1189
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Db      1190 TGGCGTCTGCTCTGTGAGGCGCATGACGCTGAGAGGCTCTGCTGATGCGCATGAGCGCCTGG 1249
Qy      881 GTCTAG 886
Db      1250 GTCTAG 1255

RESULT 9
US-08-486-270-11
; Sequence 11, Application US/08486270
; Patent No. 5807689
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen
; APPLICANT: Ponteler, Aaron
; APPLICANT: Johnson, Edwin C.
; APPLICANT: Hess, Stephen D.
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,270
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/072,574
; FILING DATE: 04-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 370..3003
; OTHER INFORMATION: /product= "HUMAN MGLUR5C"
; OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."
US-08-486-270-11

Query Match 15.4%; Score 171; DB 1; Length 3282;
Best Local Similarity 98.8%; Pred. No. 1,5e-76;
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

461 TAGCATTTCAGGTGCAGAAATTGGCTCCAGCTTTCAACATACCTCAGATTGCTTACTACAG 520
|||||
830 TAGCATTTCAGGTGCAGAAATTGGCTCCAGCTTTCAACATACCTCAGATTGCTTACTACAG 889

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OY      521  CACCATCATGAACTGTGATGACAGAGCTCTGTTCAATATATTTATGAGGGTTGTGCTT  580
Db      890  CACCCAGATGGAATCTGATGTACAGAGCTCTGTTCAATATATTTATGAGGGTTGTGCTT  949
OY      581  CAGATGCTCAGCAGGCAAGGTCATGTGTGACATAGTGAAGAGGTACAATGACCTATG  640
Db      950  CAGATGCTCAGCAGGCAAGGTCATGTGTGACATAGTGAAGAGGTACAATGACCTATG  1009
OY      641  TATCAGCCGTTCACACAGAAAGGCAATATGGAAGAAAGTGGATGGAAGCTTCAAGATA  700
Db      1010  TATCAGCCGTTCACACAGAAAGGCAATATGGAAGAAAGTGGATGGAAGCTTCAAGATA  1069
OY      701  TGTGAGCGAAGAAAGGATTTGTCATGTGCCCACTCTTACAAATATCTACAGTATGCAAGGG  760
Db      1070  TGTGAGCGAAGAAAGGATTTGTCATGTGCCCACTCTTACAAATATCTACAGTATGCAAGGG  1129
OY      761  AGCAGAGCTTGTATGAGCTGCTGAAGAAAGCTCACAGAGCTCACTTGCCCAAGGCCCGGGTGG  820
Db      1130  AGCAGAGCTTGTATGAGCTGCTGAAGAAAGCTCACAGAGCTCACTTGCCCAAGGCCCGGGTGG  1189
OY      821  TGGCTACTTCTGTGAGAGGCGCATGACGGTGAAGAGCTGTCGTATGAGGCGGCTTGG  880
Db      1190  TGGCTACTTCTGTGAGAGGCGCATGACGGTGAAGAGCTGTCGTATGAGGCGGCTTGG  1249
OY      881  GTCTAG 886
Db      1250  GTCTAG 1255

RESULT 10
US-08-367-264-11
: Sequence 11, Application US/08367264
: Patent No. 6001581
: GENERAL INFORMATION:
: APPLICANT: Daggett, Lorrle
: APPLICANT: Ellis, Steven B.
: APPLICANT: Liaw, Chen
: APPLICANT: Pontsler, Aaron
: APPLICANT: Johnson, Edwin C.
: APPLICANT: Hess, Stephen D.
: TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.
: TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pretzy, Schroeder, Brueggemann & Clark
: STREET: 444 South Flower Street, Suite 2000
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/367,264
: FILING DATE: 02-JUN-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/072,574
: FILING DATE: 04-JUN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Reiter, Stephen E.
: REGISTRATION NUMBER: 31,192
: REFERENCE/DOCKET NUMBER: FP41 9772
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-546-4737
: TELEFAX: 619-546-9392
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3282 base pairs
:

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TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-367-264-11

Query Match 15.4%; Score 171; DB 3; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 521 CAACCATCATGATCTGAGTGAAGAGACTCTGTTCAATATTTCATGAGGGTTGCTT 580  
DB 890 CAACCATCATGATCTGAGTGAAGAGACTCTGTTCAATATTTCATGAGGGTTGCTT 949  
QY 581 CAGATCTCAGCAGGCAAGGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 640  
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QY 641 TATCAGCCGTACACAGAGGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 700  
DB 1010 TATCAGCCGTACACAGAGGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 1069  
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DB 1070 TGTCAAGGAGGAGGATTTGATGCGCCACTTAACTTCAAGTAATGCAAGGG 1129  
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DB 1190 TGGCCTACTTCTGTGAGGCGCATGACGCTGATGAGGCTTCTGATGCGCATGAGCGCTG 1249  
QY 881 GTCTAG 886  
DB 1250 GTCTAG 1255

RESULT 11  
US-09-153-757-11

Sequence 11, Application US/09153757  
Patent No. 6413764

GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.

Liaw, Chen  
Pomslar, Aaron  
Johnson, Edwin C.

Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match 15.4%; Score 171; DB 4; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 461 TAGCCATTGAGTCCGAAATTTGCTCCAGCTTTTCAACATACCTGAGATTGCTTACG 520  
DB 830 TAGCCATTGAGTCCGAAATTTGCTCCAGCTTTTCAACATACCTGAGATTGCTTACG 889  
QY 521 CAACCATCATGATCTGAGTGAAGAGACTCTGTTCAATATTTCATGAGGGTTGCTT 580  
DB 890 CAACCATCATGATCTGAGTGAAGAGACTCTGTTCAATATTTCATGAGGGTTGCTT 949  
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QY 641 TATCAGCCGTACACAGAGGCACTATGAGAAAGTGGATGAGAGCTTCAAGATA 700  
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QY 761 AGCAGAGCTTTGATAAGTCTGTAAGAGCTCAAGTCACTTCCCAAGCCGGGTG 820  
DB 1130 AGCAGAGCTTTGATAAGTCTGTAAGAGCTCAAGTCACTTCCCAAGCCGGGTG 1189  
QY 821 TGGCCTACTTCTGTGAGGCGCATGACGCTGATGAGGCTTCTGATGCGCATGAGCGCTG 880  
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QY 881 GTCTAG 886  
DB 1250 GTCTAG 1255

RESULT 12  
US-09-459-715-11  
Sequence 11, Application US/09459715  
Patent No. 6485919

GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Liew, Chen  
Pontleier, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11

Query Match 15.4%; Score 171; DB 4; Length 3282;  
Best Local Similarity 98.8%; Pred. No. 1.5e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

461 TAGCCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTAGATTGCTTACTAG 520  
830 TAGCCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTAGATTGCTTACTAG 889  
521 CAACCATGATGATCTGAGTGAACAAGCTGTTCAAATATTTTCATGAGGGTTGCTT 580  
890 CAACCATGATGATCTGAGTGAACAAGCTGTTCAAATATTTTCATGAGGGTTGCTT 949  
581 CAATGCTGACGAGCAAGTCCATGCTGACATGAGTGAAGAGTACATGACCTATG 640  
950 CAATGCTGACGAGCAAGTCCATGCTGACATGAGTGAAGAGTACATGACCTATG 1009  
641 TATCAGCCGTGACACAGAGCAACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 700  
1010 TATCAGCCGTGACACAGAGCAACTATGAGAAAGTGGATGGAAGCCTTCAAGATA 1069  
701 TGTCAAGCAAGAGGATTGATGCGCCACTTTCAAAATCTACAGTAAATGCAAGGG 760

DB 1070 TGTCAAGCAAGAGGATTGATGCGCCACTTTACAAATCTACAGTAAATGCAAGGG 1129  
QY 761 AGCAGAGCTTTGATTAAGTGTCTGAAGAGTCAAGATGACTGAGCCCAAGCCGGGTG 820  
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QY 881 GTCTAG 886  
DB 1250 GTCTAG 1255

RESULT 13  
US-08-072-574-7  
Sequence 7, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Liew, Chen  
Pontleier, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7

Query Match 15.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.6e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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830 TAGCCATTGAGTCCAGATTGCTCCAGCTTTCAACATACCTAGATTGCTTACTAG 889  
521 CAACCATGATGATCTGAGTGAACAAGCTGTTCAAATATTTTCATGAGGGTTGCTT 580

Db 890 CAACGACATGATCTGAGTGAACAAGCTCTGTTCAATATTTTCAATGAGGGTTGTGCTT 949  
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Db 950 CAGATGCTCAGCAGGAGGTCATGCTGAGCATAGTGAAGAGTCACTGAGACCTATG 1009  
QY 641 TATCAGCCGTACACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 700  
Db 1010 TATCAGCCGTACACACAGAGGCACTATGAGAAAGTGGATGGAAGCTTCAAGATA 1069  
QY 701 TGTGACGGAAGAGGATTTGATGAGCCCACTCTTCAAAATCTACATGATGCAAGGG 760  
Db 1070 TGTGACGGAAGAGGATTTGATGAGCCCACTCTTCAAAATCTACATGATGCAAGGG 1129  
QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGCCCGGGTGG 820  
Db 1130 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGCCCGGGTGG 1189  
QY 821 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTGATGAGCCATGAGCGCTGG 880  
Db 1190 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTGATGAGCCATGAGCGCTGG 1249  
QY 881 GTCTAG 886  
Db 1250 GTCTAG 1255

RESULT 14  
US-08-486-270-7  
; Sequence 7, Application US/08486270  
; Patent No. 5807689  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lottie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hess, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,270  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ. ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4085 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-486-270-7  
Query Match 15.4%; Score 171; DB 1; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.6e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 461 TAGCCATTCAGGTCAGAAATTTGCTCAGCTTTTCAACATACCTCAGATTGCTTACAG 520  
Db 830 TAGCCATTCAGGTCAGAAATTTGCTCAGCTTTTCAACATACCTCAGATTGCTTACAG 889  
QY 521 CAACCATTCATGATCTGAGTGAACAAGCTCTGTGTAATATTTTCATGAGGTTGTGCTT 580  
Db 890 CAACCATTCATGATCTGAGTGAACAAGCTCTGTGTAATATTTTCATGAGGTTGTGCTT 949  
QY 581 CAGATGCTCAGCAGGAGGATTCATGAGTGAACAATGATGAGTGAAGTGAAGTGAAGTGA 640  
Db 950 CAGATGCTCAGCAGGAGGATTCATGAGTGAACAATGATGAGTGAAGTGAAGTGAAGTGA 1009  
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QY 761 AGCAGAGCTTTGATAGCTGCTGAAGAGTCAAGTCACTTCCCAAGCCCGGGTGG 820  
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Db 1190 TGGCCTACTTCTGTGAGGCGATGACGGTGAAGAGTCTGTGATGAGCCATGAGCGCTGG 1249  
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RESULT 15  
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; Sequence 7, Application US/08367264  
; Patent No. 6001581  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lottie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hess, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/367,264  
; FILING DATE: 02-JUN-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGURSA"  
US-08-367-264-7

Query Match 15.4%; Score 171; DB 3; Length 4085;  
Best Local Similarity 98.8%; Pred. No. 1.6e-76;  
Matches 421; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	461	TAGCCATTGAGTCCAGATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACTAG	520
DB	830	TAGCCATTGAGTCCAGATTTGCTCCAGCTTTCAACATACCTCAGATTGCTTACTAG	889
QY	521	CAACCATCAGATGATCGAGTGAACAAGCTGTTCAATATTTTCATGAGGGTTGCTT	580
DB	890	CAACCATCAGATGATCGAGTGAACAAGCTGTTCAATATTTTCATGAGGGTTGCTT	949
QY	581	CAGATGCTCAGCAGGCAAGGTCCATGCTGATGACATAGTGAAGAGTACAACTGACCTATG	640
DB	950	CAGATGCTCAGCAGGCAAGGTCCATGCTGATGACATAGTGAAGAGTACAACTGACCTATG	1009
QY	641	TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGGAAGCCTTCAAAGATA	700
DB	1010	TATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGGAAGCCTTCAAAGATA	1069
QY	701	TGTCAGGGAAGAAAGGATTTGCATGCGCCACTCTTCAAAATCTACAGTAATGCAAGGG	760
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DB	1250	GTCTAG 1255	

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OM nucleic - nucleic search, using sw model

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Title: US-10-027-923-3

Perfect score: 1110

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Post-Processing: Listing first 45 summaries

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28: gb\_ges1:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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22	40	3.6	647	10	BB625841
23	40	3.6	661	14	BY721282
24	40	3.6	1013	13	BQ070358
25	40	3.1	409	28	AQ227301
26	33	3.0	507	10	BG187881
27	33	2.7	532	29	BZ930457
28	30	2.6	463	28	AQ228293
29	29	2.5	960	10	BG335390
30	28	2.4	229	29	BZ914334
31	27	2.4	997	10	BF025698
32	27	2.3	450	28	AQ471966
C	33	2.2	657	13	BU351729
34	26	2.2	669	13	BU393781
35	24	2.2	673	13	BU390603
36	24	2.2	746	10	AW941949
37	23	2.1	419	14	CA026495
C	38	2.1	480	13	BX279584
39	21	1.9	599	10	BE892280
40	21	1.9	629	21	BE409094
41	21	1.9	643	28	BH467481
C	42	1.9	700	28	AQ325894
43	21	1.9	1201	13	BX358386
44	21	1.8	231	9	AA339052
C	45				

#### ALIGNMENTS

RESULT 1  
BE467477 499 bp mRNA linear EST 27-JUL-2000  
LOCUS h266d08.x1 NCI\_CGAP\_Lu24 Homo sapiens CDNA clone IMAGE:3212943 3'  
DEFINITION similar to SW:MG85\_HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
PRECUSOR ., mRNA sequence.

ACCESSION BE467477  
VERSION BE467477.1 GI:9513252

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS 1 (bases 1 to 499)  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Christopher Mokaluk, M.D., Ph.D., Michael R.  
Zimmer-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:

infoimage.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 493.  
Location/Qualifiers

# FEATURES

source

1. 499  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP LUS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 107 c 138 g 113 t  
ORIGIN

Query Match 45.0%; Score 499; DB 10; Length 499;  
Best Local Similarity 100.0%; Pred. No. 3,1e-234;  
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

497 ACAATACCTGAGATTGCTTACTCAGCAACATCATGATGATGAGTACAGACCTCTGTCA 556  
1 ACATACCTGAGATTGCTTACTCAGCAACATCATGATGATGAGTACAGACCTCTGTCA 60  
557 AATTTTTCAGAGGTTGCTTCTCAGATGCTCAGCAGGAGGATCCATGCTGACATAG 616  
61 AATATTTTCAGAGGTTGCTTCTCAGATGCTCAGCAGGAGGATCCATGCTGACATAG 120  
617 TGAAGAGTCACTGAGCCTATGATCAGCCGTAACACAGAAAGCACTATGAGAGAA 676  
121 TGAAGAGTCACTGAGCCTATGATCAGCCGTAACACAGAAAGCACTATGAGAGAA 180  
677 GTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGAAAGGATTTGATGCCCACTCT 736  
181 GTGGAGTGAAGGCTTCAAGATATGTCAGCGAAGAAAGGATTTGATGCCCACTCT 240  
737 ACAAAATCTTCAGTAATGCGAGGAGCAGAGCTTTGATTAAGCTGCTAAAGAGTCA 796  
241 ACAAAATCTTCAGTAATGCGAGGAGCAGAGCTTTGATTAAGCTGCTAAAGAGTCA 300  
797 GTCACTTGCCCAAGGCGCGGTGGTGGCTTACTCTGTGAGGGGATGACGGTGAAGGTC 856  
301 GTCACTTGCCCAAGGCGCGGTGGTGGCTTACTCTGTGAGGGGATGACGGTGAAGGTC 360  
857 TGGTGAATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTGCTTCTGGGACGGGAC 916  
361 TGGTGAATGCGCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTGCTTCTGGGACGGGAC 420  
917 CAGATGCGCATCTTTATGAGATCTCAAGAAACAGCATCTTATGAGAAAGCAAGAAAT 976  
421 CAGATGCGCATCTTTATGAGATCTCAAGAAACAGCATCTTATGAGAAAGCAAGAAAT 480  
977 GCCAAGGTGCTTCTCTTCA 995  
481 GCCAAGGTGCTTCTCTTCA 999

RESULT 2  
BE674422 519 bp mRNA linear EST 08-SEP-2000  
LOCUS BE674422  
DEFINITION 7E0104.X1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166 3.  
ACCESSION BE674422  
VERSION BE674422.1 GI:10034963

KEYWORDS  
SOURCE  
ORGANISM

# REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 519)  
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncigap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-rc@mail.nih.gov](mailto:cgaps-rc@mail.nih.gov)  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
infoimage.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 499.  
Location/Qualifiers

# FEATURES

source

1. 519  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:3281166"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_1lb="NCI CGAP Lu24"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP LUS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 143 a 114 c 143 g 119 t  
ORIGIN

Query Match 44.1%; Score 489; DB 10; Length 519;  
Best Local Similarity 100.0%; Pred. No. 2.6e-225;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

508 ATTGCTTACTCAGCAACATCATGATGATGAGTACAGACCTCTGTTCAATTTTCATG 567  
31 ATTGCTTACTCAGCAACATCATGATGATGAGTACAGACCTCTGTTCAATTTTCATG 90  
568 AGGGTTGCTTCAAGTCTCAGCAGGAGGATCCATGCTGAGCAATGAGAGCTAC 627  
91 AGGGTTGCTTCAAGTCTCAGCAGGAGGATCCATGCTGAGCAATGAGAGCTAC 150  
628 AACTGACCTATGATCAGCCGTAACACAGAAAGCACTATGAGAAAGTGGAGTGA 687  
151 AACTGACCTATGATCAGCCGTAACACAGAAAGCACTATGAGAAAGTGGAGTGA 210  
688 GCCTCAAGATATGTCAGCAGAAAGGATTTGATGATGCCCACTTTACAAATCTAC 747  
211 GCCTCAAGATATGTCAGCAGAAAGGATTTGATGATGCCCACTTTACAAATCTAC 270  
748 AGTATGACAGGGAGAGAGCTTTGATTAAGCTGCTGAAGAGTCAAGATCACTTGGCCC 807  
271 AGTATGACAGGGAGAGAGCTTTGATTAAGCTGCTGAAGAGTCAAGATCACTTGGCCC 330  
808 AAGGCGGCGGTGGTGGCTTCTGTGAGGGGATGACGGTGAAGAGTCTGCTGATGGCC 867  
331 AAGGCGGCGGTGGTGGCTTCTGTGAGGGGATGACGGTGAAGAGTCTGCTGATGGCC 390  
868 ATGAGCGCGTGGGTCTAGTGGAGAAATTTCTGCTTCTGGGACGGGACCAAGATGCATC 927

	Db	391	MTGAGCGCCGTGGTCTAGTGGAAGAATTTCTGCTTCGGGAGGGAACCAATGCCATC	450
Oy		928	TTTATTGACATTCGAAGAACAAGCATCTCTATGGGAAGACAGAAAGAAATGCCAGTGC	987
Db		451	TTTATTGAGATTCGAAGAACAAGCATCTCTATGGGAAGACAGAAAGAAATGCCAGTGC	510
Oy		988	TTCCTTCAG	996
Db		511	TTCTTCAG	519
RESULT 3				
LOCUS		AM015382		
DEFINITION		UT-H-B10-aac-d-06-0-Ut-s1 NCI CGAP_Sub1 Homo sapiens cDNA clone		
ACCESSION		AM015382		
VERSION		AM015382.1		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		NCI-CGAP http://www.ncbi.nlm.nih.gov/hcicgap.		
AUTHORS		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
TITLE		Tumor Gene Index		
JOURNAL		Unpublished		
COMMENT		Contact: Robert Strausberg, Ph.D. Email: rgsapbs@mai.nih.gov Oligo-dT track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://www-bio.lnl.gov/bbrp/image/image.html">www-bio.lnl.gov/bbrp/image/image.html</a> Seq primer: M13 Forward		
FEATURES				
Source		Location/Qualifiers		
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		/organism="Homo sapiens"		
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		/clone="IMAGE:2710331"		
		/lab_host="DH10B (Life Technologies)"		
		/clone_id="NCI CGAP Sub1"		
		/note="Vector: pRTD-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NCI_CGAP_Sub1 library is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI CGAP Co6, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP Co10, NCI CGAP Kid5, NCI CGAP Kid2, NCI CGAP Kid3, NCI CGAP Kid1, NCI CGAP Trm2, NCI CGAP Br2, NCI CGAP Co8, NCI CGAP Cui1, NCI CGAP Le12, NCI CGAP Brn23, NCI CGAP Lus , NCI CGAP Lu24, NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6 , NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_Kid3 pool 1 LLM 3334-3337, 3682-3683, 3788-3803 (IMAGE Clonides 1322376-1323911, 1456008-1456775, 1500552-1502855 ) NCI CGAP Kid5 pool 1 LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonide 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP Lus pool 1 LLM 3575-3582, 3851-3854 (IMAGE Clonides 141620-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1 LLM 3164-3167, 3736-3720, 3733-3735 (IMAGE Clonides 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonides 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 530,000 recombinants.		

Query Match	37.1%	Score 412	DB 9	Length 442
Best Local Similarity	100.0%	Prod. No. 2e-191		
Matches 412	Conservative 0	Mismatches 0	Indels 0	Gaps 0
<p>Subtraction was performed as previously described (Bonaldo, Lemon &amp; Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.            TAG LIB=NCI CGAP Le12            TAG TISSUE=le1omyosarcoma            TAG_SEQ=AATCG"</p>				
BASE COUNT	118 a	97 c	127 g	100 t
ORIGIN				
QY	486	CCAGCTTTCAACATPACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGTACAA	545	
DB	7	CCAGCTTTCAACATPACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGTACAA	66	
QY	546	GACCTGTGTTCAATTTCAATGAGGGTTTGCCCTTCAGATGCTCAGCAGCGCAAGTCCAT	605	
DB	67	GACCTGTGTTCAATTTCAATGAGGGTTTGCCCTTCAGATGCTCAGCAGCGCAAGTCCAT	126	
QY	606	GGTGACACATGATGAAAGGTACCACTGACCTATGATACAGCCGTACACAGAAAGCAA	665	
DB	127	GGTGACACATGATGAAAGGTACCACTGACCTATGATACAGCCGTACACAGAAAGCAA	186	
QY	666	CTATGAGAAAGTGGATGGAAGCCCTTCAAGATATGTCAAGCGAAGGAGGATTTGCAT	725	
DB	187	CTATGAGAAAGTGGATGGAAGCCCTTCAAGATATGTCAAGCGAAGGAGGATTTGCAT	246	
QY	726	CGCCCACTTTTACAAATCTACAGTAAATGCAAGGGAGACAGACTTTGATTAAGCTGCTGAA	785	
DB	247	CGCCCACTTTTACAAATCTACAGTAAATGCAAGGGAGACAGACTTTGATTAAGCTGCTGAA	306	
QY	786	GAAGCTCAACAAGTCACTTGGCCCAAGGCCCGGGTGGTGGCCCTTCTGTGAGGCGATGAC	845	
DB	307	GAAGCTCAACAAGTCACTTGGCCCAAGGCCCGGGTGGTGGCCCTTCTGTGAGGCGATGAC	366	
QY	846	GGTAGAGAGTCTGCTGATGCGCATGAGCGCGCTGGTCTAGTGGGAGAAATTT	897	
DB	367	GGTAGAGAGTCTGCTGATGCGCATGAGCGCGCTGGTCTAGTGGGAGAAATTT	418	
RESULT 4	BG150163	414 bp	mRNA	linear
LOCUS	add46b03.x1	NCI CGAP Lu24	Homo sapiens	cdna clone IMAGE:3358404 3'
DEFINITION	similar to SW:WGR5	HUMAN P41594	MEYABOTROPIC GLUTAMATE RECEPTOR 5	
ACCESSION	PRECURSOR. 11	;	mRNA sequence.	
VERSION	BG150163			
KEYWORDS	BG150163.1	GI:12662193		
SOURCE	EST.			
ORGANISM	Homo sapiens	(human)		
REFERENCE	Bukayrouti; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Euteleostomi; Primates; Catarrhini; Homiidae; Homo.			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
COMMENT	Tumor Gene Index			
	Unpublished			
	Contact: Robert Straubeberg, Ph.D.			
	Email: cgaabs-remail.nih.gov			
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.			
	Emmett-Buck, M.D., Ph.D.			
	CDNA Library Preparation: M. Bento Soares, Ph.D.			
	CDNA Library Arrayed by: Greg Lemon, Ph.D.			
	DNA Sequencing by: Washington University Genome Sequencing Center			
	found through the I.M.A.G.E. Consortium/LINL, send email to:			
	info@image.lnl.gov			
	Seq primer: -40UP from Gibco			
	High quality sequence stop: 354.			



FEATURES  
source

Location/Qualifiers

1. 414  
/organism="Homo sapiens"  
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/clone="IMAGE:3368404"  
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/lab\_host="DH109"  
/clone\_lib="NCI\_CGAP\_Lu24"  
/note="Organ: Lung; Vector: pT7TD-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu2 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtracted hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN

110 a 91 c 118 g 95 t

## Query Match

Best Local Similarity 100.0%; Score 384; DB 10; Length 414;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 502 CCTCAGATTGCTTACAGACCAATCATGATGATGACAGACCTGTTCAATAT 561  
DB 25 CCTCAGATTGCTTACAGACCAATCATGATGATGACAGACCTGTTCAATAT 84  
QY 562 TTGATGAGGGTGGCTTCAGATGCTCAGACGAGCATGTCATGTCAGATGAG 621  
DB 85 TTGATGAGGGTGGCTTCAGATGCTCAGACGAGCATGTCATGTCAGATGAG 144  
QY 622 AGGTACACTGAGACCTATGATACGCCGTACACAGAGGCACTATGAGAAAGTGG 681  
DB 145 AGGTACACTGAGACCTATGATACGCCGTACACAGAGGCACTATGAGAAAGTGG 204  
QY 682 ATGGAACCTTCAAGATATGTCAGGAGAGGAGATTGTCATGCGCCACTTACAA 741  
DB 205 ATGGAACCTTCAAGATATGTCAGGAGAGGAGATTGTCATGCGCCACTTACAA 264  
QY 742 ATCTACAGTATGAGGAGAGACAGCTTGTATAGTGTGTGAGAGAGTCAAGTCA 801  
DB 265 ATCTACAGTATGAGGAGAGACAGCTTGTATAGTGTGTGAGAGAGTCAAGTCA 324  
QY 802 TTGCCCCAAGGCCCGGTGTGCTTCTGTGAGGAGCATGACGCTGAGAGTCTG 861  
DB 325 TTGCCCCAAGGCCCGGTGTGCTTCTGTGAGGAGCATGACGCTGAGAGTCTG 384  
QY 862 ATGGCCATGAGGCGCGCTGGGTCTA 885  
DB 385 ATGGCCATGAGGCGCGCTGGGTCTA 408

## RESULT 5

CB153433

LOCUS CB153433 449 bp mRNA linear EST 29-JAN-2003  
DEFINITION K-EST0210877 B1T694954 Homo sapiens cDNA clone B1T694954-28-C09 5',  
mRNA sequence.

ACCESSION

CB153433

VERSION

CB153433.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

ATTNORS

TITLE

JOURNAL

COMMENT

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Kim, Y.S.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
21C Frontier Korean EST Project 2001  
Contact: Kim YS

FEATURES  
source

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Beom-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 28 row: C column: 09  
High quality sequence stop: 449.

Location/Qualifiers

1. 449

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="B1T694954-28-C09"

/sex="M"

/lab\_host="Top10P"

/clone\_lib="B1T694954"

/note="Organ: Brain; Vector: pCNS-D2; Site 1: EcoRI;  
Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then dephosphorylated  
with tobacco acid pyrophosphatase (TAP). The dephosphorylated  
infect mRNA was ligated with DNA-RNA linker including  
EcoRI site by treatment of 14 RNA ligase and the first  
strand cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10P by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

BASE COUNT  
ORIGIN

106 a 112 c 112 g 119 t

## Query Match

Best Local Similarity 99.6%; Score 347; DB 14; Length 449;  
Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 120 CTTTCTGTTCACTACAGCTTACTGTGACGAGTTCAATGAGAGAGTGTGGGCACT 179  
DB 1 CTTTCTGTTCACTACAGCTTACTGTGACGAGTTCAATGAGAGAGTGTGGGCACT 60  
QY 180 CCGTGAACAGTATGAGATTCAGAGAGGAGGATGAGTCAATCCCTGGAAGATCAA 239  
DB 61 CCGTGAACAGTATGAGATTCAGAGAGGAGGATGAGTCAATCCCTGGAAGATCAA 120  
QY 240 TTGAGACCCACACTCTTGCCCAACATCACTAGGCTGTGAGATTAAGGATTCCTGCTG 299  
DB 121 TTGAGACCCACACTCTTGCCCAACATCACTAGGCTGTGAGATTAAGGATTCCTGCTG 180  
QY 300 GCATTGGCTGTGGCCCTTGAAGAGACGATGAGATTCATTAAGATTCCTCATTTCTTC 359  
DB 181 GCATTGGCTGTGGCCCTTGAAGAGACGATGAGATTCATTAAGATTCCTCATTTCTTC 240  
QY 360 GGAAGAGAGAGAGGCTTGATGCTGTGATGAGTGGCTCTCTCTTCCCTCCGCTCCAA 419  
DB 241 GGAAGAGAGAGAGGCTTGATGCTGTGATGAGTGGCTCTCTCTTCCCTCCGCTCCAA 300  
QY 420 GAAGCCATAGTGGGATCATTTGGGCTGTGATGAGTGGCTCTCTCTTCCCTCCGCTCCAA 479  
DB 301 GAAGCCATAGTGGGATCATTTGGGCTGTGATGAGTGGCTCTCTCTTCCCTCCGCTCCAA 360  
QY 480 TTGCTCCAGCTTTTCAACATACCTCAGATTTGTTACTAGCAACATCATCATGATTTGAG 539  
DB 361 TTGCTCCAGCTTTTCAACATACCTCAGATTTGTTACTAGCAACATCATCATGATTTGAG 420  
QY 540 TGAACAAGCTCTTTCAATATTTTCATGA 568  
DB 421 TGAACAAGCTCTTTCAATATTTTCATGA 449



RESULT 8  
BC031602 1297 bp mRNA linear HTC 04-MAR-2003  
LOCUS Homo sapiens, clone IMAGE:5167902, mRNA.  
DEFINITION BC031602  
ACCESSION BC031602.1 GI:21594893  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gamarine, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louised, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaev, A.N.,  
Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAC Plate: 51 Row: a Column: 11  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4504142  
This clone has the following problem: retained intron.

## FEATURES

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1.1297  
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BASE COUNT 343 a 301 c 325 g 328 t  
ORIGIN

Query Match 11.8%; Score 131; DB 11; Length 1297;  
Best Local Similarity 99.5%; Pred. No. 6.5e-53;  
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 178 GTCCGTAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 237  
DB 548 GTCCGTAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 607  
QY 238 AATTCAGACCCACACCTTGGCCCAATCAGACTGGGCTGTGAGATTAAGGATTCCTGC 297  
DB 608 AATTCAGACCCACACCTTGGCCCAATCAGACTGGGCTGTGAGATTAAGGATTCCTGC 667  
QY 298 TGGCATTGGGCTGTGGCCCTAGAGCAGAGCATTGATTAAGATTCCTCATTTCT 357  
DB 668 TGGCATTGGGCTGTGGCCCTAGAGCAGAGCATTGATTAAGATTCCTCATTTCT 727  
QY 358 TC 359  
DB 728 TC 729

RESULT 9  
B1826234 664 bp mRNA linear EST 04-OCT-2001  
LOCUS 603075928F1 NIH\_MGC\_119 Homo sapiens CDNA clone IMAGE:5167902 5',  
DEFINITION B1826234  
ACCESSION B1826234  
VERSION B1826234.1 GI:15937784  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov/>  
COMMENT Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Inceye Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
plate: LLM11417 row: g column: 07  
High quality sequence stop: 662.

## FEATURES

## source

1.664  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5167902"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_119"  
/note="Organ: brain; Vector: PCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

BASE COUNT 151 a 177 c 179 g 157 t  
ORIGIN

Query Match 10.2%; Score 113; DB 12; Length 664;  
Best Local Similarity 100.0%; Pred. No. 3.6e-44;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 GTCCGTAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 237  
DB 547 GTCCGTAACAGATGATTCAGAGAGTGGAGCCATGCTGATACCTCGAAGAGATC 606  
QY 238 AATTCAGACCCACACCTTGGCCCAATCAGACTGGGCTGTGAGATTAAGGATTCCTGC 290  
DB 607 AATTCAGACCCACACCTTGGCCCAATCAGACTGGGCTGTGAGATTAAGGATTCCTGC 659

RESULT 10  
F05449 268 bp mRNA linear EST 19-FEB-1995  
LOCUS HSC0BC11 normalized infant brain CDNA Homo sapiens CDNA clone  
DEFINITION F05449  
ACCESSION F05449  
VERSION F05449.1 GI:669265  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 268)  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Juneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Picu, G., Poulliot, Y., Sebasticani-Kabekchie, C. and Tessier, A.  
 IMAGE: molecular integration of the analysis of the human genome and its expression  
 C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
 9527534  
 7757816  
 COMMENT Contact: Genethon  
 Genexpress-Genethon  
 Genethon Centre de recherche sur le Genome Humain  
 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE  
 Tel: 33169472800  
 Fax: 33160778698  
 Email: genexpress@genethon.fr  
 Single read.  
 Genexpress\_library\_idt: C; Genexpress\_sequence\_idt: y1c-obc11  
 Seq primer: (-21)M13 universal.  
 Location/Qualifiers  
 1..268  
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 /db\_xref="taxon:9606"  
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 /sex="Female"  
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 /dev\_stage="3 months old"  
 /clone\_1lb="normalized infant brain cDNA"  
 /note="Organ: brain; Vector: lafmid B; Site\_1: HindIII;  
 Site\_2: NotI; sex:Female; dev\_stage=3 months old;  
 isolate=muscular atrophy patient; tissue\_type=total brain  
 ; total mRNA was oligo-(dT) primed and directionally  
 cloned 5' -> 3' into the HindIII -> NotI sites of the  
 lafmid BA vector. Clone library from B.Souares, Psychiatry  
 Dept. Columbia University, USA. Normalization\_method:  
 Bento Soares, P.N.A.S in press"  
 BASE COUNT 70 a 61 c 69 g 67 t 1 others  
 ORIGIN  
 Query Match 9.2%; Score 102; DB 14; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-39;  
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 699 TATGTACGAGGAGGAGGATTCATCGCCCACTTTCAAAATCTACAGTAATGCAG 758  
 DB 167 TATGTACGAGGAGGAGGATTCATCGCCCACTTTCAAAATCTACAGTAATGCAG 226  
 QY 759 GGAGCAGAGCTTTGATTAAGCTGCTGAAGAAGCTCACAATCA 800  
 DB 227 GGAGCAGAGCTTTGATTAAGCTGCTGAAGAAGCTCACAATCA 268  
 RESULT 11  
 LOCUS BX282658 516 bp mRNA linear EST 04-MAR-2003  
 DEFINITION BX282658 NIH MGC 119 Homo sapiens cDNA clone IMAGE:5167902 ;  
 IMAGE:5167902, mRNA sequence.  
 ACCESSION BX282658  
 VERSION BX282658  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 516)  
 Ebert, L., Helli, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radelet, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 TITLE Unpublished  
 JOURNAL Contact: Ina Rolfe  
 COMMENT

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD, IMAGE:5167902, mRNA  
 RZPDLIB: 1.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
 http://www.rzpd.de/CloneCards/cgl-  
 bin/showLib.pl.cgi?response=11BN0972 Contact: Ina Rolfe  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13. Primer sequence: GGTGTAAACAGCAGCCAGT.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE5167902"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"  
 /clone\_1lb="NIH MGC 119"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source: normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH MGC Library."  
 BASE COUNT 110 a 143 c 135 g 128 t  
 ORIGIN  
 Query Match 8.5%; Score 94; DB 13; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-35;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGGTCCTTCCTGATCCTGCTGATCTTCTTGAAGAAGATCCGCGAGTGA 60  
 DB 371 ATGGTCCTTCCTGATCCTGCTGATCTTCTTGAAGAAGATCCGCGAGTGA 430  
 QY 61 CAGTCCAGTGAAGAGGAGGCTGCTCATATGC 94  
 DB 431 CAGTCCAGTGAAGAGGAGGCTGCTCATATGC 464  
 RESULT 12  
 LOCUS AI201184 456 bp mRNA linear EST 14-OCT-1998  
 DEFINITION qf70d05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755369  
 3' similar to gb:Y00281 RHOPHORIN I PRECURSOR (HUMAN);, mRNA  
 sequence.  
 ACCESSION AI201184  
 VERSION AI201184.1 GI:3753790  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 456)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
 , Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.lnl.gov/db/ftp/image/image.html](http://www-bio.lnl.gov/db/ftp/image/image.html)

Seq primer: -40UP from Glibco  
High quality sequence stop: 432.  
Location/Qualifiers

## FEATURES

source

1..456  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1755369"  
/sex="male"  
/lab\_host="DH10B"

/clone\_lib="Soares testis\_NHT"  
/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - Oligo(dT) primer (5' TGTTACCATCTGAGTGGAGCGCGCCCATTTTCTTTTCTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 122 a 100 c 90 g 144 t

## ORIGIN

Query Match 6.6%; Score 73; DB 9; Length 456;  
Best Local Similarity 100.0%; Pred. No. 1.5e-24;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 CATGATCTGAGGACAAAGCTCTGTCAATATTTGATGAGGTTTGCTTCAGATGC 587  
DB 431 CATGATCTGAGGACAAAGCTCTGTCAATATTTGATGAGGTTTGCTTCAGATGC 372  
QY 588 TCAGCAGGCAAG 600  
DB 371 TCAGCAGGCAAG 359

## RESULT 13

AG046849 667 bp DNA linear GSS 02-NOV-2001  
LOCUS AG046849

DEFINITION Pan troglodytes DNA, clone: PTB-026D03.F, genomic survey sequence.

ACCESSION AG046849.1 GI:16583741

VERSION GSS.  
KEYWORDS Pan troglodytes (chimpanzee)

## SOURCE

ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

## REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB

2 (bases 1 to 667)  
Unpublished

3 (bases 1 to 667)  
Unpublished

## JOURNAL

Submitted (02-NOV-2001) Aao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: [chimbdb@gsc.riken.go.jp](mailto:chimbdb@gsc.riken.go.jp); URL: <http://hsp.gsc.riken.go.jp/>;  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

## REFERENCE

Submitted (02-NOV-2001) Aao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: [chimbdb@gsc.riken.go.jp](mailto:chimbdb@gsc.riken.go.jp); URL: <http://hsp.gsc.riken.go.jp/>;  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

## AUTHORS

Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the Red process and may have higher chance of  
clone tracking errors.

## COMMENT

PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : PKS145  
R.Site 1 : SacI

R.Site 2 : SacI.  
Location/Qualifiers  
1..667  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-026D03.F"  
/sex="male"  
/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"  
BASE COUNT 156 a 142 c 158 g 210 t 1 others

## ORIGIN

Query Match 5.9%; Score 66; DB 29; Length 667;  
Best Local Similarity 100.0%; Pred. No. 5e-21;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 178 GTCCGTGAACAGTATGATTCAGAGAGTGAAGCCATGTCATACCTGAAAGATC 237  
DB 132 GTCCGTGAACAGTATGATTCAGAGAGTGAAGCCATGTCATACCTGAAAGATC 191  
QY 238 AATTCA 243  
DB 192 AATTCA 197

## RESULT 14

AG695213 682 bp mRNA linear EST 04-MAY-2001  
LOCUS AG695213  
DEFINITION NISC i4v3g09.w1 Soares NMBP2 pituitary Mus musculus cDNA clone  
IMAGE:4317880 5', mRNA sequence.

ACCESSION AG695213 GI:13954900  
VERSION EST.  
KEYWORDS Mus musculus (house mouse)

## SOURCE

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 682)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## REFERENCE

1 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
Tumor Gene Index  
Unpublished

Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
CDNA Library Preparation: M. Bento Soares Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[infoimage.llnl.gov](http://infoimage.llnl.gov)

MG1:1598648  
Plate: L1AM922 row: M column: 17  
Seq primer: T7 primer.

Location/Qualifiers  
1..682

/organism="Mus musculus"  
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/clone="IMAGE:4317880"  
/issue\_type="pituitary gland"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="Soares NMBP2 pituitary"  
/note="Organ: brain; Vector: pT73D-Pac; Site 1: NotI;  
Site 2: EcoRI; 1st strand cDNA was primed with a NotI -  
oligo(dT) primer

5'-ACTGGAAGATTCGCGCGCGCGCTTTTCTTTTCTTTT-3';  
double-stranded cDNA was ligated to EcoRI adaptors  
5'-ATTGCGCAGG-3' AND 5'-CTTCGCGG-3' (Pharmacia),  
digested with NotI and cloned into the NotI and EcoRI  
sites of the pT73D-PacI vector. Library went through one

round of normalization, and was constructed in the laboratory of M. Bento Soares (University of Iowa).  
 BASE COUNT 190 a 121 c 162 g 209 t  
 ORIGIN

Query Match 5.3%; Score 59; DB 10; Length 682;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 TTCGAAGATATGTCAGCGAAGAGGATTTCATGCCCTTACAAATCTACAG 749  
 Db 142 TTCGAAGATATGTCAGCGAAGAGGATTTCATGCCCTTACAAATCTACAG 200

RESULT 15  
 AK032422 3879 bp mRNA linear HTC 05-DEC-2002  
 LOCUS  
 DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
 enriched library, clone:6430542K11 product:METABOTROPIC GLUTAMATE  
 RECEPTOR MGLURS PRECURSOR homolog [Rattus norvegicus], full insert  
 sequence.

ACCESSION AK032422  
 VERSION AK032422.1 GI:26082838  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279252  
 PUBMED 10349636

REFERENCE  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
 Komano, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE  
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
 Aizawa, T., Hara, A., Fukunishi, Y., Komano, H., Adachi, J., Fukuda, S.,  
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I.,  
 Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R.,  
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
 Fleischmann, M., Gasteierland, T., Gissi, C., King, B., Kochiwa, H.,  
 Kuenli, P., Lewis, S., Matsuo, Y., Nakaido, I., Pesole, G.,  
 Quackenbush, J., Schriml, L. M., Staudil, F., Suzuki, R., Tomita, M.,  
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
 Balarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
 Carinci, P., de Bona, M. F., Brownstein, M. J., Bult, C.,  
 Fletcher, C., Fujita, M., Gariboldi, M., Guernicchi, S., Hill, D.,  
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
 Marchionni, L., Mashima, U., Mazzarelli, J., Mombaur, P., Nordone, P.,  
 Ring, B., Rungwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
 Sato, K., Schobach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
 Toyooka, K., Wang, K. H., Wetz, C., Whitaker, C., Wilmberg, L.,

Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohseki, S.,  
 and Hayashizaki, Y.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851

REFERENCE  
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 MEDLINE 12117851

REFERENCE  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hasegawa, Y., Hara, A., Hashizume, M.,  
 Hayashida, K., Hayatsu, N., Hironaka, K., Hirose, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komano, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnishi, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M., and Hayashizaki, Y.

REFERENCE  
 AUTHORS Muramatsu, M., and Hayashizaki, Y.  
 TITLE Direct Subtraction  
 JOURNAL Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,  
 URL: http://genome.resgsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.resgsc.riken.go.jp/  
 URL: http://phantom.resgsc.riken.go.jp/  
 URL: http://location.qualifiers

FEATURES  
 source 1..3879  
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 /strain="C57BL/6J"  
 /db\_xref="PANTOM DB:6430542K11"  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,  
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4	1050.8	94.7	2149	6	AX068374
5	919.8	82.9	2349	6	AX068368
6	907.8	81.8	2064	6	AX068376
7	888.4	80.0	4078	6	AR270570
8	888.4	80.0	4207	6	AR145364
9	888.4	80.0	4207	6	AR145365
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#### ALIGNMENTS

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AX709349

LOCUS

DEFINITION

AX709349

ACCESSION

AX709349.1

VERSION

AX709349.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

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Bates, B.G., Xie, Y., Gulukota, K. and Paulsen, J.E.

Glutamate receptor modulatory proteins and nucleic acids encoding

chem

Pred. No. is the number of results predicted by chance to have a

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 REFERENCE  
 AUTHORS Bates,B.G., Xie,Y., Gulukota,K. and Paulsen,J.B.  
 TITLE Glutamate receptor modulatory proteins and nucleic acids encoding  
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 ORGANISM Homo sapiens  
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REFERENCE 1  
 AUTHORS Schwarz, D.A. and Makl, R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 3 11-JAN-2001;  
 Neuroscience Biosciences, Inc. (US)

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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1  
 AUTHORS Schwarz, D.A. and Makl, R.A.  
 TITLE Metabotropic glutamate receptors and methods of use therefor  
 JOURNAL Patent: WO 0102566-A 11 11-JAN-2001;  
 Neuroscience Biosciences, Inc. (US)

FEATURES  
 source 1.2064  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

BASE COUNT 518 a 466 c 519 g 561 t

ORIGIN

Query Match 81.8%; Score 907.8; DB 6; Length 2064;  
 Best Local Similarity 99.8%; Pred. No. 3,1e-256;  
 Matches 909; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTCCTTCTGTGATCTCTGCTGCTTCACTTTTGAAGAAGATGCTGGAGTGA 60  
 DB 365 ATGGTCCTTCTGTGATCTCTGCTGCTTCACTTTTGAAGAAGATGCTGGAGTGA 424  
 QY 61 CAGTCAG 120  
 DB 425 CAGTCAG 484

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QY 121 TTTCTGTTTCATGACGAGCTTGTGGAAGAGTTTCATGAGAGAGTGTGGGCGAGTC 180
DB 485 TTTTCTGTTTCATGACGAGCTTGTGGAAGAGTTTCATGAGAGAGTGTGGGCGAGTC 544
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGCAATACCTTGAAAGAGATCAAT 240
DB 545 CGTGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGCAATACCTTGAAAGAGATCAAT 604
QY 241 TCAGACCCCACTCTTGGCCCAATCATGACTGGGCTGTGAGATTAAGGGATTCCTGTG 300
DB 605 TCAGACCCCACTCTTGGCCCAATCATGACTGGGCTGTGAGATTAAGGGATTCCTGTG 664
QY 301 CATTCGGCTGTGGCCCTTAAGAGAGCATTAAGAGATTCCTCATATTTCTTTCG 360
DB 665 CATTCGGCTGTGGCCCTTAAGAGAGCATTAAGAGATTCCTCATATTTCTTTCG 724
QY 361 GAAAGAGAGAGGCTTGTGATGTCTGTGAGATGGCTCTCTCTTCTTCCGCTCAAG 420
DB 725 GAAAGAGAGAGGCTTGTGATGTCTGTGAGATGGCTCTCTCTTCTTCCGCTCAAG 784
QY 421 AAGCCCATATAGGGGCTTATGGGCTGTGATTCAGATTCCTTAAGCATTCAGGTCAGAAAT 480
DB 785 AAGCCCATATAGGGGCTTATGGGCTGTGATTCAGATTCCTTAAGCATTCAGGTCAGAAAT 844
QY 481 TTGCTCCAGCTTTTCAACATACCTCAGATTCCTTAAGCATTCAGGTCAGAAAT 540
DB 845 TTGCTCCAGCTTTTCAACATACCTCAGATTCCTTAAGCATTCAGGTCAGAAAT 904
QY 541 GACAAAGCTTTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCAAG 600
DB 905 GACAAAGCTTTGTTCAAAATTTTCAATGAGGTTGTGCTTCAATGCTCAGAGCAAG 964
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DB 965 TCCATGTTGACATAGTGAAGAGGTACATGAGCCATATGATCAAGCCGATCACAGAA 1024
QY 661 GGCACATATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAAGGAGAGAGGAT 720
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QY 721 TGCATGCCCCATCTTCAAAATCTTACATGATATGACAGGAGAGAGAGCTTTGATTAAGCTG 780
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DB 1145 CTGAAGAGCTCAAGTCACTTGGCCAGGCGCGGTGTGCTACTCTGTGAGAGGC 1204
QY 841 ATGACGTTGAGAGGTCTGCTGATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 900
DB 1205 ATGACGTTGAGAGGTCTGCTGATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 1264
QY 901 CTTCTGGGCGAG 911
DB 1265 CTTCTGGGCGAG 1275

RESULT 7
AR270570 4078 bp DNA linear PAT 10-Apr-2003
LOCUS AR270570
DEFINITION Sequence 1133 from patent US 6500938.
ACCESSION AR270570
VERSION AR270570.1 GI:29701804
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4078)
AUTHORS Au-Young, J. and Sellhammer, J. J.
TITLES Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1133 31-DEC-2002;
FEATURES
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BASE COUNT 994 a 1074 c 1076 g 934 t
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Query Match 80.0%; Score 888.4; DB 6; Length 4078;
Best Local Similarity 98.2%; Pred. No. 1,7e-250;
Matches 888; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGTCTTCTGTGATATCCGTGACGCTTACTTTGAAAGAGATGCGTGGAGATGCA 60
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QY 61 CAGTCCAGTGAAGAGAGGTGTGGCTCATATGCTGGGTGACATCATTAATGAGCTTC 120
DB 211 CAGTCCAGTGAAGAGAGGTGTGGCTCATATGCTGGGTGACATCATTAATGAGCTTC 270
QY 121 TTTTCTGTTTCATGACGAGCTTACTGTGACGAAATTCATGAGAGAGTGTGGGCGAGTC 180
DB 271 TTTTCTGTTTCATGACGAGCTTACTGTGACGAAATTCATGAGAGAGTGTGGGCGAGTC 330
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGGAGCCATGCTGATACCTTGAAAGAGATCAAT 240
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DB 391 TCAGACCCCACTCTTGGCCCAATCATGACTGGGCTGTGAGATTAAGGATTCCTGCTGG 450
QY 301 CATTCGGCTGTGGCCCTTAAGAGAGCATTAAGATTCCTCATATTTCTTTCG 360
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QY 361 GAAAGAGAGAGGCTTGTGATGTCTGTGAGATGGCTCTCTCTTCTTCCGCTCAAG 420
DB 511 GAAAGAGAGAGGCTTGTGATGTCTGTGAGATGGCTCTCTCTTCTTCCGCTCAAG 570
QY 421 AAGCCCATATAGGGGCTTATGGGCTGTGATTCAGATTCCTTAAGCATTCAGGTCAGAAAT 480
DB 571 AAGCCCATATAGGGGCTTATGGGCTGTGATTCAGATTCCTTAAGCATTCAGGTCAGAAAT 630
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DB 631 TTGCTCCAGCTTTTCAACATACCTCAGATTCCTTAAGCATTCAGGTCAGAAAT 590
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QY 661 GGCACATATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAAGGAGAGAGGAT 720
DB 811 GGCACATATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAAGGAGAGAGGAT 870
QY 721 TGCATGCCCCATCTTCAAAATCTTACATGATATGACAGGAGAGAGAGCTTTGATTAAGCTG 780
DB 871 TGCATGCCCCATCTTCAAAATCTTACATGATATGACAGGAGAGAGAGCTTTGATTAAGCTG 930
QY 781 CTGAAGAGCTCAAGTCACTTGGCCAGGCGCGGTGTGCTACTCTGTGAGAGGC 840
DB 931 CTGAAGAGCTCAAGTCACTTGGCCAGGCGCGGTGTGCTACTCTGTGAGAGGC 990
QY 841 ATGACGTTGAGAGGTCTGCTGATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 900
DB 991 ATGACGTTGAGAGGTCTGCTGATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 1050
QY 901 CTTCTGGGCGAG 914
DB 1051 CTTCTGGGCGAG 1064

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RESULT 8	ARI45364	4207 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	ARI45364				
DEFINITION	Sequence 1 from patent US 6211353.				
ACCESSION	ARI45364				
VERSION	ARI45364.1				
KEYWORDS	GI:15107231				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unpublished.				
AUTHORS	1 (bases 1 to 4207) Burnett, J. Paul. Jr., Mayne, N. Gail., Sharp, R. Leon. and Snyder, Y. Marie.				
TITLE	Isolated nucleic acid encoding a human mGLR5				
JOURNAL	Patent: US 6211353-A 1 03-APR-2001;				
FEATURES	Location/Qualifiers 1..4207				
BASE COUNT	1011 a 1120 c 1112 g 964 t				
ORIGIN	/organism="unknown"				
Query Match	80.0%; Score 888.4; DB 6; Length 4207;				
Best Local Similarity	98.2%; Pred. No. 1.7e-250;				
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;					
QY	1 ATGGTCCTTCGTGTGATCCCTGACGCTTACTTTTGAAGAAGATGCCGTGGAGTGA	60			
DB	460 ATGGTCCTTCGTGTGATCCCTGACGCTTACTTTTGAAGAAGATGTCGTGGAGTGA	519			
QY	61 CAGTCCAGTGAAGAGAGGGGTGGCTCACATGCTGGTGA CATCATTTGAGACTTC	120			
DB	520 CAGTCCAGTGAAGAGAGGGGTGGCTCACATGCCGGGTGACATCTATTGAGACTTC	579			
QY	121 TTTTCTGTTCATCACACGCTTACTGTGAGCAAGTTCTATGAGAGAAATGTGGGGCA	180			
DB	580 TTTTCTGTTCATCACACGCTTACTGTGAGCAAAAGTTCAATGAGAGAAATGTGGGGCG	639			
QY	181 CGTAAACATATATGATTCATGAGATGAGAGGCCATGCTGCATPACCCTGGAAAGATCA	240			
DB	640 CGTAAACATATATGATTCATGAGATGAGAGGCCATGCTGCATPACCCTGGAAAGATCA	699			
QY	241 TCAGACCCCACTCTTGGCCCAACATCA CACTGGGCTGTGAGATTAAGGATTCCTG	300			
DB	700 TCAGACCCCACTCTTGGCCCAACATCA CACTGGGCTGTGAGATTAAGGATTCCTG	759			
QY	301 CATTGGCTGTGGCCCTTGAAGACAGCATTTGATTCATTAAGATTCCTCATTTCTTG	360			
DB	760 CATTGGCTGTGGCCCTTGAAGACAGCATTTGATTCATTAAGATTCCTCATTTCTTG	819			
QY	361 GAAGAGGAAGAGGGCTGTATGCTGTGTGATGGCTCTCTCTCTCTCTCTCTCTCTCT	420			
DB	820 GAAGAGGAAGAGGGCTGTATGCTGTGTGATGGCTCTCTCTCTCTCTCTCTCTCTCT	879			
QY	421 AAGCCCATATGAGGGGCTATTGGGCTGTGTTCAAGTTCTTTAGCCATTCAAGTCCA	480			
DB	880 AAGCCCATATGAGGGGCTATTGGGCTGTGTTCAAGTTCTTTAGCCATTCAAGTCCA	939			
QY	481 TTGCTCCAGCTTTTCAACATACCTTCAGATTGCTTACTGACGACCATATGAGATCT	540			
DB	940 TTGCTCCAGCTTTTCAACATACCTTCAGATTGCTTACTGACGACCATATGAGATCT	999			
QY	541 GACAAGACTCTGTTCAAAATATTTATATGAGGGGTGGGCTTCAGATGCTCACAAGG	600			
DB	1000 GACAAGACTCTGTTCAAAATATTTATATGAGGGGTGGGCTTCAGATGCTCACAAGG	1059			
QY	601 TCCATGCTGACATATGTAAGAGGTACAATCTGATCTATATCCCTGACACACAGA	660			
DB	1060 GCCATGTGGGACATATGTAAGAGGTACAATCTGATCTATATCCCTGACACACAGA	1119			
QY	661 GGCAACTATATGAGAAATGAGGATGGAACCTTCAAAAGTATATGTACAGCAAGAAG	720			
DB	1120 GGCAACTATATGAGAAATGAGGATGGAACCTTCAAAAGTATATGTACAGCAAGAAG	1179			

Qy	721	TGCATGCCCACTCTTACAAATCTACAGTAATGACAGAGGAGCAGACCTTGGATTAACGTG	780
Db	1180	TGCATGCCCACTCTTACAAATCTACAGTAATGACAGAGGAGCAGACCTTGGATTAACGTG	1239
Qy	781	CTGAAGAAGCTCACAAATCACTTGCCCAAGGCCCGGGTGGTGCCCTACTTCTGTGAAGGC	840
Db	1240	CTGAAGAAGCTCACAAATCACTTGCCCAAGGCCCGGGTGGTGCCCTACTTCTGTGAAGGC	1299
Qy	841	ATGACGGTGAAGGCTCTGCTGATGCGCATGAGCGCGCTGGGTCTAGTGGAGAAATTTCTG	900
Db	1300	ATGACGGTGAAGGCTCTGCTGATGCGCATGAGCGCGCTGGGTCTAGCGGAGAAATTTCTG	1359
Qy	901	CTTCTGGGCAGGGA 914	
Db	1360	CTTCTGGGCAGTGA 1373	
RESULT 9			
LOCUS	ARI45365	4207 bp	DNA
DEFINITION	Sequence 3 from patent US 6211353.		linear
ACCESSION	ARI45365		
VERSION	ARI45365.1	GI:15107232	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 4207)		
AUTHORS	Burnett,J.Paul, Jr., Mayne,N.Gall., Sharp,R.Leon. and Snyder,Y.Marie.		
TITLE	Isolated nucleic acid encoding a human mgluR5		
JOURNAL	Patent: US 6211353-A 3 03-Apr-2001;		
FEATURES	Location/Qualifiers		
source	1..4207		
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Best Local Similarity	98.2%; Pred. No. 1,7e-250;		
Matches	898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;		
Qy	1	ATGCTCTTCTGTTGATCTGTCAGTCTTACTTTGAAAGAGATGTCGTGGAGTGA 60	
Db	460	ATGCTCTTCTGTTGATCTGTCAGTCTTACTTTTGAAGAGATGTCGTGGAGTGA 519	
Qy	61	CAGTCCAGTAGAGAGAGGGTGGTGGCTCAATCTGGGTGATCAATTAATTGAGCTCTC 120	
Db	520	CAGTCCAGTAGAGAGAGGGTGGTGGCTCAATCTGGGTGATCAATTAATTGAGCTCTC 579	
Qy	121	TTTTCTGTTATCAACCAAGCTTACTGTGAGCGAAGTTGATGAGAGAAATGTGGGGCAGTC 180	
Db	580	TTTTCTGTTATCAACCAAGCTTACTGTGAGCGAAGTTGATGAGAGAAATGTGGGGCGCTC 639	
Qy	181	CGTGAACGATATGGCATTCAGAGAGTGGAGGCCATGCTGCATACCTTGAAGAGATCAAT 240	
Db	640	CGTGAACGATATGGCATTCAGAGAGTGGAGGCCATGCTGCATACCTTGAAGAGATCAAT 699	
Qy	241	TTCGACCCCACTCTTGGCCCAATCAATCACTGGCGCTGTGAGATTAAGGATTTCTGCTGG 300	
Db	700	TTCGACCCCACTCTTGGCCCAATCAATCACTGGCGCTGTGAGATTAAGGAGCTCTGCTGG 759	
Qy	301	CATTGGCTGTGGCCCTAGAGCAGAGCATGAGTTCAATTAAGCATTCCTCATTTCTTGG 360	
Db	760	CATTGGCTGTGGCCCTAGAGCAGAGCATGAGTTCAATTAAGCATTCCTCATTTCTTGA 819	
Qy	361	GAAAGAGAAAGAGGCTTGTATGCTCTGTGATGGCTCTCTCTTCTTCCGCTCCAG 420	
Db	820	GAAAGAGAAAGAGGCTTGTATGCTGTGATGGCTCTCTCTTCTTCCGCTCCAG 879	
Qy	421	AAGCCCATTAATTAAGGGGTCATTTGGGGCTGGTTCAGATTTTAAACCATTAAGGTCCAGAT 480	
Db	880	AAGCCCATTAATTAAGGGGTCATTTGGGGCTGGTTCAGATTTTAAACCATTAAGGTCCAGAT 939	



QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTACTCAGACCATCATGATCTAGT 540  
DB 940 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTACTCAGACCATCATGATCTAGT 999  
QY 541 GACAAAGCTCTGTTCAATATTTTCATGAGGGTTGCTTCAGATGCTCAGCAGCAAG 600  
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QY 841 ATGACGGTGAAGGTCTGCTGATGCGCATGAGGGGCGCTGCTTATGAGGAGATTCTG 900  
DB 1300 ATGACGGTGAAGGTCTGCTGATGCGCATGAGGGGCGCTGCTTATGAGGAGATTCTG 1359  
QY 901 CTTCCTGGGAGGGA 914  
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LOCUS ARI45366  
DEFINITION Sequence 4 from patent US 6211353.  
ACCESSION ARI45366  
VERSION ARI45366.1 GI:15107233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 4303)  
AUTHORS Burnet,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mglur5  
JOURNAL Patent: US 6211353-A 4 03-APR-2001;  
FEATURES  
source location/Qualifiers  
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/organism="unknown"  
BASE COUNT 1044 a 1138 c 1144 g 977 t  
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Query Match 80.0%; Score 888.4; DB 6; Length 4303;  
Best Local Similarity 98.2%; Pred.No.1.7e-250;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGTCCCTTCTGTGATCTGTCACTCTTACTTTTGAAGAAGATGTCCTGGAGATGCA 60  
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QY 61 CAGTCCAGTGAAGAGGGTGTGGCTCACAATGCTGGGTGACATCATTTATGAGCTTC 120  
DB 520 CAGTCCAGTGAAGAGGGTGTGGCTCACAATGCTGGGTGACATCATTTATGAGCTTC 579  
QY 121 TTTTCTGTTATCAACAGCTCTGCTGACGAAGTTCAATGAGAGAAAGTGTGGGCGATC 180  
DB 580 TTTTCTGTTATCAACAGCTCTGCTGACGAAGTTCAATGAGAGAAAGTGTGGGCGATC 639  
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QY 241 TCAGACCCCACTCTTGGCCCAATCACAATGGGCTGTGAATTAAGGATTTCTGCTGG 300  
DB 700 TCAGACCCCACTCTTGGCCCAATCACAATGGGCTGTGAATTAAGGATTTCTGCTGG 759  
QY 301 CATTCGGCTGTGGCCCTTGAAGCAGACATTTGATTAAGATTTCCCTCATTTCTTCG 360  
DB 760 CATTCGGCTGTGGCCCTTGAAGCAGACATTTGATTAAGATTTCCCTCATTTCTTCG 819  
QY 361 GAAAGAGAGAGGGCTTGTGATGCTGTGATGAGGCTCTCTCTTCTTCCCTCCAG 420  
DB 820 GAAAGAGAGAGGGCTTGTGATGCTGTGATGAGGCTCTCTCTTCTTCCCTCCAG 879  
QY 421 AAGCCCATATAGGGGTCAATTTGGGCTGTGCTTCAAGTTCTTACCAATCAGTCCAGAT 480  
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QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTACTCAGCAACCATCATGATCTAGT 540  
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DB 1000 GACAAAGCTCTGTTCAAAATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGCAAG 1059  
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DB 1060 GCGATGCTGACATATGTAAGAGGTACACTGACCTATGATATCAGCCGTACACAGAA 1119  
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QY 901 CTTCCTGGGAGGGA 914  
DB 1360 CTTCCTGGGAGGGA 1373

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LOCUS ARI45367  
DEFINITION Sequence 6 from patent US 6211353.  
ACCESSION ARI45367  
VERSION ARI45367.1 GI:15107234  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 4303)  
AUTHORS Burnet,J.Paul, Jr., Mayne,N.Gail., Sharp,R.Leon. and Snyder,Y.Marie.  
TITLE Isolated nucleic acid encoding a human mglur5  
JOURNAL Patent: US 6211353-A 6 03-APR-2001;  
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source location/Qualifiers  
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Query Match 80.0%; Score 888.4; DB 6; Length 4303;





QY 901 CTTCTGGGAGGGA 914  
 Db 1051 CTTCTGGGAGGGA 1064

RESULT 14  
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 LOCUS  
 DEFINITION Human mRNA for metabotropic glutamate receptor subtype 5b, complete cds.

ACCESSION D28539.1 GI:1408053  
 VERSION D28539.1  
 KEYWORDS metabotropic glutamate receptor.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 TITLE 1 (bases 1 to 4614)  
 Minakami, R., Katsuki, F., Yamamoto, T., Nakamura, K. and Sugiyama, H.  
 Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5  
 Biochem. Biophys. Res. Commun. 199 (3), 1136-1143 (1994)

JOURNAL  
 MEDLINE  
 PUBMED 7908515  
 2 (bases 1 to 4614)  
 Katsuki, F.  
 Direct Submission  
 Submitted (14-FEB-1994) Fujika Katsuki, Faculty of Science, Kyushu University, Department of Biology; 6-10-1 Hakozaki, Higashi-ku, Fukuoka, Fukuoka 812, Japan (Tel:092-642-2630, Fax:092-642-2645)  
 On Jul 10, 1996 this sequence version replaced GI:483426.  
 Sequence updated (03-Jul-1996) by: Fujika Katsuki.

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3'UTR 3790..->4614  
 BASE COUNT 1147 a 1188 c 1177 g 1102 t  
 ORIGIN

Query Match 80.0%; Score 888.4; DB 9; Length 4614;  
 Best Local Similarity 98.2%; Pred. No. 1,8e-250;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGTCCTTCTGTGTAATCTCTGTCAGTCTTACTTTGAAAGAGATGCCGTGGAGTGA 60  
 Db 151 ATGTCCTTCTGTGTAATCTCTGTCAGTCTTACTTTGAAAGAGATGCCGTGGAGTGA 210  
 QY 61 CAGTCCAGTGAAGAGAGGAGGAGTGTCTCAAGCTGGGTGACATCATTTAGAGCTTC 120  
 Db 211 CAGTCCAGTGAAGAGAGGAGTGTCTCAAGCTGGGTGACATCATTTAGAGCTTC 270  
 QY 121 TTTTCTGTTATCACCAGCTTACTGTGACGAAGTTTATGAGAGAGTGTGGGAGTTC 180  
 Db 271 TTTTCTGTTATCACCAGCTTACTGTGACGAAGTTTATGAGAGAGTGTGGGAGTTC 330  
 QY 181 CCGTGAACAGTATGACATTCAGAGAGTGAAGCCATGCTGATCCTCGGAAAGATCAAT 240  
 Db 331 CCGTGAACAGTATGACATTCAGAGAGTGAAGCCATGCTGATCCTCGGAAAGATCAAT 390  
 QY 241 TCAGACCCCACTCTTGCCCAACATCAGCTGGGCTGTGATAGATAGGATTCCTGCTG 300  
 Db 391 TCAGACCCCACTCTTGCCCAACATCAGCTGGGCTGTGATAGATAGGATTCCTGCTG 450  
 QY 301 CATTGCGCTGTGGCCCTTGAAGAGAGATGATGATTAAGATTCCTCATTTCTTCTG 360  
 Db 451 CATTGCGCTGTGGCCCTTGAAGAGAGATGATGATTAAGATTCCTCATTTCTTCTG 510  
 QY 361 GAAGAGAGAGAGGCTGTGATGCTGTGTGATGCTCTCTCTCTTCTTCCGCTCAAG 420  
 Db 511 GAAGAGAGAGAGGCTGTGATGCTGTGTGATGCTCTCTCTCTTCTTCCGCTCAAG 570  
 QY 421 AAGCCATGATGAGGAGTCAATGGGCTGTGATGCTCTCTCTCTTCTTCCGCTCAAG 480  
 Db 571 AAGCCATGATGAGGAGTCAATGGGCTGTGATGCTCTCTCTCTTCTTCCGCTCAAG 630  
 QY 481 TTGCTTCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACATCATGATCTGAGT 540  
 Db 631 TTGCTTCAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACATCATGATCTGAGT 690  
 QY 541 GACAAAGCTCTGTCAATATTTTCAAGAGGTTGCTTCTCAGATCTCAGAGGCAAG 600  
 Db 691 GACAAAGCTCTGTCAATATTTTCAAGAGGTTGCTTCTCAGATCTCAGAGGCAAG 750  
 QY 601 TCCATGCTGACATGTAAGAGTCACTGACCTTAAGTATCAGCCGTACACAGAA 660  
 Db 751 TCCATGCTGACATGTAAGAGTCACTGACCTTAAGTATCAGCCGTACACAGAA 810  
 QY 661 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATATGTCAAGAGAGAGGATT 720  
 Db 811 GGCACATATGAGAAAGTGGATGGAAGCTTCAAGATATATGTCAAGAGAGAGGATT 870  
 QY 721 TGCATGCGCCACTCTTACAAATCTTACAGTAATGACGAGGAGCAGGCTTTGATAAGCTG 780  
 Db 871 TGCATGCGCCACTCTTACAAATCTTACAGTAATGACGAGGAGCAGGCTTTGATAAGCTG 930  
 QY 781 CTGAAGAAGCTCAAGATCACTTGCACAGGCGCGGCTGTGCTTCTGTGAGGCG 840  
 Db 931 CTGAAGAAGCTCAAGATCACTTGCACAGGCGCGGCTGTGCTTCTGTGAGGCG 990  
 QY 841 ATGACGATGAGAGTCTGCTGATGAGCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 900  
 Db 991 ATGACGATGAGAGTCTGCTGATGAGCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 1050  
 QY 901 CTTCTGGGAGGGA 914  
 Db 1051 CTTCTGGGAGGGA 1064

RESULT 15  
AR038828 AR038828 3282 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 11 from patent US 5807689.  
DEFINITION AR038828  
ACCESSION AR038828  
VERSION AR038828.1 GI:5958191  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3282)  
AUTHORS Daggott, L., Ellis, S.B., Liaw, C., Pontsler, A., Johnson, E.C. and Hesse, S.D.  
TITLE Methods for identifying compounds that modulate metabotropic glutamate receptor activity  
JOURNAL Patent: US 5807689-A 11 15-SEP-1998;  
FEATURES  
Location/Qualifiers  
source 1..3282  
BASE COUNT 840 a 769 c 848 g 825 t  
ORIGIN  
Query Match 79.7%; Score 885.2; DB 6; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 1.5e-249;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 ATGCTCTTCTGTGATCCCTGATCTTCTTGAAGAAGATGCCGGGAGTGA 60  
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DB 430 CAGTCCAGTGAAGAGAGGAGTGTGCTCAGATGCTGGGTGACATATTATGAGCTCTC 489  
QY 121 TTTTCTGTTCATCAACCACTTCTGTGACGAAGTTCATGAAGAAAGTGTGGGCACTC 180  
DB 490 TTTTCTGTTCATCAACCACTTCTGTGACGAAGTTCATGAAGAAAGTGTGGGCACTC 549  
QY 181 CGTGAACAGTATGGCATTCAAGAGTGAAGGCCATGCTGCATACCTTGGAAGAAGTCAAT 240  
DB 550 CGTGAACAGTATGGCATTCAAGAGTGAAGGCCATGCTGCATACCTTGGAAGAAGTCAAT 609  
QY 241 TCAGACCCCACTCTTGCCCAATCACTGAGCTGTGAGATTAAGGAATTCCTGCTGG 300  
DB 610 TCAGACCCCACTCTTGCCCAATCACTGAGCTGTGAGATTAAGGAATTCCTGCTGG 669  
QY 301 CATTCGGCTGTGGCCCTAGAGCAGAGCATTGATTAAGAAAGTTCCTCATTTCTTCG 360  
DB 670 CATTCGGCTGTGGCCCTAGAGCAGAGCATTGATTAAGAAAGTTCCTCATTTCTTCG 729  
QY 361 GAAGAGAAAGAGGCTTGTGATGCTGTGATGAGCTCTCTTCTCCGCTCCAAG 420  
DB 730 GAAGAGAAAGAGGCTTGTGATGCTGTGATGAGCTCTCTTCTCCGCTCCAAG 789  
QY 421 AAGCCCATAGTAGGGGCTATTGGGCTGTTCAGTCTTTAGCCATTTCAGGTCAGAAAT 480  
DB 790 AAGCCCATAGTAGGGGCTATTGGGCTGTTCAGTCTTTAGCCATTTCAGGTCAGAAAT 849  
QY 481 TTGCTCAAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 540  
DB 850 TTGCTCAAGCTTTTCAACATCACTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 909  
QY 541 GACAAGACTGTCTTCAAAATTTTCATAGAGGTTGTGCTTCAAGTCTCAGCAGGCAAG 600  
DB 910 GACAAGACTGTCTTCAAAATTTTCATAGAGGTTGTGCTTCAAGTCTCAGCAGGCAAG 969  
QY 601 TCCATGCTGACATAGTGAAGAGTACACTGACCTATATATCAGCCGTACACAGAA 660  
DB 970 GGCATGCTGACATAGTGAAGAGTACACTGACCTATATATCAGCCGTACACAGAA 1029  
QY 661 GGCACCTATGAGAAAGTGGAGTGAAGCCTTCAAGATATGTCAGGAAAGAGGATTT 720  
DB 1030 GGCACCTATGAGAAAGTGGAGTGAAGCCTTCAAGATATGTCAGGAAAGAGGATTT 1089

QY 721 TGCATGCCCACTCTTACAAAATCTACAGTAATGACGGGAGACAGACTTTGATTAAGCTG 780  
DB 1090 TGCATGCCCACTCTTACAAAATCTACAGTAATGACGGGAGACAGACTTTGATTAAGCTG 1149  
QY 781 CTGAAGAAGCTCAAGAGTCACTTGCCCAAGGCCCGGGTGTGTGCTTCTGTGAGGGC 840  
DB 1150 CTGAAGAAGCTCAAGAGTCACTTGCCCAAGGCCCGGGTGTGTGCTTCTGTGAGGGC 1209  
QY 841 ATGACGCTGAGAGTGTGCTGATGAGCCATGAGCGGCTGGTCTAGTGGAGAAATTTCTG 900  
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QY 901 CTTCTGGGACAGGA 914  
DB 1270 CTTCTGGGACAGTA 1283

Search completed: December 14, 2003, 13:24:31  
Job time : 4202.01 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 06:48:22 ; Search time 319.792 Seconds  
(without alignments)  
9369.765 Million cell updates/sec

Title: US-10-027-923-3

Perfect score: 1110  
Sequence: 1 atgcgcctctctgtatcctct.....tgagagacagctcatctaa 1110

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: N\_Geneseq\_19jun03.\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
26: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1823	24	ABV73899 Human glutamate re
2	1108	99.8	1788	24	AA862274 CDNA sequence #61
3	1106.8	99.7	2172	22	AA299933 Human GRMX-1c DNA.
4	1050.8	94.7	2149	22	AA299934 Human GRMX-1f DNA.
5	919.8	82.9	2349	22	AA299930 Human GRMX-1b DNA.
6	907.8	81.8	2064	22	AA299935 Human GRMX-1g DNA.
7	888.4	80.0	2826	22	AA299935 Human GRMX-1g DNA.
8	888.4	80.0	3129	22	AA299935 Human GRMX-1g DNA.

9	888.4	80.0	4078	25	ACA56535 Human signalling p
10	888.4	80.0	4207	22	AA204990 Human metabotropic
11	888.4	80.0	4207	22	AA205029 Human metabotropic
12	888.4	80.0	4207	22	AA205030 Human metabotropic
13	888.4	80.0	4207	22	AA205033 Human metabotropic
14	888.4	80.0	4207	22	AA204991 Human metabotropic
15	888.4	80.0	4207	22	AA205031 Human metabotropic
16	888.4	80.0	4207	22	AA205032 Human metabotropic
17	888.4	80.0	4207	22	AA205033 Human metabotropic
18	888.4	80.0	4207	22	AA205034 Human metabotropic
19	888.4	80.0	4207	22	AA205035 Human metabotropic
20	888.4	80.0	4207	22	AA205036 Human metabotropic
21	888.4	80.0	4207	22	AA205037 Human metabotropic
22	888.4	80.0	4207	22	AA205038 Human metabotropic
23	888.4	80.0	4207	22	AA205039 Human metabotropic
24	888.4	80.0	4207	22	AA205040 Human metabotropic
25	888.4	80.0	4207	22	AA205041 Human metabotropic
26	888.4	80.0	4207	22	AA205042 Human metabotropic
27	888.4	80.0	4207	22	AA205043 Human metabotropic
28	888.4	80.0	4207	22	AA205044 Human metabotropic
29	888.4	80.0	4207	22	AA205045 Human metabotropic
30	888.4	80.0	4207	22	AA205046 Human metabotropic
31	888.4	80.0	4207	22	AA205047 Human metabotropic
32	888.4	80.0	4207	22	AA205048 Human metabotropic
33	888.4	80.0	4207	22	AA205049 Human metabotropic
34	888.4	80.0	4207	22	AA205050 Human metabotropic
35	888.4	80.0	4207	22	AA205051 Human metabotropic
36	888.4	80.0	4207	22	AA205052 Human metabotropic
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41	888.4	80.0	4207	22	AA205057 Human metabotropic
42	888.4	80.0	4207	22	AA205058 Human metabotropic
43	888.4	80.0	4207	22	AA205059 Human metabotropic
44	888.4	80.0	4207	22	AA205060 Human metabotropic
45	888.4	80.0	4207	22	AA205061 Human metabotropic

#### ALIGNMENTS

RESULT 1	ABV73899	standard; CDNA; 1823 BP.
XX	ABV73899	
XX	08-JUN-2003	(first entry)
XX	Human glutamate receptor modulatory protein mGluR5m CDNA.	
XX	Metabotropic glutamate receptor subtype 5 modulatory protein;	
XX	mGluR5m; human; G-protein coupled receptor; receptor; schizophrenia;	
XX	schizophrenia; bipolar affective disorder; bipolar affective disorder;	
XX	unipolar affective disorder; adolescent conduct disorder;	
XX	neuroleptic; neuroprotective; neuroleptic; chromosome 11;	
XX	gene therapy; gene; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	4..1113
XX	FT	/*tag= a
XX	FT	/product= "mGluR5m"
XX	FT	/note= "the CDS is specifically claimed in Claim 1"
XX	FT	sig_peptide
XX	FT	4..63
XX	FT	/*tag= b
XX	FT	mat_peptide
XX	FT	64..1110
XX	FT	/*tag= c
XX	PN	MO200270708-A2.



PD 12-SEP-2002.  
 XX  
 PF 21-DEC-2001; 2001MO-US49817.  
 XX  
 PR 22-DEC-2000; 2000US-257589P.  
 XX  
 PA (AMHP) WYETH.  
 PI Bates BG, Xie Y, Gulukota K, Paulsen JE.  
 XX  
 DR WPI; 2002-750462/81.  
 XX P-PSDB; ABP54921.  
 PT New mgluR5M nucleic acid molecules and proteins, useful for treating  
 PT neurological or psychiatric disorders such as schizophrenia,  
 PT schizoaffective disorder, bipolar or unipolar affective disorder, or  
 PT adolescent conduct disorder.  
 XX  
 XX Claim 11; Fig 1A; 99pp; English.  
 XX  
 CC The present sequence is that of cDNA clone Y1176 (deposited as  
 CC ATCC PTA-2775) encoding a novel human metabotropic glutamate  
 CC receptor subtype modulatory protein (mgluR5M). The cDNA was  
 CC isolated from a human brain cDNA library. Expression of mgluR5M  
 CC is predominant in cells and tissues of the central nervous system.  
 CC The gene maps to a region of chromosome 11 associated with  
 CC schizophrenia and related psychiatric disorders. The invention  
 CC provides mgluR5M polypeptides and nucleic acids, and methods for  
 CC their detection, as well as methods for using them to identify  
 CC compounds that modulate metabotropic receptor (mgluR) activity.  
 CC Such modulators include a mgluR5M nucleic acid, a mgluR5M antibody,  
 CC a ribozyme, an antisense oligonucleotide, a small molecule  
 CC modulator, a peptide and a peptidomimetic. They can be used in a  
 CC claimed method for treating a subject having a neurological  
 CC disorder, especially a psychiatric disorder selected from  
 CC schizophrenia, schizoaffective disorder, bipolar affective disorder,  
 CC unipolar affective disorder or adolescent conduct disorder (all  
 CC claimed). mgluR5M polypeptides, nucleic acids and antibodies are  
 CC also useful for screening assays, and in predictive medicine, e.g.  
 CC diagnostic assays (e.g. chromosome mapping and tissue typing),  
 CC prognostic assays, monitoring clinical trials, and pharmacogenomics.  
 CC  
 CC Sequence 1823 BP; 488 A; 397 C; 444 G; 493 T; 1 other;  
 SQ  
 Query Match 100.0%; Score 1110; DB 24; Length 1823;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 364 GAAGAGAAAGGCGTTGGATGCTGTGAGATGGCTCCCTCTTCCGCTCAAG 423  
 QY 421 AAGCCATAGTAGGGGTCATTGGGCGCTGGTTCAGATTCTTTAGCCATTGACAGAT 480  
 DB 424 AAGCCATAGTAGGGGTCATTGGGCGCTGGTTCAGATTCTTTAGCCATTGACAGAT 483  
 QY 481 TTGCTCAGCTTTCAACATACCTCAGATTGCTTACACGCAACCATATGATCTGAGT 540  
 DB 484 TTGCTCAGCTTTCAACATACCTCAGATTGCTTACACGCAACCATATGATCTGAGT 543  
 QY 541 GACAAAGCTCTGTTCAATATTTTCATGAGGGTTGTCCTTCAGATGCTCAGCAGCAAG 600  
 DB 544 GACAAAGCTCTGTTCAATATTTTCATGAGGGTTGTCCTTCAGATGCTCAGCAGCAAG 603  
 QY 601 TCATGATGACATAGTGAAGAGGTACACTGGAACCTATGATACCCGTACACAGAA 660  
 DB 604 TCATGATGACATAGTGAAGAGGTACACTGGAACCTATGATACCCGTACACAGAA 663  
 QY 661 GGCAACTATGGAAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGCAAGAAAGGAAAT 720  
 DB 664 GGCAACTATGGAAGAAAGTGGATGGAAGCCTTCAAGATATGTCAGCAAGAAAGGAAAT 723  
 QY 721 TGATGCGCCCACTTTACAAATCTACAGTAATGACAGGGAGCAGACTTTGATTAAGCT 780  
 DB 724 TGATGCGCCCACTTTACAAATCTACAGTAATGACAGGGAGCAGACTTTGATTAAGCT 783  
 QY 781 CTGAAGAGCTCAAGACTCATTTGCCAAGGCCCGGGTGTGGCTTCTGTGAGGCG 840  
 DB 784 CTGAAGAGCTCAAGACTCATTTGCCAAGGCCCGGGTGTGGCTTCTGTGAGGCG 843  
 QY 841 ATACAGGTGAGAGTGTGCTGATGAGCCATGAGGCGCTGGGTATGAGGAGAAATTTCT 900  
 DB 844 ATACAGGTGAGAGTGTGCTGATGAGCCATGAGGCGCTGGGTATGAGGAGAAATTTCT 903  
 QY 901 CTTCGGGCGGAGAACAGATGCTATTTATGAGATCTCAAGAACAGCATCTATGG 960  
 DB 904 CTTCGGGCGGAGAACAGATGCTATTTATGAGATCTCAAGAACAGCATCTATGG 963  
 QY 961 GAAGACAAAGAAATATGCCAAGGTGCTTCTTCAAGGTTTGGAGACATATTACACAA 1020  
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 DB 1024 AGTAGGTCGGTGTGCTGACATGCGCCAGCTCTGAATCTATAGGCTCAGTTCAGGGCCC 1083  
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 DB 1084 ATCACTGACTGAGGACAGGCTCATCTAA 1113

RESULT 2  
 AAS62274  
 ID AAS62274 standard; cDNA; 1788 BP.  
 XX  
 AC AAS62274;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE cDNA sequence #61 encoding novel human secreted protein.  
 XX  
 KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KW immune deficiency disorder; blood disorder; inflammatory disorder;  
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
 KW immunosuppressive; antineumatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200177291-A2.  
 XX  
 PD 18-OCT-2001.





PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 7; 59pp; English.  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX Sequence 2172 BP; 554 A; 488 C; 544 G; 586 T; 0 other;  
 SO  
 Query Match 99.7%; Score 1106.8; DB 22; Length 2172;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGGTCTTCTGTTGATCTCTGATCTCTTCTTCTTGAAGAAGATGCGGGAGTGA 60  
 DB 365 ATGGTCTTCTGTTGATCTCTGATCTCTTCTTCTTGAAGAAGATGCGGGAGTGA 424  
 QY 61 CAGTCCAGTGAAGAGAGGAGTGTGGTCAATGCTGGGTGACATCTTATTTGAGCTCTC 120  
 DB 425 CAGTCCAGTGAAGAGAGGAGTGTGGTCAATGCTGGGTGACATCTTATTTGAGCTCTC 484  
 QY 121 TTTTCTGTTGATCAACAGCTTCTGTGAGCAAGTTGATGAGGAAGTGTGGGAGTC 180  
 DB 485 TTTTCTGTTGATCAACAGCTTCTGTGAGCAAGTTGATGAGGAAGTGTGGGAGTC 544  
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 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGGCTGTGAGATPAAGGAATTCCTGCTGG 300  
 DB 605 TCAGACCCCACTCTTGGCCCAATCACTGGGGCTGTGAGATPAAGGAATTCCTGCTGG 664  
 QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGATTCATPAAGATTCCTCATTTCTTTCG 360  
 DB 665 CATTGGCTGTGGCCCTAGAGCAGAGCATTGATTCATPAAGATTCCTCATTTCTTTCG 724  
 QY 361 GAAGAGAAAGAGGCTTGTGATGCTGTGAGATGAGTCCCTCTTCTTCCGCTCCAAG 420  
 DB 725 GAAGAGAAAGAGGCTTGTGATGCTGTGAGATGAGTCCCTCTTCTTCCGCTCCAAG 784  
 QY 421 AAGCCCATAGTAGGGGCTATTGGGCTGTGCTTCAGTTCTTAAAGCATTCAAGTCCAGAAT 480  
 DB 785 AAGCCCATAGTAGGGGCTATTGGGCTGTGCTTCAGTTCTTAAAGCATTCAAGTCCAGAAT 844  
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 DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT 904  
 QY 541 GACAAAGCTCTTCAATATTTTCAAGAGGTTGTGCTTCAATGCTCAGCAGGCAAG 600  
 DB 905 GACAAAGCTCTTCAATATTTTCAAGAGGTTGTGCTTCAATGCTCAGCAGGCAAG 964  
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 DB 965 TCCATGATGACATAGTAGAGAGTCAACTGACCTATGATCAGCCGTACACAGAA 1024  
 QY 661 GGGCAATAGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGGGAAGAGGAGT 720  
 DB 1025 GGGCAATAGAGAAAGTGGATGGAAGCTTCAAGATATGTCAGGGAAGAGGAGT 1084  
 QY 721 TGCATGCCCACTCTTCAAAATTTACATGATGACAGGGAGCAGACTTTGATAGCTG 780  
 DB 1085 TGCATGCCCACTCTTCAAAATTTACATGATGACAGGGAGCAGACTTTGATAGCTG 1144  
 QY 781 CTGAAGAAGTCACAAGTCACTTGGCCCAAGGCCGGGTGGTGGCTACTTCTGTGAGGCG 840

DB 1145 CTGAAGAAGTCACAAGTCACTTGGCCCAAGGCCGGGTGGTGGCTTACTTGTGAGGCG 1204  
 QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCAGAGGCGCTGGTATGAGGAATTTCTG 900  
 DB 1205 ATGACGGTGAAGAGTCTGCTGATGAGCAGAGGCGCTGGTATGAGGAATTTCTG 1264  
 QY 901 CTTCTGGGAGGGAACAGATGTCATCTTATTTAGATCTCAAGAAAGACATCTATGG 960  
 DB 1265 CTTCTGGGAGGGAACAGATGTCATCTTATTTAGATCTCAAGAAAGACATCTATGG 1324  
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 QY 1081 ATCACTGGAAGTGAAGGACAGGCTCATCTAA 1110  
 DB 1445 ATCACTGGAAGTGAAGGACAGGCTCATCTAA 1474  
 RESULT 4  
 AAF29994  
 ID AAF29994 standard; DNA; 2149 BP.  
 XX AAF29994;  
 AC AAF29994;  
 XX 06-APR-2001 (first entry)  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRMX-1f DNA.  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRMX;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200102566-A1.  
 PN 11-JAN-2001.  
 XX 27-JUN-2000; 2000MO-US17798.  
 PE 02-JUL-1999; 99US-0346326.  
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA Schwarz DA, Maki RA;  
 PI WPI; 2001-123112/13.  
 DR Novel metabotropic glutamate receptor for prevention, treatment of  
 XX PT conditions associated with undesirable glutamate levels, e.g.  
 XX PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 XX PT schizophrenia -  
 XX PS Claim 2; Fig 9; 59pp; English.  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX Sequence 2149 BP; 547 A; 485 C; 538 G; 579 T; 0 other;  
 SO  
 Query Match 94.7%; Score 1050.8; DB 22; Length 2149;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 1085; Conservative 0; Mismatches 2; Indels 23; Gaps 1;

QY 1 ATGGCTCTTGTGATGATCGTCAAGTCTTAATTTTGAAGAAGATGTCGGTGGAGTGA 60  
 DB 365 ATGGCTCTTGTGATGATCGTCAAGTCTTAATTTTGAAGAAGATGTCGGTGGAGTGA 424  
 QY 61 CAGTCCAGTGAAGAGAGGTGGTGGCTCACATGCTGGGTGACATTAATTTGAGCTTC 120  
 DB 425 CAGTCCAGTGAAGAGAGGTGGTGGCTCACATGCTGGGTGACATTAATTTGAGCTTC 484  
 QY 121 TTTTCTGTTTCAATCAACGAGCTACTGTGAGAGAAATTATAGAGAGAAAGTGGGGCAGTC 180  
 DB 485 TTTTCTGTTTCAATCAACGAGCTACTGTGAGAGAAATTATAGAGAGAAAGTGGGGCAGTC 544  
 QY 181 CGTGAACAGTATGAGCAATTCAGAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 240  
 DB 545 CGTGAACAGTATGAGCAATTCAGAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 604  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300  
 DB 605 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 664  
 QY 301 CATTGGCTGTGGCCCTTAAGAGAGAGATTTGATTAAGAGATTCCTCATTTCTTGG 360  
 DB 665 CATTGGCTGTGGCCCTTAAGAGAGAGATTTGATTAAGAGATTCCTCATTTCTTGG 724  
 QY 361 GAAGAGAGAGAGAGAGAGTGTGATGCTGTGAGAGTGGCTCCCTCTTCCGCTCCCAAG 420  
 DB 725 GAAGAGAGAGAGAGAGAGTGTGATGCTGTGAGAGTGGCTCCCTCTTCCGCTCCCAAG 784  
 QY 421 AAGCCCAATGATAGAGAGTCAATTTGGGCTGTGATTCAGATTCCTTAAGCAATTCAGAT 480  
 DB 785 AAGCCCAATGATAGAGAGTCAATTTGGGCTGTGATTCAGATTCCTTAAGCAATTCAGAT 844  
 QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTAAGCAATTCAGATTCCTTAAGCAAT 540  
 DB 845 TTGCTCAGCTTTTCAACATACCTCAGATTCCTTAAGCAATTCAGATTCCTTAAGCAAT 904  
 QY 541 GACAAGACTGTGTTCAAAATTTTCAAGAGAGTGTGCTTCAATGCTCAGAGGAGGCAAG 600  
 DB 905 GACAAGACTGTGTTCAAAATTTTCAAGAGAGTGTGCTTCAATGCTCAGAGGAGGCAAG 964  
 QY 601 TCCATGTGAGCAATGATGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 660  
 DB 965 TCCATGTGAGCAATGATGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 1024  
 QY 661 GGCACATATGAGAAAGTGGATGAAGCCCTTCAAAAGATATGTCAGGGAAGAGAGAT 720  
 DB 1025 GGCACATATGAGAAAGTGGATGAAGCCCTTCAAAAGATATGTCAGGGAAGAGAGAT 1084  
 QY 721 TGCATGCCCCACTCTTAACAAATCTACAGTATGTCAGGGAAGAGAGTGAAGAGTGAAG 780  
 DB 1085 TGCATGCCCCACTCTTAACAAATCTACAGTATGTCAGGGAAGAGAGTGAAGAGTGAAG 1144  
 QY 781 CTGAAGAAGCTCAAGTCACTTGGCCCAAGCCCGGGTGGTGAATCTTCTGTAAGAGGC 840  
 DB 1145 CTGAAGAAGCTCAAGTCACTTGGCCCAAGCCCGGGTGGTGAATCTTCTGTAAGAGGC 1204  
 QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCCTGGGCTTAAGTGGAGAAATTTCTG 900  
 DB 1205 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGCGCCTGGGCTTAAGTGGAGAAATTTCTG 1264  
 QY 901 CTCTTGGGAGGAGAACCAAGTGCATCTTATTTGAAGTCTCAAGAACAGAGATCTTAAG 960  
 DB 1265 CTCTTGGGAGGAGAACCAAGTGCATCTTATTTGAAGTCTCAAGAACAGAGATCTTAAG 1324  
 QY 961 GAAGAGAGAGAAATATGCAAGGTGCTCTTCAAGGTTTGTGAAGCATATTAACAGAG 1020  
 DB 1325 GAAGAGAGAGAAATATGCAAGGTGCTCTTCAAGGTTTGTGAAGCATATTAACAGAG 1361  
 QY 1021 AGTGAAGTCCGTGCTGCAATGCCCCAGACCTCTGAATCTGAAGCTCAAGGAGCC 1080  
 DB 1362 AGTGAAGTCCGTGCTGCAATGCCCCAGACCTCTGAATCTGAAGCTCAAGGAGCC 1421

QY 1081 ATCACTGACTGAGGAGACAGCTCATCTAA 1110  
 DB 1422 ATCACTGACTGAGGAGACAGCTCATCTAA 1451  
 RESULT 5  
 ID AAF29990  
 AAF29990 strand; DNA; 2349 BP.  
 AC AAF29990;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human GRM-X-1b DNA.  
 KW Human; metabotropic glutamate receptor; schizophrenia; GRM-X;  
 KW Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.  
 OS Homo sapiens.  
 PN M0200102566-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000MO-US17798.  
 PR 02-JUL-1999; 99US-0346326.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PI Schwarz DA, Maki RA;  
 XX  
 DR WPI; 2001-123112/13.  
 XX  
 PT Novel metabotropic glutamate receptor for prevention, treatment of  
 PT conditions associated with undesirable glutamate levels, e.g.  
 PT Alzheimer's, Parkinson's disease, stroke, depression, anxiety, pain and  
 PT schizophrenia -  
 PS Claim 2; Fig 3; 59pp; English.  
 XX  
 CC The present invention relates to human metabotropic glutamate  
 CC receptor. An agent that decreases expression or activity of the  
 CC metabotropic glutamate receptor is useful for treating schizophrenia.  
 CC Metabotropic glutamate receptor polynucleotides, polypeptides  
 CC are useful for treating diseases associated with undesirable  
 CC levels of glutamate, such as Alzheimer's disease, Parkinson's  
 CC disease, stroke, depression, anxiety, pain and schizophrenia.  
 XX  
 SQ Sequence 2349 BP; 588 A; 538 C; 586 G; 637 T; 0 other;  
 Query Match 82.9%; Score 919.8; DB 22; Length 2349;  
 Best Local Similarity 86.1%; Pred. No. 1,8e-280;  
 Matches 1108; Conservative 0; Mismatches 2; Indels 177; Gaps 1;  
 QY 1 ATGGCTCTTGTGATGATCGTCAAGTCTTAATTTTGAAGAAGATGTCGGTGGAGTGA 60  
 DB 365 ATGGCTCTTGTGATGATCGTCAAGTCTTAATTTTGAAGAAGATGTCGGTGGAGTGA 424  
 QY 61 CAGTCCAGTGAAGAGAGGTGGTGGCTCACATGCTGGGTGACATTAATTTGAGCTTC 120  
 DB 425 CAGTCCAGTGAAGAGAGGTGGTGGCTCACATGCTGGGTGACATTAATTTGAGCTTC 484  
 QY 121 TTTTCTGTTTCAATCAACGAGCTACTGTGAGAGAAATTATAGAGAGAAAGTGGGGCAGTC 180  
 DB 485 TTTTCTGTTTCAATCAACGAGCTACTGTGAGAGAAATTATAGAGAGAAAGTGGGGCAGTC 544  
 QY 181 CGTGAACAGTATGAGCAATTCAGAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 240  
 DB 545 CGTGAACAGTATGAGCAATTCAGAGAGTGAAGCCATGCTGATCCCTGGAAGAGATCAAT 604  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGGATTCCTGCTGG 300

Db	605	TCAGACCCCA	CAC	CTTGGCCCA	ATCA	CAC	TGGGCTGTGA	AT	TAAGGA	TTCTGCTGG	664						
QY	301	CATTCCGCTGTGG	CCCTTAG	ACAGAC	ATTGA	CTTCA	TAA	GAT	TCCCTCA	TTTCTTGG	360						
Db	665	CATTCCGCTGTGG	CCCTTAG	ACAGAC	ATTGA	CTTCA	TAA	GAT	TCCCTCA	TTTCTTGG	724						
QY	361	GAAGAGGA	AGGGCTTGG	TATGCTGT	GTGATGG	CTCTCTCT	CTTCCGCTCC	CAAG			420						
Db	725	GAAGAGGA	AGGGCTTGG	TATGCTGT	GTGATGG	CTCTCTCT	CTTCCGCTCC	CAAG			784						
QY	421	AAGCCCAT	ATAGTAGGG	GTCA	TTTGGGCTGTGG	TTCCAG	TTCTTTA	AGCCATT	CAAGTCCAGAT		480						
Db	785	AAGCCCAT	ATAGTAGGG	GTCA	TTTGGGCTGTGG	TTCCAG	TTCTTTA	AGCCATT	CAAGTCCAGAT		844						
QY	481	TTTGCTCC	AGCTTTTCA	ATAC	TCTCA	ATTGGCTTA	CTAGCA	ACCATAT	TGATGTGAGT	540							
Db	845	TTTGCTCC	AGCTTTTCA	ATAC	TCTCA	ATTGGCTTA	CTAGCA	ACCATAT	TGATGTGAGT	904							
QY	541	GACAAGACT	CTGTTCA	AAATATTTC	ATGAGGGTGTGG	CTCTCAG	ATGCTCAG	ACAGGCAAG		600							
Db	905	GACAAGACT	CTGTTCA	AAATATTTC	ATGAGGGTGTGG	CTCTCAG	ATGCTCAG	ACAGGCAAG		964							
QY	601	TCCATGTGTGA	CAT	TAGTGA	AGAGGTATCA	CTGACCTAT	TGTATCAT	CGCCTTAC	ACACAGA	-	659						
Db	965	TCCATGTGTGA	CAT	TAGTGA	AGAGGTATCA	CTGACCTAT	TGTATCAT	CGCCTTAC	ACACAGA	1024							
QY	660	-----	-----	-----	-----	-----	-----	-----	-----	659							
Db	1025	GGTTCA	AGCTAT	TTCTCAT	GTCTCAG	CTCAG	AGAGGCT	ATGGCTGTCT	TCAACTTTGG	1084							
QY	660	-----	-----	-----	-----	-----	-----	-----	-----	659							
Db	1085	CCTCA	ATGATCT	GCTGCTTGG	CTTGGCCTT	CCAA	ATTCTGG	GAATTA	TGGGCAT	TAGCCACC	1144						
QY	660	-----	-----	-----	-----	-----	-----	-----	-----	AGGC	663						
Db	1145	ACAGAC	CCCGGCC	AGTGGCCG	ATCTTA	BAACA	CTTTB	AGGCTTT	CTGATTTTA	TAGGC	1204						
QY	664	AAC	TATGAGAA	AGTGGATGGA	AGCCCTT	CA	AA	GTAT	TCTACG	CAAGAAAGG	ATTGGC	723					
Db	1205	AAC	TATGAGAA	AGTGGATGGA	AGCCCTT	CA	AA	GTAT	TCTACG	CAAGAAAGG	ATTGGC	1264					
QY	724	ATCGCCCA	CTCTT	ACAA	AAATCTA	CA	GTAA	TGCA	GGGGAG	CAGACCTT	GTAT	TAGCTGCTG	783				
Db	1265	ATCGCCCA	CTCTT	ACAA	AAATCTA	CA	GTAA	TGCA	GGGGAG	CAGACCTT	GTAT	TAGCTGCTG	1324				
QY	784	AAGAA	AGCTCA	CA	AGTCA	CTT	GGCCCA	GGCCGG	GTGTGG	CCCTA	TTCTGT	TGAGGG	CATG	843			
Db	1325	AAGAA	AGCTCA	CA	AGTCA	CTT	GGCCCA	GGCCGG	GTGTGG	CCCTA	TTCTGT	TGAGGG	CATG	1388			
QY	844	ACGGT	GAGAGGT	CTGTG	TATGG	CCATG	AGGCGC	CTGGG	TTAG	TGGAGAA	TTTCTG	CTT		903			
Db	1385	ACGGT	GAGAGGT	CTGTG	TATGG	CCATG	AGGCGC	CTGGG	TTAG	TGGAGAA	TTTCTG	CTT		1444			
QY	904	CTTGG	CAAGGA	ACCA	ATGCCAT	TTTTAT	TGAGAT	CTTAA	GA	AA	AGAT	CTTAT	GGGA	963			
Db	1445	CTTGG	CAAGGA	ACCA	ATGCCAT	TTTTAT	TGAGAT	CTTAA	GA	AA	AGAT	CTTAT	GGGA	1504			
QY	964	GAC	AGAA	GA	AAATG	CCAG	ATGCGCTT	CTT	CAGGG	TTTTT	TGAG	ACAT	TTTCA	CAGA	AGT	1023	
Db	1505	GAC	AGAA	GA	AAATG	CCAG	ATGCGCTT	CTT	CAGGG	TTTTT	TGAG	ACAT	TTTCA	CAGA	AGT	1566	
QY	1024	GAGT	CCGTGTG	CTG	CA	ATG	CCCGG	CTCT	GA	ATCTA	GA	AGCT	CAGTT	CA	AGG	CCCATC	1083
Db	1565	GAGT	CCGTGTG	CTG	CA	ATG	CCCGG	CTCT	GA	ATCTA	GA	AGCT	CAGTT	CA	AGG	CCCATC	162
QY	1084	ACT	GACT	TGAG	GGAG	CA	AGGCT	CAT	CTTA	1110							
Db	1625	ACT	GACT	TGAG	GGAG	CA	AGGCT	CAT	CTTA	1651							

ID	AAE29995 standard; DNA; 2064 BP.
XX	
AC	AAE29995;
XX	
DT	06-APR-2001 (first entry)
XX	
DE	Human GRMx-Ig DNA.
XX	
KW	Human; metabotropic glutamate receptor; schizophrenia; GRMx;
KM	Alzheimer's; Parkinson's; stroke; depression; anxiety; pain; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200102566-A1.
XX	
ED	11-JAN-2001.
XX	
PF	27-JUN-2000; 2000WO-US17798.
XX	
PR	02-JUL-1999; 99US-0346326.
XX	
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
XX	
PI	Schwarz DA, Maki RA;
XX	
DR	WPI; 2001-123112/13.
XX	
PT	Novel metabotropic glutamate receptor for prevention, treatment of
CC	conditions associated with undesirable glutamate levels, e.g.
PT	Alzheimer's; Parkinson's disease, stroke, depression, anxiety, pain and
XX	schizophrenia -
PS	Claim 2; Fig 11; 59pp; English.
XX	
CC	The present invention relates to human metabotropic glutamate
CC	receptor. An agent that decreases expression or activity of the
CC	metabotropic glutamate receptor is useful for treating schizophrenia.
CC	Metabotropic glutamate receptor polynucleotides, polypeptides
CC	are useful for treating diseases associated with undesirable
CC	levels of glutamate, such as Alzheimer's disease, Parkinson's
CC	disease, stroke, depression, anxiety, pain and schizophrenia.
XX	
SEQ	Sequence 2064 BP; 518 A; 466 C; 519 G; 561 T; 0 other:
Query Match	81.8%; Score 907.8; DB 22; Length 2064;
Best Local Similarity	99.8%; Pred. No. 1.1e-276;
Matches 909; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 ATGCTCCTTCGTGGTATCTCCTGCAGCTCTACTTTTGAAAAGAAGATGCGTGGAGATGCA 60
DB	365 ATGGTCCCTTCGTGGATCTCTGTCAAGTCTTACTTTTGAAAAGAAGATGTCGGTAGATCCA 424
QY	61 CAGTCCAGTAGAGAGAGAGGTGATGCTCACATGCTGGGTGACATCATATTGAGACTCTC 120
DB	425 CAGTCCAGTAGAGAGAGGTGATGCTCACATGCTGGGTGACATCATATTGAGACTCTC 484
QY	121 TTTTCTGTTCATCACACAGCTTACTGTGAGCAGAACTTCATGAGAGGAAGTGGGGCAGTC 180
DB	485 TTTTCTGTTCATCACACAGCTTACTGTGAGCAGAACTTCATGAGAGGAAGTGGGGCAGTC 544
QY	181 CGTGAACAGTATGGCATTACAAGAGGTGAGGCCAATGCTGCATPACCCTGGAAAAGATCAAT 240
DB	545 CGTGAACAGTATGGCATTACAAGAGGTGAGGCCAATGCTGCATPACCCTGGAAAAGATCAAT 604
QY	241 TCAGACCCCACTCTTGSCCAATCACTCATGSGCTGTGAGATTAAGGATTTCTGCTGG 300
DB	605 TCAGACCCCACTCTTGSCCAATCACTCATGSGCTGTGAGATTAAGGATTTCTGCTGG 664
QY	301 CATTCGGCTGTGGCCCTAGAGCAGAGCATTAAGTTCAATAGAAGATTCCTCATTTCTTGG 360
DB	665 CATTCGGCTGTGGCCCTAGAGCAGAGCATTAAGTTCAATAGAAGATTCCTCATTTCTTGG 724
QY	361 GAAGAGAGAGAGGCTTGATGCTCTGTGATGAGTGCCTCTCTTCTTCCGCTCCAG 420

Db	725	GAAAGGAAAGAGGGCTTGGTGTGCTCTGTGGATGGCTCTCTCTCTTCTTCCGCTCCAG	784
QY	421	AAGCCCATAGTAGGGGTCATTTGGGCTTGCTTCAAGTCTTTAGCCATTCAAGTCCAGAT	480
Db	785	AAGCCCATAGTAGGGGTCATTTGGGCTTGCTTCAAGTCTTTAGACCATTCAGGTCAGAT	844
QY	481	TTGCTCCAGCTTTTCCACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT	540
Db	845	TTGCTCCAGCTTTTCCACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGT	904
QY	541	GACAAAGACTCTGTTCAATATTTTCATGAGGTTGTGCTTCAAGTCTCAGACGCAAGG	600
Db	905	GACAAAGACTCTGTTCAATATTTTCATGAGGTTGTGCTTCAAGTCTCAGACGCAAGG	964
QY	601	TCCATGGTGGACATAGTGAAGAGGACAACTGGACCTATGTATCAAGCCGTTCACACAA	660
Db	965	TCCATGGTGGACATAGTGAAGAGGACAACTGGACCTATGTATCAAGCCGTTCACACAA	1024
QY	661	GGCAACTATGAGAAAGTGGAGTGAAGACCTTCAAGATATGTCCAGCAAGAAAGGAGTT	720
Db	1025	GGCAACTATGAGAAAGTGGAGTGAAGACCTTCAAGATATGTCCAGCAAGAAAGGAGTT	1084
QY	721	TGCATGCGCCCACTCTTACAAATCTACAGTATGCAAGGAGACAGACTTTGATTAAGCTG	780
Db	1085	TGCATGCGCCCACTCTTACAAATCTACAGTATGCAAGGAGACAGACTTTGATTAAGCTG	1144
QY	781	CTGAAGAAGCTCACAAAGTCACTTGCCCAAGGCCCGGGTGTGTGCGCTTACTTGTGTAGGGC	840
Db	1145	CTGAAGAAGCTCACAAAGTCACTTGCCCAAGGCCCGGGTGTGTGCGCTTACTTGTGTAGGGC	1204
QY	841	ATGACGGTGAAGAGTCTGCTGATATGGCCATGAGGCGCTGGGCTCTAGTGGAGAAATTTCTG	900
Db	1205	ATGACGGTGAAGAGTCTGCTGATATGGCCATGAGGCGCTGGGCTCTAGTGGAGAAATTTCTG	1264
QY	901	CTTCTGGGCGAG 911	
Db	1265	CTTCTGGGCGAG 1275	

XX	RESULT 7
XX	AAC85785
ID	AAC85785 standard; cDNA; 2826 BP.
XX	
AC	AAC85785;
XX	
DT	18-JUL-2001 (first entry)
XX	
DE	cDNA encoding metabotropic glutamate receptor.
XX	
Human; metabotropic glutamate receptor; mglur; splice variant;	
mglur5; G-protein-coupled receptor; glutamate; neurological disorder	
anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;	
muscle relaxant; ss.	
XX	
OS	Homo sapiens.
XX	
PN	WO200130829-A1.
XX	
PD	03-MAY-2001.
XX	
PF	25-OCT-2000; 2000WO-US29356.
XX	
PR	25-OCT-1999; 99US-0161481.
PR	24-OCT-2000; 2000US-0695481.
XX	
PA	(NPSF-) NPS PHARM INC.
PI	
Krapcho K, Storzmann T, Levinthal C, Hammerland L, Storzjohann L;	
WPI; 2001-308615/32.	
P-PSDB; AAB47217.	
DR	
XX	

PT New nucleic acid encoding an isoform of human metabotropic glutamate  
PT receptor, for identifying potential therapeutic agents for neurological  
PT disease .  
XX  
XX  
PS Claim 2; Page 51-56; 86pp; English.  
CC This sequence encodes a human metabotropic glutamate receptor (mglur).  
CC mglur is a splice variant of human metabotropic glutamate receptor 5  
CC (mglur5). mglur5 are G-protein-coupled receptors capable of activating  
CC a variety of intracellular second messenger systems following the  
CC binding of glutamate. Recombinant mglur DNA and compounds that bind to,  
CC or modulate activity of mglur are useful for diagnosing or treating  
CC neurological disorders, e.g. as anticonvulsants, neuroprotectants,  
CC analgesics, cognitive enhancers and muscle relaxants.  
XX  
XX Sequence 2826 BP; 729 A; 679 C; 712 G; 706 T; 0 other;  
SQ  
Query Match 80.0%; Score 888.4; DB 22; Length 2826;  
Best Local Similarity 98.2%; Pred. No. 1,88-270;  
Matches 899; Conservative 0; Mismatches 16; Indels 0; Gaps 0

Qy	1	ATGTCCTCTGTGTAACCTGTCAGTCTTACTTTTGAAGAAGATGTCCTGCGGAGTCA	60
Db	1	ATGTCCTCTGTGTAACCTGTCAGTCTTACTTTTGAAGAAGATGTCCTGCGGAGTCA	60
Qy	61	CAGTCCAGTAGAGAGAGGGTGTGTGCTCAACATGCTGGGTGACATCATTTATTTGAGCTTC	120
Db	61	CAGTCCAGTAGAGAGAGGGTGTGTGCTCAACATGCTGGGTGACATCATTTATTTGAGCTTC	120
Qy	121	TTTTCTGTTATACACCGCCTACTGTGTGAGGAAGTTTCATAGAGAAAGTGTGTGGGCACTC	180
Db	121	TTTTCTGTTATACACCGCCTACTGTGTGAGGAAGTTTCATAGAGAAAGTGTGTGGGCGCTC	180
Qy	181	CGTGAACAGTATGGCATTACAGAGGTGAGAGGCCATGCTGCATACCTTGAAAGATCAAT	240
Db	181	CGTGAACAGTATGGCATTACAGAGGTGAGAGGCCATGCTGCATACCTTGAAAGATCAAT	240
Qy	241	TCAGACCCCACTCTTGTCCCAATCATCACTTGGCTGTGTGAGTAAAGGATTCCTGTGG	300
Db	241	TCAGACCCCACTCTTGTCCCAATCATCACTTGGCTGTGTGAGTAAAGGATTCCTGTGG	300
Qy	301	CATTGGCTGTGGCCCTTGAAGCAGAGCATTTGAGTTCTAAGAGATTCCTCATTTCTTGG	360
Db	301	CATTGGCTGTGGCCCTTGAAGCAGAGCATTTGAGTTCTAAGAGATTCCTCATTTCTTCA	360
Qy	361	GAAAGGGAAGAGGGCTTGTATGCTCTGTGGAATGGCTCCTCTTCCCTTCCGCTCCAG	420
Db	361	GAAAGGGAAGAGGGCTTGTATGCTGTGTGGAATGGCTCCTCTTCCCTTCCGCTCCAG	420
Qy	421	AAGCCATATGTAAGGGTCAATTGGGGCTGTTCAGATTCTTTAGCCATTACAGSTCCAGAT	480
Db	421	AAGCCATATGTAAGGGTCAATTGGGGCTGTTCAGATTCTTTAGCCATTACAGSTCCAGAT	480
Qy	481	TTGCTCCAGCTTTTCAACATATCTCAGATTGCTTACTTCAGCAACCATCATGATCTGAGT	540
Db	481	TTGCTCCAGCTTTTCAACATATCTCAGATTGCTTACTTCAGCAACCATCATGATCTGAGT	540
Qy	541	GAAAGATCTGTTCAAATATTTTCAAGAGGGTGTGCTTCAGATGTCTCAGACAGCAAGG	600
Db	541	GAAAGATCTGTTCAAATATTTTCAAGAGGGTGTGCTTCAGATGTCTCAGACAGCAAGG	600
Qy	601	TTCATGGTGAACATATGTAAGAGGTATCAACTGACCTATGTATAGCGCTATCACAGAA	660
Db	601	TTCATGGTGAACATATGTAAGAGGTATCAACTGACCTATGTATAGCGCTATCACAGAA	660
Qy	661	GCGAATATGAGAAAGTGGGATGGAAGCCTTCAGAAATATGTTCAGCGAAGGAAGGATT	720
Db	661	GCGAATATGAGAAAGTGGGATGGAAGCCTTCAGAAATATGTTCAGCGAAGGAAGGATT	720
Qy	721	TGATATGCCCATCTTTACAAATATCTACAGTATATGACGGGAGCAGACCTTTGATTAAGCTG	780
Db	721	TGATATGCCCATCTTTACAAATATCTACAGTATATGACGGGAGCAGACCTTTGATTAAGCTG	780

QY 781 CTGAAGAGCTCAAGATCTGTCCTGACCAAGCCCGGATGCTGCTACTTCTGAGAGGC 840  
DB 781 CTGAAGAGCTCAAGATCTGTCCTGACCAAGCCCGGATGCTGCTACTTCTGAGAGGC 840  
QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCTGAGTCTAGTGGAGAAATTTCTG 900  
DB 841 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCTGAGTCTAGTGGAGAAATTTCTG 900  
QY 901 CTTCTGGGAGGGA 914  
DB 901 CTTCTGGGAGGGA 914

RESULT 8  
AAC85787  
ID AAC85787 standard; cDNA; 3129 BP.  
XX AAC85787;  
XX  
XX 18-JUL-2001 (first entry)  
XX  
XX cDNA encoding chimeric receptor containing hmGluR5d portion.  
XX  
XX Human; metabotropic glutamate receptor; mglur; splice variant;  
XX mglur5; G-protein-coupled receptor; glutamate; neurological disorder;  
XX anticonvulsant; neuroprotectant; analgesic; cognitive enhancer;  
XX muscle relaxant; calcium receptor; CaR; mglur5d; ss.  
XX  
XX Chimeric - Homo sapiens.  
XX  
XX MO200130829-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 25-OCT-2000; 2000MO-US29356.  
XX  
XX 25-OCT-1999; 99US-0161481.  
XX PR 24-OCT-2000; 2000US-0695481.  
XX  
XX (NPSP-) NPS PHARM INC.  
XX  
XX Krapcho K, Stormann T, Levinthal C, Hammerland L, Storchmann L;  
XX WPI; 2001-308615/32.  
XX DR P-PSDB; AAB47219.  
XX  
XX New nucleic acid encoding an isoform of human metabotropic glutamate  
XX receptor, for identifying potential therapeutic agents for neurological  
XX disease -  
XX  
XX Claim 18; Page 70-75; 86pp; English.  
XX  
XX This sequence encodes a chimeric receptor comprising the intracellular  
XX cytoplasmic tail of the human calcium receptor (CaR) and the extra-  
XX cellular and seven transmembrane domains of the human metabotropic  
XX glutamate receptor (mglur) splice variant of human metabotropic  
XX glutamate receptor 5 (mglur5), mglur5d. mglur5 are G-protein-coupled  
XX receptors capable of activating a variety of intracellular second  
XX messenger systems following the binding of glutamate. Recombinant  
XX mglur5d DNA and compounds that bind to, or modulate activity of it  
XX are useful for diagnosing or treating neurological disorders, e.g.  
XX as anticonvulsants, neuroprotectants, analgesics, cognitive enhancers  
XX and muscle relaxants.  
XX  
XX Sequence 3129 BP; 806 A; 782 C; 804 G; 737 T; 0 other;

QY Query Match 80.0%; Score 888.4; DB 22; Length 3129;  
Best Local Similarity 98.2%; Pred. No. 1.9e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGCTCTTGTGATCTGTCAGTCTTACTTTTGAAGAAGATGCTCGTGGAGTGA 60  
DB 1 ATGGCTCTTGTGATCTGTCAGTCTTACTTTTGAAGAAGATGCTCGTGGAGTGA 60

QY 61 CAGTCCAGTGAAGAGAGGGGTGGTGCATATGCTGGTGAACATCATTTATGAGCTCTG 120  
DB 61 CAGTCCAGTGAAGAGAGGGGTGGTGCATATGCTGGTGAACATCATTTATGAGCTCTG 120  
QY 121 TTTTCTGTTTCATCAGAGCTTACTGTGAAGAAATTCATGAGAGAAAGTGGGGAGTC 180  
DB 121 TTTTCTGTTTCATCAGAGCTTACTGTGAAGAAATTCATGAGAGAAAGTGGGGAGTC 180  
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGCTGCATCCCTGGAAAGATCAAT 240  
DB 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCCATGCTGCATCCCTGGAAAGATCAAT 240  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGAGGATTCCTGCTG 300  
DB 241 TCAGACCCCACTCTTGGCCCAATCACTGAGGCTGTGAGATTAAGAGGATTCCTGCTG 300  
QY 301 CATTGCGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAAGATTCCTCATTTCTTGG 360  
DB 301 CATTGCGCTGTGGCCCTAGAGCAGAGCATTTAGATTCAAGATTCCTCATTTCTTGG 360  
QY 361 GAAAGAGAGAGGGCTTTGGTATGCTCTGTGATGCTCTCTCTTCTTCCGCTCCAAG 420  
DB 361 GAAAGAGAGAGGGCTTTGGTATGCTCTGTGATGCTCTCTCTTCTTCCGCTCCAAG 420  
QY 421 AAGCCCATGTAAGGGGTCAATGGGCTGGTTCAGTTCTTTAGCCATTGACGTCAGAAAT 480  
DB 421 AAGCCCATGTAAGGGGTCAATGGGCTGGTTCAGTTCTTTAGCCATTGACGTCAGAAAT 480  
QY 481 TTGCTCAGCTTTTCAACATACCTCAATGCTTACTCAAGCAACATCATGATCTGAGT 540  
DB 481 TTGCTCAGCTTTTCAACATACCTCAATGCTTACTCAAGCAACATCATGATCTGAGT 540  
QY 541 GACAAAGCTCTGTTCAAAATTTTCATGAGGGTTGCTTCAAGTCTCAGAGGGAAG 600  
DB 541 GACAAAGCTCTGTTCAAAATTTTCATGAGGGTTGCTTCAAGTCTCAGAGGGAAG 600  
QY 601 TCCATGATGAGCATGATGAGAGGATCACTGACCTATGATCAACCGTACACAGAA 660  
DB 601 TCCATGATGAGCATGATGAGAGGATCACTGACCTATGATCAACCGTACACAGAA 660  
QY 661 GGCACATGAGAGAAAGTGGATGAGAGGCTTCAAAAGATATGTCAGAGAAAGGATTT 720  
DB 661 GGCACATGAGAGAAAGTGGATGAGAGGCTTCAAAAGATATGTCAGAGAAAGGATTT 720  
QY 721 TGCATGCCCACTCTTACAAATCTACATGATGACGGGAGAGAGCTTTGATTAAGCTG 780  
DB 721 TGCATGCCCACTCTTACAAATCTACATGATGACGGGAGAGAGCTTTGATTAAGCTG 780  
QY 781 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCCCGGGTGGCTCAATCTGTAAGGGC 840  
DB 781 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCCCGGGTGGCTCAATCTGTAAGGGC 840  
QY 841 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 900  
DB 841 ATGACGGTGAAGAGTCTGCTGATGAGCCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 900  
QY 901 CTTCTGGGAGGGA 914  
DB 901 CTTCTGGGAGGGA 914

RESULT 9  
ACA56535  
ID ACA56535 standard; cDNA; 4078 BP.  
XX ACA56535;  
XX  
XX 06-JUN-2003 (first entry)  
XX  
XX Human signalling pathway polynucleotide probe SEQ ID NO 1133.  
XX  
XX Human; probe; ss; array element; Parkinson's disease;



KM signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KM immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 OS Homo sapiens.  
 XX US6500938-BI.  
 PN 31-DEC-2002.  
 PD 30-JAN-1998; 98US-0016434.  
 PF 30-JAN-1998; 98US-0016434.  
 XX 30-JAN-1998; 98US-0016434.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Au-Young J, Sellhammer JI;  
 PI WPI; 2003-352189/33.  
 DR Combination of polynucleotide probes, useful as array elements in a  
 PT microarray for monitoring the expression of a number of target  
 PT polynucleotides -  
 PS Claim 1; SEQ ID NO 1133; 65bp; English.  
 XX  
 XX The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensic and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding  
 CC for different signalling pathway populations which can be used to diagnose  
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
 CC and Parkinson's disease. The present sequence represents a polynucleotide  
 CC probe of the invention. Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?docID=06500938B1.  
 CC  
 SO Sequence 4078 BP; 994 A; 1074 C; 1076 G; 934 T; 0 other:  
 Query Match 80.0%; Score 888.4; DB 25; Length 4078;  
 Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ATGGTCCTTGTGATCCTGAGCTTACTTTGAAAGAAATGCGTGGAGAGCA 60  
 DB 151 ATGGTCCTTGTGATCCTGAGCTTACTTTGAAAGAAATGCGTGGAGAGCA 210  
 QY 61 CAGTCCAGTGAAGAGGAGTGTGCTCAGCATCTGGGTGACATCATTTAGAGCTTC 120  
 DB 211 CAGTCCAGTGAAGAGGAGTGTGCTCAGCATCTGGGTGACATCATTTAGAGCTTC 270  
 QY 121 TTTTCTGTTTATCAGAGCTTACTGTGAGCAAGTTATGAGAGAAAGTGTGGGCAATC 180  
 DB 271 TTTTCTGTTTATCAGAGCTTACTGTGAGCAAGTTATGAGAGAAAGTGTGGGCAATC 330  
 QY 181 CGTGAACAGTATGAGCAATTGAGAGTGAAGGCAATGTCATCCCTGGAAGAAAGATCAAT 240  
 DB 331 CGTGAACAGTATGAGCAATTGAGAGTGAAGGCAATGTCATCCCTGGAAGAAAGATCAAT 390  
 QY 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGAGTTCTGCTGG 300  
 DB 391 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGATTAAGGAGTTCTGCTGG 450

QY 301 CATTGGGCTGTGGCCCTAGAGCAGAGCATTTGAGTTCATAAGAGATTCCCTATTCTTGG 360  
 DB 451 CATTGGGCTGTGGCCCTAGAGCAGAGCATTTGAGTTCATAAGAGATTCCCTATTCTTCA 510  
 QY 361 GAAGAGAAAGAGGCTTGGTATGCTGTGATGAGTGCCTCTCTTCCGCTCCAG 420  
 DB 511 GAAGAGAAAGAGGCTTGGTATGCTGTGATGAGTGCCTCTCTTCCGCTCCAG 570  
 QY 421 AAGCCATATGAGGAGTCAATGGGCTGTGCTTCAAGTTCTTACCAATTCAGTCCAGAT 480  
 DB 571 AAGCCATATGAGGAGTCAATGGGCTGTGCTTCAAGTTCTTACCAATTCAGTCCAGAT 630  
 QY 481 TTGCTCAGCTTTTAACTACTGAGTTGCTTACTCAGCAACCAATCATGATCTGAGT 540  
 DB 631 TTGCTCAGCTTTTAACTACTGAGTTGCTTACTCAGCAACCAATCATGATCTGAGT 690  
 QY 541 GACAAAGCTCTGTTCAAAATATTTATGAGGAGTGTGCTTCAAGATGCTCAGCAGCAAG 600  
 DB 691 GACAAAGCTCTGTTCAAAATATTTATGAGGAGTGTGCTTCAAGATGCTCAGCAGCAAG 750  
 QY 601 TCCATGCTGAGCACTAGTGAAGAGTCAACTGAGCCTATGATCAGCCGTACACAGAA 660  
 DB 751 TCCATGCTGAGCACTAGTGAAGAGTCAACTGAGCCTATGATCAGCCGTACACAGAA 810  
 QY 661 GCGAAGTATGAGAAAGTGGATGGAAGGCTTCAAGATATGTCAGCGAAGAGGATTT 720  
 DB 811 GCGAAGTATGAGAAAGTGGATGGAAGGCTTCAAGATATGTCAGCGAAGAGGATTT 870  
 QY 721 TGCATGCGCCACTCTTACAAATCTACAGTAATGACGGAGAGCAAGCTTGTAAAGCTG 780  
 DB 871 TGCATGCGCCACTCTTACAAATCTACAGTAATGACGGAGAGCAAGCTTGTAAAGCTG 930  
 QY 781 CTGAGAGAGCTCAAGATCACTTGGCCAAAGCCGGGTGGTGGCTTCTGTGAGAGGC 840  
 DB 931 CTGAGAGAGCTCAAGATCACTTGGCCAAAGCCGGGTGGTGGCTTCTGTGAGAGGC 990  
 QY 841 ATGACGCTGAGAGGTTGCTGATGAGCATGAGAGCCGCTGGTCTAGTGGAGAAATTTCTG 900  
 DB 991 ATGACGCTGAGAGGTTGCTGATGAGCATGAGAGCCGCTGGTCTAGTGGAGAAATTTCTG 1050  
 QY 901 CTTCTGGGAGGGA 914  
 DB 1051 CTTCTGGGAGGGA 1064  
 RESULT 10  
 AAD04990  
 ID AAD04990 standard; cDNA; 4207 BP.  
 AC AAD04990;  
 XX  
 DT 17-JUL-2001 (first entry)  
 XX  
 DE Human metabolotropic glutamate receptor, mGluR5A cDNA mutant.  
 XX  
 KW Human; metabolotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 KM postsynaptic sensitivity; glutamate excitation; mutant; ss.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT mutation /tag= a  
 FT mutation /tag= b  
 FT mutation /tag= b  
 FT mutation /tag= b  
 PN US6211353-B1.  
 XX  
 PD 03-APR-2001.



PF 07-JUN-1996; 96US-0660148.  
 XX 29-JUL-1994; 94US-0282853.  
 XX (ELIL ) LILLY & CO ELI.  
 PA Burnette JP, Mayne NG, Sharp RL, Snyder YM;  
 PI WPI; 2001-289639/30.  
 XX  
 XX New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptor, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 XX  
 PS Disclosure; Column -; 53bp; English.  
 XX  
 CC The present sequence is a cDNA mutant encoding human metabotropic  
 CC glutamate receptor, mglur5A. L-glutamate, the most abundant  
 CC neurotransmitter in the central nervous system (CNS), mediates excitatory  
 CC pathway in mammals. L-glutamate is referred to as excitatory amino acid  
 CC (EAA) and the receptors that respond to glutamate are EAA receptors. The  
 CC receptors are useful for modulating the presynaptic release of glutamate  
 CC and the postsynaptic sensitivity of the neuronal cell to glutamate  
 CC excitation.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the sequence referred as SEQ ID NO:1, shown in column  
 CC 59-68 (AAd05029) of the specification.  
 CC  
 XX Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 T; 0 other;  
 XX  
 Query Match 80.0%; Score 888.4; DB 22; Length 4207;  
 Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ATGGCTCTTCTGTTGATCTGTCACTCTTCTTGAAGAAGATGTCGGGAGATGCA 60  
 DB 460 ATGGCTCTTCTGTTGATCTGTCACTCTTGAAGAAGATGTCGGGAGATGCA 519  
 QY 61 CAGTCCAGTGAAG 120  
 DB 520 CAGTCCAGTGAAG 579  
 QY 121 TTTTCTGTTATCAACGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
 DB 580 TTTTCTGTTATCAACGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639  
 QY 181 CGTGAACAGTATGAGCATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
 DB 640 CGTGAACAGTATGAGCATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 699  
 QY 241 TCAGAACCCCACTCTTGGCCCAATCACTGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 DB 700 TCAGAACCCCACTCTTGGCCCAATCACTGAGAGAGAGAGAGAGAGAGAGAGAG 759  
 QY 301 CATTGGCTGAG 360  
 DB 760 CATTGGCTGAG 819  
 QY 361 GAAG 420  
 DB 820 GAAG 879  
 QY 421 AAGCCATAGTAG 480  
 DB 880 AAGCCATAGTAG 939  
 QY 481 TTGCTCAGCTTTCAACATACCTCAATGCTTACAGAGAGAGAGAGAGAGAGAGAG 540  
 DB 940 TTGCTCAGCTTTCAACATACCTCAATGCTTACAGAGAGAGAGAGAGAGAGAGAG 999  
 QY 541 GACAAAGCTGTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

DB 1000 GACAAAGCTGTGTTCAATATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059  
 QY 601 TCATAGTGGACATAGTGAAGAGAGTCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
 DB 1060 GCCATGAGTGAACATAGTGAAGAGAGTCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1119  
 QY 661 GGCACATATGAG 720  
 DB 1120 GGCACATATGAG 1179  
 QY 721 TGCATGAG 780  
 DB 1180 TGCATGAG 1239  
 QY 781 CTGAG 840  
 DB 1240 CTGAG 1299  
 QY 841 ATGACGAGTGAAG 900  
 DB 1300 ATGACGAGTGAAG 1359  
 QY 901 CTCTGAG 914  
 DB 1360 CTCTGAG 1373  
 RESULT 11  
 AAD05029  
 ID AAD05029 standard; cDNA; 4207 BP.  
 XX  
 AC AAD05029;  
 XX  
 DT 17-JUL-2001 (first entry)  
 XX  
 DE Human metabotropic glutamate receptor, mglur5A cDNA.  
 XX  
 KW Human; metabotropic glutamate receptor; mglur5A; excitatory amino acid;  
 KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 KW postsynaptic sensitivity; glutamate excitation; 88.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 460..4002  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mglur5A"  
 PN US6211353-B1.  
 XX  
 PD 03-APR-2001.  
 XX  
 PP 07-JUN-1996; 96US-0660148.  
 XX  
 PR 29-JUL-1994; 94US-0282853.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Burnette JP, Mayne NG, Sharp RL, Snyder YM;  
 DR WPI; 2001-289639/30.  
 XX  
 DR P-PSDB; AAB01156.  
 XX  
 XX New isolated nucleic acids for producing human metabotropic glutamate  
 PT receptor, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 XX  
 XX Claim 2; Column 59-68; 53bp; English.  
 CC The present sequence is a cDNA encoding human metabotropic glutamate  
 CC receptor, mglur5A. L-glutamate, the most abundant neurotransmitter in

CC the central nervous system (CNS), mediates excitatory pathway in  
 CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
 CC the receptors that respond to glutamate are EAA receptors. The receptors  
 CC are useful for modulating the presynaptic release of glutamate and the  
 CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
 CC Note: The present sequence is stated as being the same as that shown as  
 CC SEQ ID NO:1 (AAD05033) in column 7-18 of the specification. However the  
 CC sequences differ at several positions.  
 XX

Sequence 4207 BP; 1011 A; 1120 C; 1112 G; 964 T; 0 other;

Query Match 80.0%; Score 888.4; DB 22; Length 4207;  
 Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
 Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```

QY 1 ATGGCTCTTGTGTAATCTGTGATGCTTCTTTGAAAGATGCTCGGAGTGC 60
DB 460 ATGGCTCTTGTGTAATCTGTGATGCTTCTTTGAAAGATGCTCGGAGTGC 519
QY 61 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGGTGATCATATTGAGCTTC 120
DB 520 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGGTGATCATATTGAGCTTC 579
QY 121 TTTTCTTTCATACACGCTTCTGTGACGAAATTGATGAGAGAGTGTGGCAGTC 180
DB 580 TTTTCTTTCATACACGCTTCTGTGACGAAATTGATGAGAGAGTGTGGCAGTC 639
QY 181 CGTGAACAGTATGAGCATTGAGAGTGTGGCCATGCTGCATTCCTGGAAGATCAAT 240
DB 640 CGTGAACAGTATGAGCATTGAGAGTGTGGCCATGCTGCATTCCTGGAAGATCAAT 699
QY 241 TCAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGATGATGAGGATTCCTGTGG 300
DB 700 TCAGACCCACACTCTTGGCCCAATGACACTGGGCTGTGATGATGAGGATTCCTGTGG 759
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCATTAAGATTCCTCATTTCTTCG 360
DB 760 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCATTAAGATTCCTCATTTCTTC 819
QY 361 GAAGAGAGAGAGGCTTGTGATGCTGTGATGAGCTCTCTCTTCTTCCGCTCCAG 420
DB 820 GAAGAGAGAGAGGCTTGTGATGCTGTGATGAGCTCTCTCTTCTTCCGCTCCAG 879
QY 421 AAGCCATGTAGGGGTCAATTTGGGCTGTGCTTCAAGTTCCTTACCATTCAGGTCCAGAT 480
DB 880 AAGCCATGTAGGGGTCAATTTGGGCTGTGCTTCAAGTTCCTTACCATTCAGGTCCAGAT 939
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATGATGATGAGT 540
DB 940 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGCAACCATGATGATGAGT 999
QY 541 GACAAAGCTGTGTAATATTTTATGAGGAGTGTGCTTCAAGTGTCCAGAGGCAAG 600
DB 1000 GACAAAGCTGTGTAATATTTTATGAGGAGTGTGCTTCAAGTGTCCAGAGGCAAG 1059
QY 601 TCCATGTGACATATGAGAGAGTACATGAGCCTATATATACGCCGTACACAGAA 660
DB 1060 TCCATGTGACATATGAGAGAGTACATGAGCCTATATATACGCCGTACACAGAA 1119
QY 661 GGCAATATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGAGAAAGAGGAT 720
DB 1120 GGCAATATGAGAAAGTGGATGAGAGCTTCAAAAGATATGTCAGAGAAAGAGGAT 1179
QY 721 TGCATGCCCACTCTTCAAAATCTACATATATGACAGGGAGAGAGCTTGTAAAGCTG 780
DB 1180 TGCATGCCCACTCTTCAAAATCTACATATATGACAGGGAGAGAGCTTGTAAAGCTG 1239
QY 781 CTGAAGAAGTCAAGATCACTTGGCCCAAGCCCGGTGTGCTTACTTCTGTAGAGGC 840
DB 1240 CTGAAGAAGTCAAGATCACTTGGCCCAAGCCCGGTGTGCTTACTTCTGTAGAGGC 1299
QY 841 ATGACGGTGAAGAGTGTGATGAGCAGATGAGGCGCTGGGTCTAATGGGAAATTTCTG 900

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DB 1300 ATGACGGTGAAGAGTGTGATGAGCAGATGAGGCGCTGGGTCTAGCGGAGAAATTTCTG 1359

QY 901 CTTCCTGGCAGAGGA 914

DB 1360 CTTCCTGGCAGAGGA 1373

# RESULT 12

AAD05030  
 ID AAD05030 standard; mRNA; 4207 BP.

AC AAD05030;

DT 17-JUL-2001 (first entry)

XX Human metabotropic glutamate receptor, mGluR5A mRNA.

XX Human; metabotropic glutamate receptor; mGluR5A; excitatory amino acid;

XX EAA; central nervous system; CNS; presynaptic release; neurotransmitter;

XX postsynaptic sensitivity; glutamate excitation; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 460..4002

XX /tag= a

XX /product= "Human metabotropic glutamate receptor,

XX mGluR5A"

XX US6211353-B1.

XX PD 03-APR-2001.

XX XX 07-JUN-1996; 96US-0660148.

XX PR 29-JUL-1994; 94US-0282853.

XX PA (ELIL ) LILLY & CO ELI.

XX PI Burnett JP, Wayne NG, Sharp RL, Snyder YM;

XX DR WPI; 2001-289639/30.

XX PS P-PSDB; AAB01156.

XX PT New isolated nucleic acids for producing human metabotropic glutamate

XX PT receptors, which are useful for modulating the presynaptic release of

XX PT glutamate or the postsynaptic sensitivity of the neuronal cell to

XX PT glutamate excitation -

XX PS Claim 2; Column 43-46; 53pp; English.

XX The present sequence is a mRNA encoding human metabotropic glutamate

XX CC receptor, mGluR5A. L-glutamate, the most abundant neurotransmitter in

XX CC the central nervous system (CNS), mediates excitatory pathway in

XX CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and

XX CC the receptors that respond to glutamate are EAA receptors. The receptors

XX CC are useful for modulating the presynaptic release of glutamate and the

XX CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.

SO Sequence 4207 BP; 1010 A; 1121 C; 1112 G; 964 U; 0 other;

Query Match 80.0%; Score 888.4; DB 22; Length 4207;

Best Local Similarity 73.9%; Pred. No. 2.3e-270;

Matches 675; Conservative 223; Mismatches 16; Indels 0; Gaps 0;

```

QY 1 ATGGCTCTTGTGTAATCTGTGATGCTTCTTTGAAAGATGCTCGGAGTGC 60
DB 460 ATGGCTCTTGTGTAATCTGTGATGCTTCTTTGAAAGATGCTCGGAGTGC 519
QY 61 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGGTGATCATATTGAGCTTC 120
DB 520 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGGTGATCATATTGAGCTTC 120

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QY 121 TTTCTGTCATCCAGCCCTACTGTGACGAAGTTGATGAGAGAGTGGGGCAGTC 180  
 Db 580 UUUUCUUGUACACCGCCUACUGUGGACAAAGUUCUAGAGAGAGUUGGGGCGGUC 639  
 QY 181 CGTGAACAGTAGGCAATTCAGAGAGTGGAGCCATGCTGCAATCCTGGAAGATCAAT 240  
 Db 640 CGUGAACAGUAGGCAUUCAGAGAGUGAGGCGCAUUGCUGACUACCCUGAAGAUCAU 699  
 QY 241 TCAGACCCCACTCTTGGCCCAATCACTAGGCTGTGAGATTAAGGATTCCTGCTGG 300  
 Db 700 UCGAGCCCACTCUCUGCCCAACUACUGGGCUGUGAGUAAAGGACUCCUGCUGG 759  
 QY 301 CATTCGCTGTGGCCCTAGAGAGAGCATTAAGTTCATTAAGATTCCTCATTTCTTGG 360  
 Db 760 CAUUGCGCUGUGGCCCTAGAGAGAGCAUUGAGUUCUAAAGAGUUCCTCUCUUCUCA 819  
 QY 361 GAAGAGAGAGAGGGCTGTGATGCTGTGAGAGGCTCTCTCTCTCTCCGCTCAAG 420  
 Db 820 GAAGAGAGAGAGGGCTGTGATGCTGTGAGAGGCTCTCTCTCTCTCCGCTCAAG 879  
 QY 421 AAGCCCATAGAGGGGCTGTGATGCTGTGAGAGGCTCTCTCTCTCTCCGCTCAAG 480  
 Db 880 AAGCCCATAGAGGGGCTGTGATGCTGTGAGAGGCTCTCTCTCTCTCCGCTCAAG 939  
 QY 481 TTGCTCAGCTTTTCAATCACTCAGATTGCTTCAAGCAACCATCAATGATGAT 540  
 Db 940 UUGUCUCCAGUUCUUCACCAUACCUCAAGUUCUUAUCAGACACCAAGUAGUAGU 999  
 QY 541 GACAAAGCTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAAGTCTCAAGCAGG 600  
 Db 1000 GACAAAGCTCTGTTCAAAATATTTCAATGAGGGTGTGCTTCAAGTCTCAAGCAGG 1059  
 QY 601 TCCATGTGAGACATAGTGAAGAGTACATCTGACCTATATATAGCCCTACACAGAA 660  
 Db 1060 GCCAUGUGUAGCAAGAGGAGGAGUACACGAGCCTAUGUAGUAGCCGAGCAGAA 1119  
 QY 661 GGCACATGAGGAGAGTGGAGTGAAGGCTTCAAGATATATGTCAGGAGAGAGGAT 720  
 Db 1120 GGCACATGAGGAGAGTGGAGTGAAGGCTTCAAGATATATGTCAGGAGAGAGGAT 1179  
 QY 721 TGCATGCCCACTCTTCAAAATATTAAGTATGAGGAGAGCAGGCTTTGATAGCTG 780  
 Db 1180 UGCATGCCCACTCTTCAAAATATTAAGTATGAGGAGAGCAGGCTTTGATAGCTG 1239  
 QY 781 CTGAAGAGCTCAAAATCACTTGCCTCAAGGCTGGGTGTGCTACTTCTGTGAGGCG 840  
 Db 1240 CTGAAGAGCTCAAAATCACTTGCCTCAAGGCTGGGTGTGCTACTTCTGTGAGGCG 1299  
 QY 841 ATGACGGTGAAGGCTGTGATGAGGAGGAGGCTGGGTGTGATGAGGAGATTTCTG 900  
 Db 1300 AUGACGGUAGAGGUCUGUGAGUAGGCGCCTGUGGUCUAGCGGAGAGAUUUCUG 1359  
 QY 901 CTTTGGGAGAGGA 914  
 Db 1360 CUUCGCGGAGUGA 1373  
 RESULT 13  
 AAD05033  
 ID AAD05033 standard; cDNA; 4207 BP.  
 XX AAD05033;  
 AC AAD05033;  
 XX 17-JUL-2001 (first entry)  
 DT 17-JUL-2001 (first entry)  
 XX Human metabotropic glutamate receptor, mGluR5A cDNA, alternative version.  
 XX Human metabotropic glutamate receptor; mGluR5A; excitatory amino acid;  
 KM EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
 KM postsynaptic sensitivity; glutamate excitation; ss.  
 XX Homo sapiens.  
 OS

FH Key Location/Qualifiers  
 FT misc\_feature 416  
 FT /tag= a  
 FT /note= "Nucleotide 'T' is present at this location  
 FT in the sequence shown in column 59-68 of the  
 FT specification (AAD05029)"  
 FT 420  
 FT misc\_feature  
 FT /tag= b  
 FT /note= "Nucleotide 'A' is present at this location  
 FT in the sequence shown in column 59-68 of the  
 FT specification (AAD05029)"  
 FT 460..4002  
 FT CDS  
 FT /tag= c  
 FT /product= "Human metabotropic glutamate receptor,  
 FT mGluR5A"  
 FT 3890  
 FT misc\_feature  
 FT /tag= d  
 FT /note= "Nucleotide 'G' is present at this location  
 FT in the sequence shown in column 59-68 of the  
 FT specification (AAD05029)"  
 FT 3999  
 FT misc\_feature  
 FT /tag= e  
 FT /note= "Nucleotide 'G' is present at this location  
 FT in the sequence shown in column 59-68 of the  
 FT specification (AAD05029)"  
 FT 4087  
 FT misc\_feature  
 FT /tag= f  
 FT /note= "Nucleotide 'G' is present at this location  
 FT in the sequence shown in column 59-68 of the  
 FT specification (AAD05029)"  
 FT 4177  
 FT misc\_feature  
 FT /tag= g  
 FT /note= "Nucleotide 'G' is present at this location  
 FT in the sequence shown in column 59-68 of the  
 FT specification (AAD05029)"  
 FT 4177  
 PN US6211353-B1.  
 XX 03-APR-2001.  
 XX 07-JUN-1996; 96US-0660148.  
 XX 29-JUL-1994; 94US-0282853.  
 XX (ELIL) LILLY & CO ELI.  
 PA Burnelt JP, Mayne NG, Sharp RL, Snyder YM;  
 PI WPI; 2001-289639/30.  
 XX P-PSDB; AAB01156.  
 DR New isolated nucleic acids for producing human metabotropic glutamate  
 XX receptors, which are useful for modulating the presynaptic release of  
 PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
 PT glutamate excitation -  
 XX  
 PS Claim 2; Column 7-18; 53pp; English.  
 XX The present sequence is an alternative version of a cDNA encoding human  
 CC metabotropic glutamate receptor, mGluR5A. L-glutamate, the most abundant  
 CC neurotransmitter in the central nervous system (CNS), mediates excitatory  
 CC pathway in mammals. L-glutamate is referred to as excitatory amino acid  
 CC (EAA) and the receptors that respond to glutamate are EAA receptors. The  
 CC receptors are useful for modulating the presynaptic release of glutamate  
 CC and the postsynaptic sensitivity of the neuronal cell to glutamate  
 CC excitation.  
 CC Note: The present sequence is stated as being the same as that shown as  
 CC SEQ ID NO:1 (AAD05029) in column 59-68 of the specification. However the  
 CC sequences differ at several positions.  
 XX  
 SQ Sequence 4207 BP; 1010 A; 1125 C; 1108 G; 964 T; 0 other;  
 Query Match 80.0%; Score 888.4; DB 22; Length 4207;

Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1 ATGCTCTTCTGTGATCCTGTCACTTACTTTTGAAGAAGATGCGGTGAGTCA 60
DB 460 ATGGCTCTTCTGTGATCCTGTCACTTACTTTTGAAGAAGATGCGGTGAGTCA 519
QY 61 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGTGAACATTAATGAGCTCTC 120
DB 520 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGTGAACATTAATGAGCTCTC 579
QY 121 TTTTCTGTTCATCAACGACCTTCTGTGACGAAGTTTCATGAGAGAGTGTGAGTTC 180
DB 580 TTTTCTGTTCATCAACGACCTTCTGTGACGAAGTTTCATGAGAGAGTGTGAGTTC 639
QY 181 CGTGAACAGTATGAGCATTCAAGAGTGAAGGCCATGCTGCATACCTGGAAGAGATCAAT 240
DB 640 CGTGAACAGTATGAGCATTCAAGAGTGAAGGCCATGCTGCATACCTGGAAGAGATCAAT 699
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAATTAAGAGATTCCTGTGG 300
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QY 301 CATTGGCTGTGGCCCTTGAAGAGAGCATTGAGTTCATTAAGATTCCTCATTTCTTCG 360
DB 760 CATTGGCTGTGGCCCTTGAAGAGAGCATTGAGTTCATTAAGATTCCTCATTTCTTCG 819
QY 361 GAAAGAGAGAGGAGCTTGTATGCTGTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCAAG 420
DB 820 GAAAGAGAGAGGAGCTTGTATGCTGTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCAAG 879
QY 421 AAGCCCATGTAGGGGTCATTGGGCTGTGCTTCAAGTCTTACCAATTCAGTTCAGCAAT 480
DB 880 AAGCCCATGTAGGGGTCATTGGGCTGTGCTTCAAGTCTTACCAATTCAGTTCAGCAAT 939
QY 481 TTGCTCAGCTTTTCAACAATCCTCAAGTGTCTTCACTGACCAACCAAGATGATCTGAGT 540
DB 940 TTGCTCAGCTTTTCAACAATCCTCAAGTGTCTTCACTGACCAACCAAGATGATCTGAGT 999
QY 541 GACAACTCTGTCTTAATATTTTCAATGAGGAGTGTGCTTCAAGTGTCTGACAGCAAGG 600
DB 1000 GACAACTCTGTCTTAATATTTTCAATGAGGAGTGTGCTTCAAGTGTCTGACAGCAAGG 1059
QY 601 TCCATGTGAGCACTATGAGAGAGTCAACTGAGCCTATATATCAAGCCGTACACAGAA 660
DB 1060 TCCATGTGAGCACTATGAGAGAGTCAACTGAGCCTATATATCAAGCCGTACACAGAA 1119
QY 661 GGCACCTATGAGAGAGAGTGAAGGCTTCAAGATATGTCAGGAGAGAGAGGATTT 720
DB 1120 GGCACCTATGAGAGAGAGTGAAGGCTTCAAGATATGTCAGGAGAGAGAGGATTT 1179
QY 721 TGCATGCCCACTCTTACAAATCTCAAGTATGACAGGAGAGAGAGCTTGTAAAGCTG 780
DB 1180 TGCATGCCCACTCTTACAAATCTCAAGTATGACAGGAGAGAGAGCTTGTAAAGCTG 1239
QY 781 CTGAAGAAGCTCAAGTCACTTGGCCCAAGGCCCGGGTGTGCTTCTGTGAGGCTC 840
DB 1240 CTGAAGAAGCTCAAGTCACTTGGCCCAAGGCCCGGGTGTGCTTCTGTGAGGCTC 1299
QY 841 ATGACGGTGAAGAGTGTGCTGATGAGCAGTGAAGGCGCTGGGCTTAAGTGAAGAAATTTCTG 900
DB 1300 ATGACGGTGAAGAGTGTGCTGATGAGCAGTGAAGGCGCTGGGCTTAAGTGAAGAAATTTCTG 1359
QY 901 CTTCTGGGAGGGA 914
DB 1360 CTTCTGGGAGGGA 1373

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RESULT 14  
AAD04991  
ID AAD04991 standard; cDNA; 4303 BP.  
XX  
AC AAD04991;

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XX 17-JUL-2001 (first entry)
DT Human metabotropic glutamate receptor, mGluR5B cDNA mutant.
XX
XX
XX Human metabotropic glutamate receptor; mGluR5B; excitatory amino acid;
XX EAA; central nervous system; CNS; presynaptic release; neurotransmitter;
XX postsynaptic sensitivity; glutamate excitation; mutant; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH replace (416, T)
FT mutation /tag= a
FT mutation replace (425, A)
FT mutation /tag= b
XX
XX US6211353-B1.
XX
XX 03-APR-2001.
XX
XX 07-JUN-1996; 96US-0660148.
XX
XX 29-JUL-1994; 94US-0282853.
XX
XX (BL1) LILLY & CO ELI.
XX
XX Burnett JP, Mayne NG, Sharp RL, Snyder YM;
XX WPI; 2001-289639/30.
XX
XX
XX New isolated nucleic acids for producing human metabotropic glutamate
XX receptors, which are useful for modulating the presynaptic release of
XX glutamate or the postsynaptic sensitivity of the neuronal cell to
XX glutamate excitation -
XX
XX Disclosure; Column 23-34; 53pp; English.
XX
XX
XX The present sequence is a cDNA mutant encoding human metabotropic
XX glutamate receptor, mGluR5B. L-glutamate, the most abundant
XX neurotransmitter in the central nervous system (CNS), mediates excitatory
XX pathway in mammals. L-glutamate is referred to as excitatory amino acid
XX (EAA) and the receptors that respond to glutamate are EAA receptors. The
XX receptors are useful for modulating the presynaptic release of glutamate
XX and the postsynaptic sensitivity of the neuronal cell to glutamate
XX excitation.
XX
XX Sequence 4303 BP; 1043 A; 1139 C; 1144 G; 977 T; 0 other;
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Query Match 80.0%; Score 888.4; DB 22; Length 4303;  
Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 1 ATGCTCTTCTGTGATCCTGTCACTTACTTTTGAAGAAGATGCGGTGAGTCA 60
DB 460 ATGGCTCTTCTGTGATCCTGTCACTTACTTTTGAAGAAGATGCGGTGAGTCA 519
QY 61 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGTGAACATTAATGAGCTCTC 120
DB 520 CAGTCCAGTGAAGAGGAGTGTGCTCATATGCTGGTGAACATTAATGAGCTCTC 579
QY 121 TTTTCTGTTCATCAACGACCTTCTGTGACGAAGTTTCATGAGAGAGTGTGAGTTC 180
DB 580 TTTTCTGTTCATCAACGACCTTCTGTGACGAAGTTTCATGAGAGAGTGTGAGTTC 639
QY 181 CGTGAACAGTATGAGCATTCAAGAGTGAAGGCCATGCTGCATACCTGGAAGAGATCAAT 240
DB 640 CGTGAACAGTATGAGCATTCAAGAGTGAAGGCCATGCTGCATACCTGGAAGAGATCAAT 699
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAATTAAGAGATTCCTGTGG 300
DB 700 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAATTAAGAGATTCCTGTGG 759

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```
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTGATTATAGAGATTCCTCATTTCTTCG 360
XX |||
DB 760 CATTGGCTGTGGCCCTAGAGCAGAGCATTTGATTATAGAGATTCCTCATTTCTTCG 819
QY 361 GAAGAGAGAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 420
XX |||
DB 820 GAAGAGAGAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 879
QY 421 AAGCCCTATAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 480
XX |||
DB 880 AAGCCCTATAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 939
QY 481 TTGCTCAGCTTTTCAACATATCTCAGATTTCTTACTCAGAACCATCATGATCTGAGT 540
DB 940 TTGCTCAGCTTTTCAACATATCTCAGATTTCTTACTCAGAACCATCATGATCTGAGT 999
QY 541 GACAGACTCTGTTCATTAATTTTCATGAGGCTGTGTGCTTCAATGCTCAGCAGCAAG 600
DB 1000 GACAGACTCTGTTCATTAATTTTCATGAGGCTGTGTGCTTCAATGCTCAGCAGCAAG 1059
QY 601 TCCATGCTGACATATGAGAGAGGATCAACTGACCTATGATGACCTGACACACAGAA 660
DB 1060 TCCATGCTGACATATGAGAGAGGATCAACTGACCTATGATGACCTGACACACAGAA 1119
QY 661 GGCACATGAGAGAGAGGATGAGAGCCTTCAAGATATGTCAGAGAGAGAGGAT 720
DB 1120 GGCACATGAGAGAGAGGATGAGAGCCTTCAAGATATGTCAGAGAGAGAGGAT 1179
QY 721 TGCAATGCCCACTCTTACAAATCTTACAGTATGACAGAGAGAGAGAGGAT 780
DB 1180 TGCAATGCCCACTCTTACAAATCTTACAGTATGACAGAGAGAGAGAGGAT 1239
QY 781 CTGAAGAGAGGCTCAAGTCACTTGGCCAGGCGCGGTGTGTGCTTCTGTGAGGCG 840
DB 1240 CTGAAGAGAGGCTCAAGTCACTTGGCCAGGCGCGGTGTGTGCTTCTGTGAGGCG 1299
QY 841 ATGACGATGAGAGGCTGTGTATGAGCAGAGGCGCTGAGCTTATGAGAGAGATTTCTG 900
DB 1300 ATGACGATGAGAGGCTGTGTATGAGCAGAGGCGCTGAGCTTATGAGAGAGATTTCTG 1359
QY 901 CTTCTGGGCAAGGA 914
DB 1360 CTTCTGGGCAAGGA 1373
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RESULT 15  
AAD05031  
ID AAD05031 standard; cDNA; 4303 BP.

XX  
AC AAD05031;

XX  
DT 17-JUL-2001 (first entry)

XX  
DE Human metabotropic glutamate receptor, mGluR5B cDNA.

XX  
KM Human; metabotropic glutamate receptor; mGluR5B; excitatory amino acid;  
KW EAA; central nervous system; CNS; presynaptic release; neurotransmitter;  
KW postsynaptic sensitivity; glutamate excitation; ss.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

FT CDS 460..4098

FT /tag= a

FT /product= "Human metabotropic glutamate receptor,  
mGluR5B"

XX  
PN US6211353-B1.

XX  
PD 03-APR-2001.

XX  
PF 07-JUN-1996; 96US-0660148.

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XX  
PR 29-JUL-1994; 94US-0282853.  
XX  
PA (BLI) LILLY & CO BLI.  
XX  
PI Burnett JP, Wayne NG, Sharp RL, Snyder YM;  
XX  
DR WPI; 2001-289639/30.  
XX  
DR P-PSDB; AAB01157.  
XX  
PT New isolated nucleic acids for producing human metabotropic glutamate  
PT receptors, which are useful for modulating the presynaptic release of  
PT glutamate or the postsynaptic sensitivity of the neuronal cell to  
PT glutamate excitation -  
XX  
PS Claim 15; Column 77-86; 53pp; English.  
XX  
CC The present sequence is a cDNA encoding human metabotropic glutamate  
CC receptor, mGluR5B. L-glutamate, the most abundant neurotransmitter in  
CC the central nervous system (CNS), mediates excitatory pathway in  
CC mammals. L-glutamate is referred to as excitatory amino acid (EAA) and  
CC the receptors that respond to glutamate are EAA receptors. The receptors  
CC are useful for modulating the presynaptic release of glutamate and the  
CC postsynaptic sensitivity of the neuronal cell to glutamate excitation.  
XX  
SQ Sequence 4303 BP; 1044 A; 1138 C; 1144 G; 977 T; 0 other;
```

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Query Match 80.0%; Score 888.4; DB 22; Length 4303;  
Best Local Similarity 98.2%; Pred. No. 2.3e-270;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 1 ATGCTCTTCTGTGATCCCTGAGTCTTACTTTTGAAGAAGATCCGTGGAGTGCA 60  
DB 460 ATGCTCTTCTGTGATCCCTGAGTCTTACTTTTGAAGAAGATCCGTGGAGTGCA 519  
QY 61 CAGTCCAGTGAAGAGAGGCTGTGTGCTCAATGCTGGTGAATCATTTTGAAGCTCTC 120  
DB 520 CAGTCCAGTGAAGAGAGGCTGTGTGCTCAATGCTGGTGAATCATTTTGAAGCTCTC 579  
QY 121 TTTTCTGTTCAACACGACTACTGTGAGCAAGTTCAAGAGAGAGTGTGGGCGATC 180  
DB 580 TTTTCTGTTCAACACGACTACTGTGAGCAAGTTCAAGAGAGAGTGTGGGCGATC 639  
QY 181 CGTGAACAGTATGGGATTCAGAGAGTGAAGGCGCATGCTCATACCTGTGAAAGATCAAT 240  
DB 640 CGTGAACAGTATGGGATTCAGAGAGTGAAGGCGCATGCTCATACCTGTGAAAGATCAAT 699  
QY 241 TCAGACCCCACTCTTGGCCCAACATCACATGGGCTGTGAGTAAAGGATTCCTGCTGG 300  
DB 700 TCAGACCCCACTCTTGGCCCAACATCACATGGGCTGTGAGTAAAGGATTCCTGCTGG 759  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTTGATTATAGAGATTCCTCATTTCTTCG 360  
DB 760 CATTGGCTGTGGCCCTAGAGCAGAGCATTTGATTATAGAGATTCCTCATTTCTTCG 819  
QY 361 GAAGAGAGAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 420  
DB 820 GAAGAGAGAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 879  
QY 421 AAGCCCTATAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 480  
DB 880 AAGCCCTATAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCCGCTCCAG 939  
QY 481 TTGCTCAGCTTTTCAACATATCTCAGATTTCTTACTCAGAACCATCATGATCTGAGT 540  
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DB 1000 GACAGACTCTGTTCATTAATTTTCATGAGGCTGTGTGCTTCAATGCTCAGCAGCAAG 1059  
QY 601 TCCATGCTGACATATGAGAGAGGATCAACTGACCTATGATGACCTGACACACAGAA 660
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Qy      661 GGCACCTATGGAGAAAGTGGGATGGAGCCTTCAAGATATGTCAGGAAGGATT 720
Db      1120 GGCACCTATGGAGAAAGTGGGATGGAGCCTTCAAGATATGTCAGGAAGGATT 1179
Qy      721 TGCATGCCCCACTCTTACAAATCTACAGTAATGCAGGGAGCAGAGCTTTGATTAAGCTG 780
Db      1180 TGCATGCCCCACTCTTACAAATCTACAGTAATGCAGGGAGCAGAGCTTTGATTAAGCTG 1239
Qy      781 CTGAAGAAAGCTCACAAAGTCACTTGCCCAAGGCCCGGGTGGTGGCTACTTCTGTAGGGC 840
Db      1240 CTGAAGAAAGCTCACAAAGTCACTTGCCCAAGGCCCGGGTGGTGGCTACTTCTGTAGGGC 1299
Qy      841 ATGACGGTGAAGAGTCTGCTGATGGCCATGAGGGCGCTGGGCTCTAGTGGAGAAATTCTG 900
Db      1300 ATGACGGTGAAGAGTCTGCTGATGGCCATGAGGGCGCTGGGCTCTAGTGGAGAAATTCTG 1359
Qy      901 CTTCTGGGCAGGGA 914
Db      1360 CTTCTGGGCAGTGA 1373
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
6777.889 Million cell updates/sec

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Perfect score: 1110

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	888.4	80.0	2826	4 US-09-695-481-1	Sequence 1, Appl1
2	888.4	80.0	3129	4 US-09-695-481-5	Sequence 5, Appl1
3	888.4	80.0	4078	4 US-09-016-434-1133	Sequence 1133, Ap
4	888.4	80.0	4207	3 US-08-660-148-1	Sequence 1, Appl1
5	888.4	80.0	4207	3 US-08-660-148-3	Sequence 3, Appl1
6	888.4	80.0	4303	3 US-08-660-148-4	Sequence 4, Appl1
7	888.4	80.0	4303	3 US-08-660-148-6	Sequence 6, Appl1
8	885.2	79.7	3282	1 US-08-072-574-11	Sequence 11, Appl1
9	885.2	79.7	3282	1 US-08-486-270-11	Sequence 11, Appl1
10	885.2	79.7	3282	1 US-08-367-264-11	Sequence 11, Appl1
11	885.2	79.7	3282	4 US-09-153-757-11	Sequence 11, Appl1
12	885.2	79.7	3282	4 US-09-459-715-11	Sequence 11, Appl1
13	885.2	79.7	4085	1 US-08-072-574-7	Sequence 7, Appl1
14	885.2	79.7	4085	1 US-08-486-270-7	Sequence 7, Appl1
15	885.2	79.7	4085	1 US-08-367-264-7	Sequence 7, Appl1
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21	885.2	79.7	4181	4 US-09-153-757-9	Sequence 9, Appl1
22	885.2	79.7	4181	4 US-09-459-715-9	Sequence 9, Appl1
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24	458.2	41.3	3321	3 US-08-367-264-1	Sequence 1, Appl1
25	458.2	41.3	3321	4 US-09-153-757-1	Sequence 1, Appl1
26	458.2	41.3	3321	4 US-09-459-715-1	Sequence 1, Appl1
27	458.2	41.3	3582	4 US-08-538-526-2	Sequence 2, Appl1

28	458.2	41.3	4074	4 US-09-016-434-1475	Sequence 1475, Ap
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31	449.2	40.5	3384	2 US-08-687-289A-1	Sequence 1, Appl1
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33	449.2	40.5	4300	1 US-08-041-538-1	Sequence 1, Appl1
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42	144.2	13.0	4095	5 PCT-US91-09422-18	Sequence 18, Appl1
43	143.6	12.9	2736	3 US-08-617-785-1	Sequence 1, Appl1
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45	143.6	12.9	3431	4 US-09-641-318-1	Sequence 1, Appl1

## ALIGNMENTS

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RESULT 1
US-09-695-481-1
; Sequence 1, Application US/09695481
; Patent No. 6534287
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHANN, LAURA
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: KAPCHO, KAREN J.
; APPLICANT: NNS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2826)
US-09-695-481-1

Query Match      80.0%; Score 888.4; DB 4; Length 2826;
Best Local Similarity 98.2%; Pred. No. 3.5e-269;
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGCTCTCTGTGTAATCTCTGTCAGCTTACTTTTGAAGAAGATGTCGTGGAGTGA 60
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DB 1 ATGCTCTCTGTGTAATCTCTGTCAGCTTACTTTTGAAGAAGATGTCGTGGAGTGA 60
    |||

QY 61 CAGTCCAGTGAAGAGAGGGGTGTGCTCAATGCTGGTGAATCATTTATTTGAGCTCTC 120
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    |||

QY 121 TTTTCTGTCATCAGGCTTACTGTGAGAGAGATTATGAGAGAGTGTGGGAGTGC 180
    |||
DB 121 TTTTCTGTCATCAGGCTTACTGTGAGAGAGATTATGAGAGAGTGTGGGAGTGC 180
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QY 181 CCGGAACAGTATGAGCTTCAAGAGTGAAGGCGCATGCTGATACCTTGGAAAGATCAAT 240
    |||
DB 181 CCGGAACAGTATGAGCTTCAAGAGTGAAGGCGCATGCTGATACCTTGGAAAGATCAAT 240
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QY 241 TCAGACCCCACTCTTGGCCCAATCATCATCTGGGCTGTGAGATTAAGGATTCCTGCTGG 300
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DB 241 TCAGACCCCACTCTTGGCCCAATCATCATCTGGGCTGTGAGATTAAGGATTCCTGCTGG 300
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RESULT 3  
US-09-016-434-1133  
Sequence 1133, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Sellhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4078 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1408051  
US-09-016-434-1133

Query Match 80.0%; Score 888.4; DB 4; Length 4078;  
Best Local Similarity 98.2%; Pred. No. 4.3e-269;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTTGATCTGTGAGTCTTCTTTGAAAGAGTCCGGGAGATGCA 60  
DB 151 ATGGCTCTTCTGTTGATCTGTGAGTCTTCTTTGAAAGAGTCCGGGAGATGCA 210  
QY 61 CAGTCCAGTGAAGAGAGGAGTGTGAGTCAATGCTGGGATCAATATTGAGCTCTC 120  
DB 211 CAGTCCAGTGAAGAGAGGAGTGTGAGTCAATGCTGGGATCAATATTGAGCTCTC 270  
QY 121 TTTTCTGTTTATCAACGAGCTTCTGTGAGAGAGTTCATGAGAGAGTGTGGGAGTGC 180  
DB 271 TTTTCTGTTTATCAACGAGCTTCTGTGAGAGAGTTCATGAGAGAGTGTGGGAGTGC 330  
QY 181 CGTGAACAGATGAGATTCAGAGAGTGAAGGAGTGTGATACCTTGAAGAGATCAAT 240  
DB 331 CGTGAACAGATGAGATTCAGAGAGTGAAGGAGTGTGATACCTTGAAGAGATCAAT 390  
QY 241 TCAGACCCCACTCTTGTCCCAATCACTGAGGCTGTGAGATTAAGGAGTTCTGTCTG 300  
DB 391 TCAGACCCCACTCTTGTCCCAATCACTGAGGCTGTGAGATTAAGGAGTTCTGTCTG 450

QY 301 CATTGGCTGTGGCCCTTGAAGCAGAGATTCATTAAGAGATTCCTCATTTCTTGG 360  
DB 451 CATTGGCTGTGGCCCTTGAAGCAGAGATTCATTAAGAGATTCCTCATTTCTTGG 420  
QY 361 GAAGAGAAAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCTTGGCTCAAG 420  
DB 511 GAAGAGAAAGAGGCTGTGTATGCTGTGTGATGAGTCTCTCTTCTTCTTGGCTCAAG 570  
QY 421 AAGCCATGATGAGGATTCATGGGCTGTGTGATGAGTCTCTCTTCTTCTTGGCTCAAG 480  
DB 571 AAGCCATGATGAGGATTCATGGGCTGTGTGATGAGTCTCTCTTCTTCTTGGCTCAAG 540  
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DB 631 TTGCTCAGCTTTTCAACATTCCTGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 541 GACAGACTCTGTTCAATATTTTCAATGAGGTTGCTGATGATGATGATGATGATGATGAT 600  
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QY 601 TCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 751 GCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810  
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DB 811 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870  
QY 721 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 871 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 930  
QY 781 CTGAAGAGTCAAGTCACTTGGCCAGAGGCTGATGATGATGATGATGATGATGATGATGAT 840  
DB 931 CTGAAGAGTCAAGTCACTTGGCCAGAGGCTGATGATGATGATGATGATGATGATGATGAT 990  
QY 841 ATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
DB 991 ATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1050  
QY 901 CTTCTGGGAGGGA 914  
DB 1051 CTTCTGGGAGGGA 1064

RESULT 4  
US-08-660-148-1  
Sequence 1, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 460..3999  
US-08-660-148-1

Query Match 80.0%; Score 888.4; DB 3; Length 4207;  
Best Local Similarity 98.2%; Pred. No. 4,4e-269;  
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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460 ATGGCTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 519  
61 CAGTCCAGTGAAGAGAGGAGTGTGCTCACTACGCTGGGTGATCATTTATTTGAGCTTC 120  
520 CAGTCCAGTGAAGAGAGGAGTGTGCTCACTACGCTGGGTGATCATTTATTTGAGCTTC 579  
121 TTTTCTGTTTCATCAACGCTTCTGTGAGCAAGTTATGAGAGAGTGTGGGAGTC 180  
580 TTTTCTGTTTCATCAACGCTTCTGTGAGCAAGTTATGAGAGAGTGTGGGAGTC 639  
181 CCGAACAAGTATGATTCATGAGAGTGTGAGAGGCTGCTGATACCTCTGAGAAAGATCAAT 240  
640 CCGAACAAGTATGATTCATGAGAGTGTGAGAGGCTGCTGATACCTCTGAGAAAGATCAAT 699  
241 TCAGACCCCACTCTTGGCCCAACATCACTGGGCTGTGAGATTAAGGAGATTCCTGCTGG 300  
700 TCAGACCCCACTCTTGGCCCAACATCACTGGGCTGTGAGATTAAGGAGATTCCTGCTGG 759  
301 CATTGGCTGTGGCCCTAGAGACAGAGCATTTGATTCAAGAGATTCCTCATTTCTTCG 360  
760 CATTGGCTGTGGCCCTAGAGACAGAGCATTTGATTCAAGAGATTCCTCATTTCTTCG 819  
361 GAAGAGAGAGAGGCTTGTATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCAAG 420  
820 GAAGAGAGAGAGGCTTGTATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCAAG 879  
421 AAGCCCACTAGAGAGGCTTGTATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 480  
880 AAGCCCACTAGAGAGGCTTGTATGCTCTGTGATGCTCTCTCTCTCTCTCTCTCTCAAG 939  
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1000 GACAAAGCTCTGTTCAAATATTTCTATGAGAGGTTGTGCTTCAATGCTCAGCAGGCAAG 1059  
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1060 GCGATGTTGACATATGAGAGAGGTTCACTGAGCTATGATGAGCCGTTACACAGAA 1119  
661 GCGAATCTATGAGAGAGGTTGAGAGGCTTCAAGATATGTCAGGAGAGAGGATTT 720  
1120 GCGAATCTATGAGAGAGGTTGAGAGGCTTCAAGATATGTCAGGAGAGAGGATTT 1179

721 TGCATGCCCACTCTTACAAATCTACGATATGAGAGGAGAGAGCTTTGATTAAGCTG 780  
1180 TGCATGCCCACTCTTACAAATCTACGATATGAGAGGAGAGAGCTTTGATTAAGCTG 1239  
781 CTGAGAGAGCTCAAGAGTCACTTCCCAAGGCCGAGGTGTGCTCACTTCTGTGAGGAGC 840  
1240 CTGAGAGAGCTCAAGAGTCACTTCCCAAGGCCGAGGTGTGCTCACTTCTGTGAGGAGC 1299  
841 ATGACGTTGAGAGGTTCTGCTGATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 900  
1300 ATGACGTTGAGAGGTTCTGCTGATGAGCCATGAGGCGCTGGGTCTAGTGGAGAAATTTCTG 1359  
901 CTTCTGGGACAGGGA 914  
1360 CTTCTGGGACAGTGA 1373

RESULT 5  
US-08-660-148-3  
Sequence 3, Application US/08660148  
Patent No. 6211353  
GENERAL INFORMATION:  
APPLICANT: Burnette, J. P.  
APPLICANT: Mayne, Nancy G.  
APPLICANT: Sharp, Robert L.  
APPLICANT: Snyder, Yvonne M.  
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND  
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,148  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-660-148-3

Query Match 80.0%; Score 888.4; DB 3; Length 4207;  
Best Local Similarity 73.9%; Pred. No. 4,4e-269;  
Matches 675; Conservative 223; Mismatches 16; Indels 0; Gaps 0;

1 ATGGCTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 60  
460 ATGGCTCTTCTGTGATCCCTGCTGCTTCTTCTTGAAGAAGATGTCCTGGAGTGA 519

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QY 61 CAGTCCAGTGAAGAGAGGGTGTGGTCAATCTGGGTGATCATTTATGAGCTCTC 120
DB 520 CAGUCCAGTGAAGAGAGGGTGTGGTCAATCTGGGTGATCATTTATGAGCTCTC 579
QY 121 TTTTCTGTTTCATCAAGCTTCTGTGAGCAAGTTTATGAGAGAGAGTGGGGCAGTC 180
DB 580 UUUUCUGUUCAUCAAGCCUAGCUUGUAGCAAGUUCAUAGAGAGAGUUGGGGGCGGUC 639
QY 181 CGTGAACAGTATGAGCTTCAAGAGAGAGAGCAATGCTGATACCTCTGGAAGAGATCAAT 240
DB 640 CGGGAACAGUAGUAGCAUUCAGAGAGAGAGAGCAUUGUAGUAGCCUUGAAGAGAGCAU 699
QY 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGTAAGAGATTCCTGCTGG 300
DB 700 UCGAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGTAAGAGATTCCTGCTGG 759
QY 301 CATTCGGCTGTGGCCCTTGAAGAGAGAGCAATTAAGATTCCTCATTTCTTGG 360
DB 760 CAUUCGGCTGTGGCCCTTGAAGAGAGAGCAATTAAGATTCCTCATTTCTTGG 819
QY 361 GAAGAGAGAGAGGGCTTGTGATCTCTGTGAGAGAGCTCTCTCTCTCTCTCTCTCAAG 420
DB 820 GAAGAGAGAGAGGGCTTGTGATCTCTGTGAGAGAGCTCTCTCTCTCTCTCTCTCAAG 879
QY 421 AAGCCCATAGTGAAGGGTCAATTGGGCTGTGAGTTCCTTGAAGATTCCTCAAGAT 480
DB 880 AAGCCCATAGTGAAGGGTCAATTGGGCTGTGAGTTCCTTGAAGATTCCTCAAGAT 939
QY 481 TTGCTCAGCTTTTCAACATATCTCAGATTTCTTACTCAGCAACATCATGATCTGAGT 540
DB 940 UUGCUCACGCUUUAACAACUACAGUUGUUGCUUACAGCAACAGCAUAGUUCUAGU 999
QY 541 GACAAAGCTCTGTTCAAAATTTTCAAGAGGTTGTGCTTCAAGATCTCAGCAAGG 600
DB 1000 GACAAAGCTCTGTTCAAAATTTTCAAGAGGTTGTGCTTCAAGATCTCAGCAAGG 1059
QY 601 TCCATGATGAGCAATGTAAGAGAGTCACTGAGACCTATGATCAGCCGTACACAGAA 660
DB 1060 GGCNAUGGAGCAUAGUAGAGAGUACUAGACCUUUAUACAGCCUUGUACAGAA 1119
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QY 781 CTGAAGAGCTCAAGATCACTTGGCCAGAGCCGGGTGTGCTTCAATCTGTGAGGCG 840
DB 1240 CTGAAGAGCTCAAGATCACTTGGCCAGAGCCGGGTGTGCTTCAATCTGTGAGGCG 1299
QY 841 ATGACGAGTGAAGAGTGTGCTGATGAGCAGTGGGCTGTGAGTGAAGAGATTTCTG 900
DB 1300 AUGACGAGTGAAGAGTGTGCTGATGAGCAGTGGGCTGTGAGTGAAGAGATTTCTG 1359
QY 901 CTCTTGGGAGAGGA 914
DB 1360 CUUCUGGGCAGUGA 1373

```

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CORRESPONDENCE ADDRESS:
ADDRESS: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ. ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 460..4095
US-08-660-148-4

Query Match 80.0%; Score 888.4; DB 3; Length 4303;
Best Local Similarity 98.2%; Pred. No. 4,4e-269;
Matches 898; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGGTCCTCTGTGATCTGTCAGTCTTACTTTGAAAGAGATCCGTGGAGTGA 60
DB 460 AAGTCTCTCTGTGATCTGTCAGTCTTACTTTGAAAGAGATCCGTGGAGTGA 519
QY 61 CAGTCCAGTGAAGAGAGGGTGTGGCTCAATGCTGGTGAATCATTTATGAGCTCTC 120
DB 520 CAGTCCAGTGAAGAGAGGGTGTGGCTCAATGCTGGTGAATCATTTATGAGCTCTC 579
QY 121 TTTTCTGTTTCATCAAGCTTCTGTGAGCAAGTTTATGAGAGAGAGTGGGGCAGTC 180
DB 580 UUUUCUGUUCAUCAAGCCUAGCUUGUAGCAAGUUCAUAGAGAGAGUUGGGGGCGGUC 639
QY 181 CGTGAACAGTATGAGCTTCAAGAGAGAGCAATGCTGATACCTCTGGAAGAGATCAAT 240
DB 640 CGTGAACAGTATGAGCTTCAAGAGAGAGCAATGCTGATACCTCTGGAAGAGATCAAT 699
QY 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGTAAGAGATTCCTGCTGG 300
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QY 301 CATTCGGCTGTGGCCCTTGAAGAGAGAGCAATTAAGATTCCTCATTTCTTGG 360
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DB 820 GAAGAGAGAGAGGGCTTGTGATCTCTGTGAGAGAGCTCTCTCTCTCTCTCTCAAG 879
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Db 1360 CUUCUGGCGAGUGA 1373

RESULT 8  
US-08-072-574-11

Sequence 11, Application US/08072574  
Patent No. 5521297

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Pontleier, Aaron

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 00719

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/072,574

FILING DATE: 19930604

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen B.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9383

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-622-7700

TELEFAX: 213-489-4210

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3282 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 370..3003

OTHER INFORMATION: /product= "HUMAN MGLUR5C"

OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."

US-08-072-574-11

Query Match

Best local Similarity 98.0%; Pred. No. 3.8e-268;

Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

1 ATGCTCTTCTGTTGATCTCTGTCAGTCTTATTTGAAAGAGATGCGTGGAGTGA 60  
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6 ATGCTCTTCTGTTGATCTCTGTCAGTCTTATTTGAAAGAGATGCGTGGAGTGA 120  
7 ATGCTCTTCTGTTGATCTCTGTCAGTCTTATTTGAAAGAGATGCGTGGAGTGA 120  
8 ATGCTCTTCTGTTGATCTCTGTCAGTCTTATTTGAAAGAGATGCGTGGAGTGA 489  
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10 ATGCTCTTCTGTTGATCTCTGTCAGTCTTATTTGAAAGAGATGCGTGGAGTGA 180  
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12 ATGCTCTTCTGTTGATCTCTGTCAGTCTTATTTGAAAGAGATGCGTGGAGTGA 549  
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250 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 789  
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265 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 720  
266 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 720  
267 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 1089  
268 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 1089  
269 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 780  
270 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 780  
271 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 1149  
272 TCAGACCCCACTCTTGGCCCAACATCAGACTGGCTGTGAGATTAAGGATCTCTGCTG 1149  
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RESULT 9  
US-08-486-270-11

Sequence 11, Application US/08486270  
Patent No. 5807689

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Pontleier, Aaron

APPLICANT: Johnson, Edwin C.

APPLICANT: Hees, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-486-270-11

Query Match 79.7%; Score 885.2; DB 1; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 3,8e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGGCTCTTCTGTTGATCTGTGCTGCTTACTTTGAAAGAGTGTCCGTGGAGTGA 60  
DB 370 ATGGCTCTTCTGTTGATCTGTGCTGCTTACTTTGAAAGAGTGTCCGTGGAGTGA 429  
QY 61 CAGTCCGATGAG 120  
DB 430 CAGTCCGATGAG 489  
QY 121 TTTTCTGTTATCCAGCCCTACTGTGGAAGAGTTCATGAGAGAGAGAGAGAGAG 180  
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QY 181 CGTGAACAGTATGAGCATTGAGAGAGTGAAGCCATGCTGATACCTGGAAGATCAAT 240  
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DB 610 TCAGACCCCACTCTTGGCCCAATCACTGGGCTGTGAGATTAAGAGATTCTGCTGG 669  
QY 301 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCAATAGAGATTCCTTCATTTCTTG 360  
DB 670 CATTGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCAATAGAGATTCCTTCATTTCTTG 729  
QY 361 GAAG 420  
DB 730 GAAG 789  
QY 421 AAGCCCATGAG 480  
DB 790 AAGCCCATGAG 849  
QY 481 TTGCTCAGCTTTTCAACATCTCAATGCTTCACTCAGAGCAACATCAAGATCTGAGT 540  
DB 850 TTGCTCAGCTTTTCAACATCTCAATGCTTCACTCAGAGCAACATCAAGATCTGAGT 909  
QY 541 GACAAAGACTCTGTTCAATATATTTTATGAGAGGTTGCTTCAATGCTCAGAGCAAGG 600  
DB 910 GACAAAGACTCTGTTCAATATATTTTATGAGAGGTTGCTTCAATGCTCAGAGCAAGG 969

QY 601 TCATGATGAGCATAGTGAAGAGTACAACTGACCTATGATACACCCGTACACAGAA 650  
DB 970 GCGATGTGAGCATATGTAAGAGTACAACTGACCTATGATACACCCGTACACAGAA 1029  
QY 661 GCGCACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCAGCGAAGAGAGAT 720  
DB 1030 GCGCACTATGAGAAAGTGGATGAGAGCTTCAAGATATGTCAGCGAAGAGAGAT 1089  
QY 721 TGCATGCCCCACTTACAAATCTACATATATGACGGGAGAGAGCTTGTATAGCTG 780  
DB 1090 TGCATGCCCCACTTACAAATCTACATATATGACGGGAGAGAGCTTGTATAGCTG 1149  
QY 781 CTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGGCTTACTTGTGAGGCG 840  
DB 1150 CTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGGCTTACTTGTGAGGCG 1209  
QY 841 ATGACGGTGAAGAGTGTGATGACCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 900  
DB 1210 ATGACGGTGAAGAGTGTGATGACCATGAGGCGCTGGTCTAGTGGAGAAATTTCTG 1269  
QY 901 CTCTGGGAGAGGA 914  
DB 1270 CTCTGGGAGAGGA 1283

RESULT 10  
US-08-367-264-11  
Sequence 11, Application US/08367264  
Patent No. 6001581  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
APPLICANT: Johnson, Edwin C.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
OTHER INFORMATION: /note= "Variant of MGLUR5A with truncated 3' end."  
US-08-367-264-11

Query Match  
Best Local Similarity 98.0%; Pred. No. 3.8e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

79.7%; Score 885.2; DB 3; Length 3282;

1 ANGTCCTTCTGTGATCCTGTCAGTCTTACCTTTGAAAGAGATGTCGGAGAGTGA 60  
370 ANGTCCTTCTGTGATCCTGTCAGTCTTACCTTTGAAAGAGATGTCGGAGAGTGA 429  
61 CAGTCAG 120  
430 CAGTCAG 489  
121 TTTTCTGTCATCAACAGCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
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181 CGTGAACAGTATGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
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241 TGAAG 300  
610 TGAAG 669  
301 CATTGGAG 360  
670 CATTGGAG 729  
361 GAAAG 420  
730 GAAAG 789  
421 AAGCCATATGAT 480  
790 AAGCCATATGAT 849  
481 TTGCTCAGCTTTTAACTACTGATGCTTACTGAGAGAGAGAGAGAGAGAGAT 540  
850 TTGCTCAGCTTTTAACTACTGATGCTTACTGAGAGAGAGAGAGAGAGAGAT 909  
541 GACAAGACTCTGTTCAATATTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAG 600  
910 GACAAGACTCTGTTCAATATTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAG 969  
601 TGCATGAT 660  
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661 GGCATGAT 720  
1030 GGCATGAT 1089  
721 TGCATGAT 780  
1090 TGCATGAT 1149  
781 CTGAAGAT 840  
1150 CTGAAGAT 1209  
841 ATGAT 900  
1210 ATGAT 969  
901 CTTCTGGAT 1269  
CTTCTGGAT

DB 1270 CTTCTGGAT 1283

RESULT 11  
US-09-153-757-11  
Sequence 11, Application US/09153757  
Patent No. 6413764  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
Ellis, Steven B.  
Law, Chen  
Pontsler, Aaron  
Johnson, Edwin C.  
Hees, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: Precity, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,757  
FILING DATE: 15-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,270  
FILING DATE: 02-JUN-1994  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reltier, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MGLUR5C"  
/note= "Variant of MGLUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-153-757-11

Query Match  
Best Local Similarity 98.0%; Pred. No. 3.8e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

79.7%; Score 885.2; DB 4; Length 3282;

1 ANGTCCTTCTGTGATCCTGTCAGTCTTACCTTTGAAAGAGATGTCGGAGAGTGA 60  
370 ANGTCCTTCTGTGATCCTGTCAGTCTTACCTTTGAAAGAGATGTCGGAGAGTGA 429  
61 CAGTCAG 120  
430 CAGTCAG 489  
121 TTTTCTGTCATCAACAGCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

Db 490 TTTTCTGTTTCATACCAAGCTTCTGTGAGCAAAAGTTTCATAGAGAGAGTGGGGGCTC 549  
Qy 181 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCGCATGTCATACCTTGAAGAGATCAAT 240  
Db 550 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCGCATGTCATACCTTGAAGAGATCAAT 609  
Qy 241 TCAGACCCCACTCTTTGGCCCAATCAACATGGGCTGTGAGATTAAGAGATTCCTGCTG 300  
Db 610 TCAGACCCCACTCTTTGGCCCAATCAACATGGGCTGTGAGATTAAGAGATTCCTGCTG 669  
Qy 301 CATTGGCTGTGGCCCTTGAAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 360  
Db 670 CATTGGCTGTGGCCCTTGAAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 729  
Qy 730 GAAG 789  
Db 421 AAGCCCATAGTATGAGGAGATTTGGGCGCTGTGAGATTCATTAAGATTAAGATTAAGAT 480  
Qy 790 AAGCCCATAGTATGAGGAGATTTGGGCGCTGTGAGATTCATTAAGATTAAGATTAAGAT 849  
Db 481 TTGCTCAGCTTTTCAACATACCTCAGATTTGCTTCAAGCAACCATCATGATCTGAGT 540  
Qy 850 TTGCTCAGCTTTTCAACATACCTCAGATTTGCTTCAAGCAACCATCATGATCTGAGT 909  
Db 541 GACAGACCTCTGTTCAAAATTTTCATGAGAGGTTGTGCTTCAATGCTCAGAGCAAGG 600  
Qy 910 GACAGACCTCTGTTCAAAATTTTCATGAGAGGTTGTGCTTCAATGCTCAGAGCAAGG 969  
Db 601 TCCATGCTGACATAGTGAAGAGGATCAATGAGCCTTATGATGAGGCTTACACACGAA 660  
Qy 970 GGCATGCTGACATAGTGAAGAGGATCAATGAGCCTTATGATGAGGCTTACACACGAA 1029  
Db 661 GGCATGCTGACATAGTGAAGAGGATCAATGAGCCTTATGATGAGGCTTACACACGAA 720  
Qy 1030 GGCATGCTGACATAGTGAAGAGGATCAATGAGCCTTATGATGAGGCTTACACACGAA 1089  
Db 721 TGCATGCTGACATAGTGAAGAGGATCAATGAGCCTTATGATGAGGCTTACACACGAA 780  
Qy 1090 TGCATGCTGACATAGTGAAGAGGATCAATGAGCCTTATGATGAGGCTTACACACGAA 1149  
Db 781 CTGAAGAGCTCACAAGTCACTTGGCCCAAGGCGGCTGTGAGGCTTCTGTGAGAGG 840  
Qy 1150 CTGAAGAGCTCACAAGTCACTTGGCCCAAGGCGGCTGTGAGGCTTCTGTGAGAGG 1209  
Db 841 ATGACGCTGAGAGGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
Qy 1210 ATGACGCTGAGAGGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1269  
Db 901 CTTCCTGGGAGAGGA 914  
Qy 1270 CTTCCTGGGAGAGGA 1283

RESULT 12  
US-09-459-715-11  
Sequence 11, Application US/09459715  
Patent No. 6485919  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lortie  
Ellis, Steven B.  
Llaw, Chen  
Pontelier, Aaron  
Johnson, Edwin C.  
Hess, Stephen D.  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/459,715  
FILING DATE: 13-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/367,264  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen B.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: PP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
MOLECULE TYPE: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3003  
OTHER INFORMATION: /product= "HUMAN MEURPSC"  
/note= "Variant of MEUR5A with truncated 3' end."  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-459-715-11  
Query Match 79.7%; Score 885.2; DB 4; Length 3282;  
Best Local Similarity 98.0%; Pred. No. 3.8e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
Qy 1 ATGATCCTTCTGTGATACCTGTGAGTCTTATCTTTGAAAGAGATGCTGGGAGTGA 60  
Db 370 ATGATCCTTCTGTGATACCTGTGAGTCTTATCTTTGAAAGAGATGCTGGGAGTGA 429  
Qy 61 CAGTCCAGTGAAGAGAGGAGTGTGCTCACATGCTGGGTGACATTTATTTGAGCTTC 120  
Db 430 CAGTCCAGTGAAGAGAGGAGTGTGCTCACATGCTGGGTGACATTTATTTGAGCTTC 489  
Qy 121 TTTTCTGTTTCATACCAAGCTTCTGTGAGCAAAAGTTTCATAGAGAGAGTGGGGCAGTC 180  
Db 490 TTTTCTGTTTCATACCAAGCTTCTGTGAGCAAAAGTTTCATAGAGAGAGTGGGGCAGTC 549  
Qy 181 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCGCATGTCATACCTTGAAGAGATCAAT 240  
Db 550 CGTGAACAGTATGAGCATTCAGAGAGTGGAGGCGCATGTCATACCTTGAAGAGATCAAT 609  
Qy 241 TCAGACCCCACTCTTTGGCCCAATCAACATGGGCTGTGAGATTAAGAGATTCCTGCTG 300  
Db 610 TCAGACCCCACTCTTTGGCCCAATCAACATGGGCTGTGAGATTAAGAGATTCCTGCTG 669  
Qy 301 CATTGGCTGTGGCCCTTGAAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 360  
Db 670 CATTGGCTGTGGCCCTTGAAGAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 729  
Qy 730 GAAG 789  
Db 421 AAGCCCATAGTATGAGGAGATTTGGGCGCTGTGAGATTCATTAAGATTAAGATTAAGAT 480  
Qy 790 AAGCCCATAGTATGAGGAGATTTGGGCGCTGTGAGATTCATTAAGATTAAGATTAAGAT 849

QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGACCAACCATGATCTGAGT 540  
DB 850 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGACCAACCATGATCTGAGT 909  
QY 541 GACAAAGCTCTGTTCAAAATATTTTCATGAGGCTTGCTTCAATGCTCAGACGCAAGG 609  
DB 910 GACAAAGCTCTGTTCAAAATATTTTCATGAGGCTTGCTTCAATGCTCAGACGCAAGG 969  
QY 601 TCATGCTGACATGATGAAAGGTACACTGACCTATGATGACGCTTACACAGAA 660  
DB 970 GCATGCTGACATGATGAAAGGTACACTGACCTATGATGACGCTTACACAGAA 1029  
QY 661 GGCACATGAGAAAGTGGAGTGAAGGCTTCAAAATATTTTCATGAGGCAAGGATTT 720  
DB 1030 GGCACATGAGAAAGTGGAGTGAAGGCTTCAAAATATTTTCATGAGGCAAGGATTT 1089  
QY 721 TGCAATGCTTCTTCAAAATATTTTCATGATGACAGGAGGAGCACTTGAATGAGT 780  
DB 1090 TGCAATGCTTCTTCAAAATATTTTCATGATGACAGGAGGAGCACTTGAATGAGT 1149  
QY 781 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCGCGGCTGCTTCTGATGAGGCT 840  
DB 1150 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCGCGGCTGCTTCTGATGAGGCT 1209  
QY 841 ATGACGCTGAGAGGCTGCTGATGAGGCTGATGAGGCTGCTGATGAGGAGATTTCTG 900  
DB 1210 ATGACGCTGAGAGGCTGCTGATGAGGCTGATGAGGCTGCTGATGAGGAGATTTCTG 1269  
QY 901 CTTCGCGGAGGAG 914  
DB 1270 CTTCGCGGAGGAGTGA 1283

RESULT 13  
US-08-072-574-7  
; Sequence 7, Application US/08072574  
; Patent No. 5521297  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrle  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Portisler, Aaron  
; TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Precely, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 00719  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/072,574  
; FILING DATE: 19930604  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213-622-7700  
; TELEFAX: 213-489-4210  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4085 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-072-574-7  
Query Match 79.7%; Score 885.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 4,3e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 ATGCTCTTCTGTTGATTCCTGATGCTTACTTTTGAAGAAGATGCTGGAGAGTGA 60  
DB 370 ATGCTCTTCTGTTGATTCCTGATGCTTACTTTTGAAGAAGATGCTGGAGAGTGA 429  
QY 61 CAGTCCAGTGAAGAGGAGTGTGCTCACAATGCTGGTGAATCAATTTAGAGTCTG 120  
DB 430 CAGTCCAGTGAAGAGGAGTGTGCTCACAATGCTGGTGAATCAATTTAGAGTCTG 489  
QY 121 TTTTCTGTTCAATCAGGAGCTTACTGTGACGAAGTTTATGAGAGAGTGTGGGAGT 180  
DB 490 TTTTCTGTTCAATCAGGAGCTTACTGTGACGAAGTTTATGAGAGAGTGTGGGAGT 549  
QY 181 CCGAAGCAGTATGAGCATTTAGAGAGTGAAGGCAATGCTGATACCTTGAAGAGTCAAT 240  
DB 550 CCGAAGCAGTATGAGCATTTAGAGAGTGAAGGCAATGCTGATACCTTGAAGAGTCAAT 609  
QY 241 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGTAAAGGATTCCTGCTG 300  
DB 610 TCAGACCCCACTCTTGGCCCAATCATCACTGGGCTGTGAGTAAAGGATTCCTGCTG 669  
QY 301 CATTCGCTGTGAGCCCTTGAAGCAGAGCATTTAGATTAAGATTCCTCATTTCTTG 360  
DB 670 CATTCGCTGTGAGCCCTTGAAGCAGAGCATTTAGATTAAGATTCCTCATTTCTTG 729  
QY 361 GAAGAGAGAGAGGCTTGTATGCTCTGTGAGATGAGTCTCTCTCTTCTTCCGCTCAAG 420  
DB 730 GAAGAGAGAGAGGCTTGTATGCTCTGTGAGATGAGTCTCTCTCTTCTTCCGCTCAAG 789  
QY 421 AAGCCATGATGAGGAGTCAATGGGCTGGTTCAGTCTTTAGCCATTCAGATCCAGAT 480  
DB 790 AAGCCATGATGAGGAGTCAATGGGCTGGTTCAGTCTTTAGCCATTCAGATCCAGAT 849  
QY 481 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGACCAACCATGATCTGAGT 540  
DB 850 TTGCTCAGCTTTTCAACATACCTCAGATTGCTTACTCAGACCAACCATGATCTGAGT 909  
QY 541 GACAAAGCTCTGTTCAAAATATTTTCATGAGGCTTGCTTCAATGCTCAGACGCAAGG 600  
DB 910 GACAAAGCTCTGTTCAAAATATTTTCATGAGGCTTGCTTCAATGCTCAGACGCAAGG 969  
QY 601 TCATGCTGACATGATGAAAGGTACACTGACCTATGATGACGCTTACACAGAA 660  
DB 970 GCATGCTGACATGATGAAAGGTACACTGACCTATGATGACGCTTACACAGAA 1029  
QY 661 GGCACATGAGAAAGTGGAGTGAAGGCTTCAAAATATTTTCATGAGGCAAGGATTT 720  
DB 1030 GGCACATGAGAAAGTGGAGTGAAGGCTTCAAAATATTTTCATGAGGCAAGGATTT 1089  
QY 721 TGCAATGCTTCTTCAAAATATTTTCATGATGACAGGAGGAGCACTTGAATGAGT 780  
DB 1090 TGCAATGCTTCTTCAAAATATTTTCATGATGACAGGAGGAGCACTTGAATGAGT 1149  
QY 781 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCGCGGCTGCTTCTGATGAGGCT 840  
DB 1150 CTGAAGAGCTCAAGTCACTTGGCCCAAGGCGCGGCTGCTTCTGATGAGGCT 1209  
QY 841 ATGACGCTGAGAGGCTGCTGATGAGGCTGATGAGGCTGCTGATGAGGAGATTTCTG 900  
DB 1210 ATGACGCTGAGAGGCTGCTGATGAGGCTGATGAGGCTGCTGATGAGGAGATTTCTG 1269

QY 901 CTTCTGGGCGAGGA 914  
Db 1270 CTTCTGGGCGAGGA 1283

## RESULT 14

US-08-486-270-7

Sequence 7, Application US/08486270

Patent No. 5807689

GENERAL INFORMATION:

APPLICANT: Daggett, Lorie

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Pontsler, Aaron

APPLICANT: Johnson, Edwin C.

APPLICANT: Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,270

FILING DATE: 02-JUN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/072,574

FILING DATE: 04-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9772

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 4085 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 370..3912

OTHER INFORMATION: /product= "HUMAN MGLUR5A"

US-08-486-270-7

Query Match 79.7%; Score 885.2; DB 1; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 4.3e-268;

Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGCTCTTCTGTTGATCTCTGCTGCTTACTTTTGAAGAAGATGTCCTGGAGAGTCA 60  
Db 370 ATGCTCTTCTGTTGATCTCTGCTGCTTACTTTTGAAGAAGATGTCCTGGAGAGTCA 429  
QY 61 CAGTCCAGTGAAGAGGAGGAGTGGCTGACATGCGGGGTGACATCATTTATTGAGCTCTC 120  
Db 430 CAGTCCAGTGAAGAGGAGGAGTGGCTGACATGCGGGGTGACATCATTTATTGAGCTCTC 489  
QY 121 TTTTCTGTTTCAACAGGCTTACTGTGACGAAAGTTCAATGAGAGAAAGTGTGGGCGAGTC 180  
Db 490 TTTTCTGTTTCAACAGGCTTACTGTGACGAAAGTTCAATGAGAGAAAGTGTGGGCGAGTC 549

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QY 241 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGATTCCTCTG 300  
Db 610 TCAGACCCCACTCTTGGCCCAATCACACTGGGCTGTGAGATTAAGGATTCCTCTG 669  
QY 301 CATTGGCTGTGGCCCTTGAAGCAGACATTTGATTAAGATATCCCATTTCTTG 360  
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Db 730 GAAGAGAAAGAGGCTTGTGATGCTGTGATGAGTCTCTCTCTTCTCCCTCCCAAG 789  
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Db 790 AACCCATAGTAGGGGTCATTGGGCTGTGTCAGTTCTTTAGCCATTCAGTCCAGAT 849  
QY 481 TTGCTCAGCTTTTCAACATACCTCAATGCTTACTCAGCAACCATATGATCTGAGT 540  
Db 850 TTGCTCAGCTTTTCAACATACCTCAATGCTTACTCAGCAACCATATGATCTGAGT 909  
QY 541 GACAGACTCTCTCAAAATATTTATGATGAGGCTTGTGCTCAGATGCTCAGAGCAAG 600  
Db 910 GACAGACTCTCTCAAAATATTTATGATGAGGCTTGTGCTCAGATGCTCAGAGCAAG 969  
QY 601 TCATGCTGACATAGTAGAAGAGTCAACCTGACCTTATGATGATGACCTGACACAGAA 660  
Db 970 TCATGCTGACATAGTAGAAGAGTCAACCTGACCTTATGATGATGACCTGACACAGAA 1029  
QY 661 GGCATCTATGAGAAAGTGGATGGAAGCTTTCAAGATATGTCAGGAAAGAGGAT 720  
Db 1030 GGCATCTATGAGAAAGTGGATGGAAGCTTTCAAGATATGTCAGGAAAGAGGAT 1089  
QY 721 TGATGCGCCACTCTTACAAATCTACATGATGACAGGAGGAGGAGCTTTGTAAGCTG 780  
Db 1090 TGATGCGCCACTCTTACAAATCTACATGATGACAGGAGGAGGAGCTTTGTAAGCTG 1149  
QY 781 CTGAGAAGCTCAACAGTCACTTCCCAAGGCCCGGGTGTGCTTACTTGTGAGGCG 840  
Db 1150 CTGAGAAGCTCAACAGTCACTTCCCAAGGCCCGGGTGTGCTTACTTGTGAGGCG 1209  
QY 841 ATGACGCTGAGAGGTCTGCTGATGAGCCATGAGGCGCTTGTGATGAGGAAATTTCTG 900  
Db 1210 ATGACGCTGAGAGGTCTGCTGATGAGCCATGAGGCGCTTGTGATGAGGAAATTTCTG 1269  
QY 901 CTTCTGGGCGAGGA 914  
Db 1270 CTTCTGGGCGAGGA 1283

## RESULT 15

US-08-367-264-7

Sequence 7, Application US/08367264

Patent No. 6001581

GENERAL INFORMATION:

APPLICANT: Daggett, Lorie

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Pontsler, Aaron

APPLICANT: Johnson, Edwin C.

APPLICANT: Hess, Stephen D.

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/367,264  
FILING DATE: 02-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/072,574  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: FP41 9772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 370..3912  
OTHER INFORMATION: /product= "HUMAN MGLUR5A"  
US-08-367-264-7

Query Match 79.7%; Score 885.2; DB 3; Length 4085;  
Best Local Similarity 98.0%; Pred. No. 4.3e-268;  
Matches 896; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGGTCTTGTGTGATCCGTGAGCTTATCTTTGAAAGAGATGTCCTGGAGTGCA 60  
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DB 490 TTTTCTGTTATGACCAAGCTTACTGTGAGCAAGTTTCATAGAGAGAGTGTGGGTGAGTC 549  
QY 181 CGTGAACAGTATGCGCATTCAGAGAGTGAAGCCATGCTGCATACCTTGAAGAGATCAAT 240  
DB 550 CGTGAACAGTATGCGCATTCAGAGAGTGAAGCCATGCTGCATACCTTGAAGAGATCAAT 609  
QY 241 TCAGACCCCACTCTTGGCCCAATCACTGGGGCTGTGAGATTAAGGGATTCTGCTGG 300  
DB 610 TCAGACCCCACTCTTGGCCCAATCACTGGGGCTGTGAGATTAAGGGATTCTGCTGG 669  
QY 301 CATTGCGCTGTGACCTTAGAGCAGAGCATGATTCATTAAGAGATTCCTCATTTCTTCG 360  
DB 670 CATTGCGCTGTGACCTTAGAGCAGAGCATGATTCATTAAGAGATTCCTCATTTCTTCG 729  
QY 361 GAAGAGAGAGAGGCTTGTGATGCTGTGTGATGAGCTCTCTCTTCTTCCGCTCCAAG 420  
DB 730 GAAGAGAGAGAGGCTTGTGATGCTGTGTGATGAGCTCTCTCTTCTTCCGCTCCAAG 789  
QY 421 AAGCCATAGTAGGGGCTATTGGGCTGTGATTCATTTAGCATTCGAGTCCAGAAAT 480  
DB 790 AAGCCATAGTAGGGGCTATTGGGCTGTGATTCATTTAGCATTCGAGTCCAGAAAT 849  
QY 481 TTGCTCAGCTTTTCAACATACCTCAAGATGCTTACTCAGCAACCATCATGATCTGAGT 540  
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QY 541 GACAAGACTCTGTTCAAAATTTTCATGAGGTTGTGCTTCAAGTGTGCAGAGGCAAG 600  
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DB 1150 CTGAAGAGCTCAAGTCACTTGCCCAAGGCCCGGGTGTGCTTACTGTGAGGGC 1209  
QY 841 ATGACGCTGAGAGGTCTGCTGATGACCATGAGGCGCTTGGGTCTAGTGGAGAAATTTCTG 900  
DB 1210 ATGACGCTGAGAGGTCTGCTGATGACCATGAGGCGCTTGGGTCTAGTGGAGAAATTTCTG 1269  
QY 901 CTTCTGGGCAAGGA 914  
DB 1270 CTTCTGGGCAAGGA 1283

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Job time : 76.2844 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 09:35:14 ; Search time 2531.84 Seconds  
(without alignments)  
10655.460 Million cell updates/sec

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Perfect score: 1110  
Sequence: 1 atgcctctctgtgctgctc.....tgaggcagcgtcctctaa 1110

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

EST.\*  
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2: em\_estbma:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vtl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	57.7	1297	11	BC031602 Homo sapi
2	509.8	45.9	519	10	BE674422 7e01a04.x
3	499	45.0	499	10	BE67477 h266d08.x
4	445.8	40.2	449	14	CB153433 K-EST0210

5	424.4	38.2	442	9	AW015382
6	417.4	37.6	667	29	AG046849 Pan trogl
7	400.6	36.1	414	10	BG150163
8	372.2	33.5	3879	11	AK032422
9	289.2	26.1	682	10	BG695213
10	287	25.9	664	12	B1826234
11	281.6	25.4	657	13	BU351729
12	281.6	25.4	669	13	BU393781
13	268.2	24.2	392	14	T78107
14	257	23.2	515	13	BX280403
15	252.2	22.7	673	13	BU390603
16	246.8	22.2	471	14	CB730684
17	228.8	20.6	439	14	CB750802
18	224.2	20.2	832	28	B2181748
19	191.6	17.3	532	28	B2930457
20	185	16.7	722	28	A2815421
21	174	15.7	744	29	CNS03K04
22	159.2	14.3	657	28	B2164680
23	155.6	14.0	456	9	AI201184
24	146	13.2	589	29	BX191055
25	142.8	12.9	516	13	BX282658
26	140	12.6	268	14	F05449
27	135	12.2	673	28	B2101647
28	134.6	12.1	763	14	CA318495
29	129.6	11.7	1065	29	CNS05504
30	125.6	11.3	3675	11	AK038395
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32	125.6	11.3	647	10	BB625841
33	119	10.7	647	10	AK020663
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35	111	10.0	455	12	BI1600148
36	110.8	10.0	664	14	CD355039
37	110.6	10.0	1430	11	AK047733
38	109	9.8	661	14	BY721282
39	106.6	9.6	1013	13	BQ070358
40	105.4	9.5	715	10	BE275390
41	105.4	9.5	806	10	BF125311
42	103.2	9.3	742	12	BI093942
43	103.2	9.3	871	12	BE893553
44	103.2	9.3	868	13	BU154755
45	101.8	9.2	916	13	BX410048

## ALIGNMENTS

RESULT 1  
BC031602  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1297)  
Strausberg, R.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Direct Submission  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,  
USA

REMARK  
COMMENT  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gumarate, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,  
Kowals, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

**FEATURES**

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INLIL at: <http://image.inlil.gov>

Series: IRAX Plate: 51 Row: a Column: 11

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504142

This clone has the following problem: retained intron.

Location/Qualifiers

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1. .1297
/organism="Homo sapiens"
/mol_type="rRNA"
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/clone="IMAGE:5167902"
/class_type="Brain, adult medulla"
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
343 a 301 c 325 g 328 t
BASE COUNT
ORIGIN

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Best Local Similarity	97.7%;	Pred. No. 1.4e-179;		
Matches 649;	Conservative	0;	Mismatches 15;	Indels 0;
				Gaps 0;

QY	ATGGCCCTTCGTGGATCTCTGCAAGCTTACTTTTGAAGAAGATGTCGCGGGAGTCA	60
Db	371 ATGGTCCCTTCGTGGATCTCTGCAAGCTTACTTTTGAAGAAGATGTCGCGGGAGTCA	430
QY	61 CAGTCCAGTGAAGAGGGGTGGCTCACATGCTGGGTGAATCATTTATTTGAGCTTC	120
Db	431 CAGTCCAGTGAAGAGGGGTGGCTCACATGCTGGGTGAATCATTTATTTGAGCTTC	490
QY	121 TTTTCTGTTCATCAACAGCCTTACTGTGACGAAATTCATGAGAGAAATGTGGGGCAATC	180
Db	491 TTTTCTGTTCATCAACAGCCTTACTGTGACGAAAGTTCATGAGAGAAATGTGGGGCGGTTC	550
QY	181 CGTGAACAGTATGGCATTCAAGAGGTGAGGCCATGCTGCATATCCCTGAAAGATCAAT	240
Db	551 CGTGAACAGTATGGCATTCAAGAGTGAAGGCCATGCTGCATATCCCTGAAAGATCAAT	610
QY	241 TCAGACCCCACTCTTTCGCCAATCACTAGTGGCTGTGAGATTAAGGATTCCTGTGG	300
Db	611 TCAGACCCCACTCTTTCGCCAATCACTAGTGGCTGTGAGATTAAGGATTCCTGTGG	670
QY	301 CATTCGGCTGTGGCCCTTAGAGCAGAGCATTAAGTTCATTAAGATATCCCTCATTTCTTCG	360
Db	671 CATTCGGCTGTGGCCCTTAGAGCAGAGCATTAAGTTCATTAAGATATCCCTCATTTCTTCA	730
QY	361 GAAAGGAAAGAGGGCTTGGTATGCTCTGTGTGAATGACTCTCTCTTCTTCCTTCGCTCAAG	420
Db	731 GAAAGGAAAGAGGGCTTGGTATGCTCTGTGTGAATGACTCTCTCTCTTCCTTCGCTCAAG	790
QY	421 AAGCCCAATGTAAGGGGTATATGGGCTGTGGTCCAGTCTTTAGCATTAAGSTCCAGAT	480
Db	791 AAGCCCAATGTAAGGGGTATATGGGCTGTGGTCCAGTCTTTAGCATTAAGSTCCAGAT	850
QY	481 TTGCTCCAGCTTTTCAACATATCACTAGATTTGCTTCTCAGCAACCATATGAGATCTAGT	540
Db	851 TTGCTCCAGCTTTTCAACATATCACTCAGATTTGCTTCTCAGCAACCATATGAGATCTAGT	910
QY	541 GACAAAGACTGTTCAAATTAATTCATGAGGGTTGTGCTTCAAGTCTCAGCAGGCAAGG	600
Db	911 GACAAAGACTGTTCAAATTAATTCATGAGGGTTGTGCTTCAAGTCTCAGCAGGCAAGG	970
QY	601 TTCATGTGTGACATATGTGAAGAAGTCAAACTGACATTAATGATACCGGTGACACAAATA	660
Db	971 GCGATGTGTGACATATGTGAAGAAGTCAAACTGACATTAATGATACCGGTGACACAAATA	1030

QY	661	GGCA	664
Db	1031	GGTA	1034

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BE674422	BE674422	519 bp mRNA linear EST 08-SEP-2000	BE674422	BE674422	761aa04.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3281166 3' similar to SW:MR5 HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR. ; mRNA sequence.	BE674422.1	GI:10034963
			EST.				
			Homo sapiens (human)				
			Homo sapiens				
			Homo sapiens				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 519)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.

Seq primer: -40UP from Gibco  
High quality sequence stop: 499.  
location/Qualifiers  
1. 519

BASE COUNT	143 a	114 c	143 g	119 t
ORIGIN				
Query Match,				
Best Local Similarity	45.9%;	Score 509.8;	DB 10;	Length 519;
Matches 511; Conservative	99.6%;	Pred. No. 6,8e-111;		
	0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy	484	TTCCAGCTTTTCAACATACCTGACATGGCTTACTCAGCAACCAATCATGGATCTTAGTGAC	543
Db	7	CGCCAGCTTTTCAACATACCTCATATTGCTTACTCAGCAACCATCATGGATCTTAGTGAC	66
Oy	544	AAGACTCTGTTCAATATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGCAAGGTCC	603
Db	67	AAGACTCTGTTCAATATATTTTCATGAGGGTTGTGCTTCAGATGCTCAGCAGCAAGGTCC	126
Oy	604	ATGTGTGACATAGTGAAGAAGGTACAACTGCACTATGATATCAGCCGTACACAGAAAGC	663
Db	127	ATGTGTGACATAGTGAAGAAGGTACAACTGCACTATGATATCAGCCGTACACAGAAAGC	186
Oy	664	AACATATGAGAAAGCTGGAGTGAAGACCTTCAMAGATATGTTCAGCAAGAAAGGATTTGC	723

Db 187 AACTATGAGAAAGTGGATGGAAGCTTCAAGATATGTACAGGAAGGATTTGC 246  
 QY 724 ATGGCCCACTTTACAAATCTACAGTAATGACAGGGAGACAGCTTTGTAAGCTG 783  
 Db 247 ATGGCCCACTTTACAAATCTACAGTAATGACAGGGAGACAGCTTTGTAAGCTG 306  
 QY 784 AAGAGCTCAAGTCACTTGGCCCAAGCCGGGTGGTGGCTTCTGTGAGGGGATG 843  
 Db 307 AAGAGCTCAAGTCACTTGGCCCAAGCCGGGTGGTGGCTTCTGTGAGGGGATG 366  
 QY 844 ACGGTGAGAGTCTGTGATGCGCATGAGCGCTGCGTCTAGTGGAGAAATTTCTG 903  
 Db 367 ACGGTGAGAGTCTGTGATGCGCATGAGCGCTGCGTCTAGTGGAGAAATTTCTG 426  
 QY 904 CTGGGCGAGGACCAAGTCCATCTTTATTTGAGATCTCAAGAAAGACATCTATGG 963  
 Db 427 CTGGGCGAGGACCAAGTCCATCTTTATTTGAGATCTCAAGAAAGACATCTATGG 486  
 QY 964 GACAGAGAAATGCGAAGGTGCTTCTTCA 996  
 Db 487 GACAGAGAAATGCGAAGGTGCTTCTTCA 519

RESULT 3  
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 LOCUS h26608.x1 NCI CGAP Lu24 Homo sapiens cDNA IMAGE:3212943 3,  
 DEFINITION similar to SW:MG95 HUMAN P41594 METABOTROPIC GLUTAMATE RECEPTOR 5  
 PRECURSOR. ; mRNA sequence.  
 BE467477  
 BE467477.1 GI:9513252  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 499)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: sgabbs-remail.nih.gov  
 Tissue Procurement: Christopher Moshalk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:  
 info@image.lnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 493.  
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 library NCI CGAP Lu2 was prepared, and ss circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (cloneids  
 1414930-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 BASE COUNT 141 a 107 c 138 g 113 t

ORIGIN  
 Query Match 45.0%; Score 499; DB 10; Length 499;  
 Best Local Similarity 100.0%; Pred.No. 1,1e-137;  
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ACATACCTGAGATGCTTACTACGACCAACATCTGATCTGATGACCAAGCTCTGTTCA 60  
 QY 557 AATATTTCAATGAGGTTGCTTCAAGATCTGAGAGGAGGATTCATGCGCACTT 616  
 Db 61 AATATTTCAATGAGGTTGCTTCAAGATCTGAGAGGAGGATTCATGCGCACTT 120  
 QY 617 TGAAGAGTTCACATGAGCTTATGATCTGAGCCCTTACACAGAGCAATATGAGAAA 676  
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 QY 857 TGTGTATGCGCATGAGAGCGCGGTGTGCTTCTTCTGAGGGCATGACGTGAGAGTTC 916  
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RESULT 4  
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 CB153433  
 CB153433.1 GI:28138427  
 EST.  
 ACCESSION CB153433.1 GI:28138427  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 449)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and.  
 Kim,Y.S.  
 21C Promoter Korean EST Project 2001  
 Unpublished  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 28 row: C column: 09  
 High quality sequence stop: 449.  
 Location/Qualifiers  
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 FEATURES  
 source

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 /note="Organ: Brain; Vector: PCNS-D2; Site 1: EcoRI;  
 Site 2: NotI. The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Bergs method. The  
 obtained cDNA vectors were used for transfection of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

BASE COUNT 106 a 112 c 112 g 119 t

Query Match 40.2%; Score 445.8; DB 14; Length 449;  
 Best Local Similarity 99.6%; Pred. No. 8.6e-122;  
 Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 120 CTTTCTGTTTCATCCAGGCTTACTGTGAGCGAAGTTCAAGAGAGAGTGTGGGAGT 179  
 Db 1 CTTTCTGTTTCATCCAGGCTTACTGTGAGCGAAGTTCAAGAGAGAGTGTGGGAGT 60  
 QY 180 CCGTGAACAGTATGCGATTCAAGAGAGTGGAGCCATGCTGCATACCTCGAAGAGATCAA 239  
 Db 61 CCGTGAACAGTATGCGATTCAAGAGAGTGGAGCCATGCTGCATACCTCGAAGAGATCAA 120  
 QY 240 TTTCAGACCCCACTCTTGGCCCAATCAACATGCGGCTGTGAGATTAAGGATTCCTGCTG 299  
 Db 121 TTTCAGACCCCACTCTTGGCCCAATCAACATGCGGCTGTGAGATTAAGGATTCCTGCTG 180  
 QY 300 GCATTCGGCTGTGGCCCTAGAGCAGACATTTAGTTCAAGAGATTCCTCATTTCTTC 359  
 Db 181 GCATTCGGCTGTGGCCCTAGAGCAGACATTTAGTTCAAGAGATTCCTCATTTCTTC 240  
 QY 360 GGAAGAGAGAGAGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCAA 419  
 Db 241 GGAAGAGAGAGAGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCAA 300  
 QY 420 GAAGCCCATATGAGGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCAA 479  
 Db 301 GAAGCCCATATGAGGGCTTGTGATGCTGTGATGCTCTCTCTCTCTCTCTCTCTCTCTCAA 360  
 QY 480 TTTCCTCAGCTTTTCAACATCTCAGATTTCTTACTCAGCAACATCATGATCTGAG 539  
 Db 361 TTTCCTCAGCTTTTCAACATCTCAGATTTCTTACTCAGCAACATCATGATCTGAG 420  
 QY 540 TGACAGAGCTCTGTTCAATATTTTCATGA 568  
 Db 421 TGACAGAGCTCTGTTCAATATTTTCATGA 449

RESULT 5  
 LOCUS AM015382  
 DEFINITION UI-H-B10-aac-d-06-0-UI.s1 NCI CGAP\_Sub1 Homo sapiens cDNA clone  
 IMAGE:2710331 3', mRNA sequence.  
 ACCESSION AM015382  
 VERSION AM015382.1 GI:5864139  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 1 (bases 1 to 442)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Oligo-dt track not found. Not 1 site shown in beginning of sequence  
 is likely internal to the message. cDNA library preparation: M.B.  
 Soares Lab cDNA distribution: NCI-CGAP clone distribution  
 information can be found through the I.M.A.G.E. Consortium/JLNUV at:  
[www-bio.11nl.gov/bdrip/image/image.html](http://www-bio.11nl.gov/bdrip/image/image.html)  
 Seq primer: M13 forward  
 POLYA=No.

FEATURES  
 source

1. 442  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2710331"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_1db="NCI-CGAP Sub1"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NCI-CGAP Sub1 library is a subcloned library derived from  
 B1. B1 constitutes a mixture of 21 normalized or  
 subcloned NCI-CGAP libraries: NCI-CGAP Co4, NCI-CGAP Co16,  
 NCI-CGAP Pr22, NCI-CGAP Pr28, NCI-CGAP Co10, NCI-CGAP Co16,  
 NCI-CGAP K145, NCI-CGAP K1412, NCI-CGAP K143, NCI-CGAP Co8,  
 NCI-CGAP K141, NCI-CGAP Lym2, NCI-CGAP Br23, NCI-CGAP Lu5,  
 NCI-CGAP Cui1, NCI-CGAP Le12, NCI-CGAP Br23, NCI-CGAP Lu5,  
 NCI-CGAP Lu24, NCI-CGAP Lu19, NCI-CGAP G4, NCI-CGAP G6,  
 NCI-CGAP Br25. These 21 libraries were pooled and a  
 single-stranded DNA preparation of the resulting mixture  
 was used as a tracer in a subtractive hybridization with a  
 driver whose composition is detailed below: NCI-CGAP K143  
 pool 1 LLM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
 CloneID: 132337C-1323911, 1456006-1456775, 1500552-1502855)  
 ) NCI-CGAP K145 pool 1 LLM 3338-3342, 3722-3725,  
 3776-3778 (IMAGE CloneID: 1323912-1325831,  
 1471368-1472903, 1492104-1493255) NCI-CGAP Lu5 pool 1 LLM  
 3575-3582, 3851-3854 (IMAGE CloneID: 141920-1417991,  
 1520964-1522439) NCI-CGAP G4 pool 1 LLM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE CloneID: 1257096-1258631,  
 1469064-1470983, 1475592-1476743) NCI-CGAP Pr22 pool 1  
 LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneID  
 985608-986759, 1101192-1101959, 1217928-1220615)  
 NCI-CGAP Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE  
 CloneID: 1057416-1061255, 1144584-1145351) The resulting  
 subcloned library contained 530,000 recombinants.  
 Subtraction was performed as previously described [Bonaldo  
 & Lemmon & Soares (1996)]. Normalization and Subtraction:  
 Two Approaches To Facilitate Gene Discovery. Genome  
 Research 6, 791-806.  
 TAG LTB=NCI CGAP Le12  
 TAG TISSUB=Telomysarcoma  
 TAG\_SEQ=AAATCG"

BASE COUNT 118 a 97 c 127 g 100 t

Query Match 38.2%; Score 424.4; DB 9; Length 442;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-115;  
 Matches 436; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 484 CTCAGCTTTTCAACATCTCAGATTTCTTACTCAGCAACATCATGATCTGAG 543  
 Db 5 CGCAGCTTTTCAACATCTCAGATTTCTTACTCAGCAACATCATGATCTGAG 64  
 QY 544 AAGACTCTGTTCAATATTTTCATGAGGTTGTGCTTCAGATCTCAGCAAGGCTCC 603  
 Db 65 AAGACTCTGTTCAATATTTTCATGAGGTTGTGCTTCAGATCTCAGCAAGGCTCC 124

Matches	489;	Conservative	0;	Mismatches	102;	Indels	1;	Gaps	1;
Qy	112	GGAGCTCTCTTTCTGTTCATCACACGCTTACTGTGACGAAAGTTTCATGAGAGAACTGT	171						
Db	66	GGAGCTCTCTTTCTGTTCATCACACGCTTACTGTGACGAAAGTTTCATGAGAGAAAGTGT	125						
Qy	172	GGGGCACTCCGTGAAACAAGTATGCGATTACAGAGATGGAAGCGCATTAACCTTGAA	231						
Db	126	GGGGCGGTCCGTGAAACAAGTATGCGATTACAGAGATGGAAGCGCATTAACCTTGAA	185						
Qy	232	AGGATCAATTACAGACCCCACTCTTGCCCAACATCACACTGGGCTGTGAGATTAAGGAT	291						
Db	186	AGGATCAATTACATACCCCACTCTTGCCCAACATCACACTGGGCTGTGAGATTAAGGAC	245						
Qy	292	TCCTGCTGGCATTCGGCTGTGGCCCTTAGACACAGCATTTGATTCATPAAGATTCCTCT	351						
Db	246	TACTGCTGGCATTCGGCTGTGGCTCTTAGAGCATTTGATTCATPAAGATTCCTCT	305						
Qy	352	ATTTCCTCGAAGAGAAAGAGGGCTTGATAGCTCTGTGTGATAGGCTCTCTCTCTCTTC	411						
Db	306	ATTTCCTTATPAAGAGAAAGGGCTTGATAGCTCTGTGTGATAGGCTCTCTCTCTCTTC	365						
Qy	412	CGCTCGAAGAGCCCATPATAGGGGTCATTGGGCGCTGGTCCAGTCTTTAGCATTGAC	471						
Db	366	CGGTCGAGAAAGCCCATPATAGGGGTTATTGATCTATATTCAGTCTTGCTCTCATTTG	425						
Qy	472	GTCCAGATTTGTCTCCAGCTTTTCCACATACCTCAGATTGCTTACTCAGAACCATCATG	531						
Db	426	GCGCAGAAATGGTGACAGTTTTCACATACCTGACATTGTTTACTGATGAAACCATG	485						
Qy	532	GATTCAGTGCACAAAGATCTCTGTTCAATATTTTCATAGGGGTTGTGCTTCAGATGCTCAG	591						
Db	486	GATTCGATGCACAAAGATCTCTGTTCAATATTTTCATAGGATGTGGCCTTTA-TTGCCTTAA	544						
Qy	592	CAGGCAAGTCCAGTGTGACATAGTGAAGAGGTAACAACGACCTATGATATCAGCCGTA	651						
Db	545	TTTCTTATGATTTATGTGTGACATACCTTATAGGCTCAATTGTGCTTATGATTTATTCGTA	604						
Qy	652	CACACAGAAAGCACTATGAGAGAAAGTGGAGTGAAGACCTTCAAGATATATGT	703						
Db	605	CTACCTATTAAGGATTTTATTTCTTTGTTATATCTGCGCTGTATATGTTATATGT	656						
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Bg150163									
LOCUS									
DEFINITION									
	Bg150163	414 bp	mRNA	linear	EST 05-FEB-2001				
		nd44603.x1	NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3368404	3'					
		similar to: sw:MG85.HUMAN P41594	METABOTROPIC GLUTAMATE RECEPTOR 5						
		PRBCNRSO. [1] ;	mRNA sequence.						
ACCESSION		Bg150163							
VERSION		Bg150163.1	GI:12662193						
KEYWORDS		EST.							
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
REFERENCE		1 (bases 1 to 414)							
AUTHORS		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.							
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),							
		Tumor Gene Index							
JOURNAL		Unpublished							
COMMENT		Contact: Robert Strausberg, Ph.D.							
		Email: cga@bcr-remail.nih.gov							
		Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.							
		Emmett-Buck, M.D., Ph.D.							
		cDNA Library Preparation: M. Bento Soares, Ph.D.							
		cDNA Library Arrayed by: Greg Lennon, Ph.D.							
		DNA Sequencing by: Washington University Genome Sequencing Center							
		clone distribution: NCI-CGAP clone distribution information can be							
		found through the I.M.A.G.E. Consortium/LINL, send email to:</							





COMMENT	DNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/ Location/Qualifiers
SOURCE	1..3879 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM,DB:6430542K11" /db_xref="taxon:10090" /clone="6430542K11" /sex="male" /tissue_type="olfactory brain" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult"
misc_feature	<1..3063 /note="METABOTROPIC GLUTAMATE RECEPTOR MGLUR5 PRECURSOR homolog (Rattus norvegicus) (SPTRLBAA01711, evidence: FASTV, 98.5%id, 87length, match=3058) putative"
BASE COUNT	1026 a 975 c 954 g 924 t
ORIGIN	
Query Match	33.5%; Score 372.2; DB 11; Length 3879; Best Local Similarity 88.4%; Pred No. 3.2e-99;
Matches	404; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY	458 CTTTAGCCATTGAGTCCAGAATTTGTCTCGACCTTTTCACATACCAGATTGGTTACT
Db	1 CTGTGGCATTCAGATTGAGTAAGTCTGCACAGCTTTCAACATACCTCAGATTGCTTACT
QY	518 CAGCAACCATATGATGATTCAGTGACAAGACTCTGTTCAAAATATTTCATGAAGGTTGTGC
Db	61 CTGCAACTGACATGATTTGATGATGACAGACTCTTATTAAGTAATTCATGAAGGTTGTGAC
QY	578 CTTGAGATGCTCAGAGGACAGGTCATGATGAGCATGTAGTAAGAGGTACAACTGGAACT
Db	121 CTTGAGATGCCAAGAACGCCGAGCATGTAGTAAGTAAGTAAGATACAACTGGAACTT
QY	638 ATGTATCAGCCGTACACACAGAAAGCACTATGAGAAAGTGGATGAAAGCTTCAAAG
Db	181 ATGTCTAGCTGTGCACACAGAAAGCACTATGAGAAAGTGGATGAAAGCTTCAAAG
QY	698 ATATGTACGAGAGAAAGGATTTGCATGCGCCACTTTACAAAATCTTACAGTATGAG
Db	241 ATATGTACGAGAGAAAGGATTTGCATGCGCCACTTTACAAAATCTTACAGTATGAG
QY	758 GGGAGCAGAGTTTGTATGATGCTGCTGAAGAAGCTCACAGTCACTTGGCCAAAGCCCGGG
Db	301 GGGAGCAGAGTTTGTATGATGCTGCTGAAGAAGCTCACAGTCACTTAAAGCCCGGG
QY	818 TGTGTGACCTACTTCTGTGAGGGAGTACGATGAGAGTCTGTGATGAGTACATGAGAGCC
Db	361 TGTGTGACCTGCTTCTGTGAGGGAGTACAGTTCAGAGTCTGTGATGAGTACATGAGAGCC
QY	878 TGAGTCTAGTGGAGAAATTTCTGCTTCTGGCAGAGGA
Db	421 TGAGTCTAGCAGGGAATTTCTACTTCTGGCAGAGGA
RESULT 9	Bg695213 682 bp mRNA linear EST 04-MAY-2001
LOCUS	Bg695213
DEFINITION	NISC i.v1j909.w1 Soares NMBP2 pituitary Mus musculus cDNA clone
ACCESSION	Bg695213
VERSION	Bg695213.1 GI:13954900
KEYWORDS	EST.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Unpublished	
2	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Tumor Gene Index	Unpublished	
3	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Contact: Robert Strausberg, Ph.D.	Unpublished	
4	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Email: <a href="mailto:cgapb-remail.nih.gov">cgapb-remail.nih.gov</a>	Unpublished	
5	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	CDNA Library Preparation: M. Bento Soares Laboratory	Unpublished	
6	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL	Unpublished	
7	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	DNA Sequencing by: National Institutes of Health Intramural	Unpublished	
8	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Sequencing Center (NISC)	Unpublished	
9	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Clone distribution: NCI-CGAP clone distribution information can be	Unpublished	
10	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	found through the I.M.A.G.E. Consortium/LNL at:	Unpublished	
11	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	<a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a>	Unpublished	
12	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	MDI:1598648	Unpublished	
13	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Plate: LLM9922	Unpublished	
14	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	row: M	Unpublished	
15	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	column: 17	Unpublished	
16	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Seq primer: T7 primer.	Unpublished	
17	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Location/Qualifiers	Unpublished	
18	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	1. 682	Unpublished	
19	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/organism="Mus musculus"	Unpublished	
20	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/mol_type="mRNA"	Unpublished	
21	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/db_xref="taxon:10090"	Unpublished	
22	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/clone="IMAG:4317880"	Unpublished	
23	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/tissue_type="pituitary gland"	Unpublished	
24	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/dev_stage="embryo, 14 dpc"	Unpublished	
25	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/lab_host="DH10B (phage-resistant)"	Unpublished	
26	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/clone_id="Soares NMBP pituitary"	Unpublished	
27	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	/note="Organ: brain; Vector: pT73D-Pac; Site 1: NotI;	Unpublished	
28	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Site 2: EcoRI; 1st strand cDNA was primed with a NotI -	Unpublished	
29	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	oligo(dT) primer	Unpublished	
30	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	5'-AATCGAAGAATTCGGCGCGCGCGCGCTTTTCTTTTCTTTTCTTTT-3';	Unpublished	
31	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	double-stranded cDNA was ligated to EcoRI adaptor	Unpublished	
32	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	5'-AATTCGGCGCGCGCG-3' AND 5'-CCCTGCGCG-3' (Pharmacia),	Unpublished	
33	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	sited with NotI and cloned into the NotI and EcoRI	Unpublished	
34	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	sites of the pT73D-Pac vector. Library went through one	Unpublished	
35	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	round of normalization, and was constructed in the	Unpublished	
36	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	laboratory of M. Bento Soares (University of Iowa)."	Unpublished	
37	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		Unpublished	
38	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		Unpublished	
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48	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		Unpublished	
49	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		Unpublished	



RESULT 10  
LOCUS BI826234 664 bp mRNA linear EST 04-OCT-2001  
DEFINITION 603075928F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5167902 5', mRNA sequence.  
ACCESSION BI826234  
VERSION BI826234  
KEYWORDS EST. 15937784  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
Plate: LAM1417 row: g column: 07  
High quality sequence, stop: 662.  
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/clone="IMAGE:5167902"  
/tissue\_type="medulla"  
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/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."  
BASE COUNT 151 a 177 c 179 g 157 t  
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Query Match 25.9%; Score 287; DB 12; Length 664;  
Best Local Similarity 98.3%; Pred. No. 3.3e-74;  
Matches 290; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 61 CAGTTCAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 430 CAGTTCAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 489  
QY 121 TTTTCTGTATCAACCAAGCTACTGTGAGCAAGTTCATGAGAGAAAGTGGGGCA 180  
DB 490 TTTTCTGTATCAACCAAGCTACTGTGAGCAAGTTCATGAGAGAAAGTGGGG 549  
QY 181 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCAATGTCATACCTCGAAAGATCA 240  
DB 550 CGTGAACAGTATGAGCATTCAGAGAGTGAAGGCAATGTCATACCTCGAAAGATCA 609  
QY 241 TCAAGCCCAACATCTTGTCCCAACATCACTGGGCTGTGAGATPAGGATTCCT 295  
DB 610 TCAAGCCCAACATCTTGTCCCAACATCACTGGGCTGTGAGATPAGGATTCCT 664

RESULT 11  
LOCUS BU351729 657 bp mRNA linear EST 28-NOV-2002  
DEFINITION 603527561F1 CSECHN69 Gallus gallus cDNA clone CHEST47616 5', mRNA sequence.  
ACCESSION BU351729  
VERSION BU351729  
KEYWORDS EST. 25859730  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
AUTHORS 1 (bases 1 to 657)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Boesch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
TITLE A Comprehensive Collection of Chicken cDNAs  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
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BASE COUNT 161 a 168 c 178 g 150 t  
ORIGIN  
Query Match 25.4%; Score 281.6; DB 13; Length 657;  
Best Local Similarity 72.4%; Pred. No. 1.4e-72;  
Matches 365; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 411 CCGCTCCAGAACCCATAGTAGGGGCTATGGGCTGCTGAGTCTTTACCATTC 470  
DB 10 CCGCTCGAGAACCCATAGTAGGGGCTATGGGCTGCTGAGTCTTTACCATTC 69  
QY 471 GGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACAT 530  
DB 70 GGTCCAGAAATTTGCTCCAGCTTTTCAACATACCTCAGATGCTTACTCAGCAACAT 129  
QY 531 GGATCTGAGTGAAGAGCTGTGCAATATTTCAATGAGGCTGTGCTTCAATGTCA 590  
DB 130 CGACTGAGTGAAGAGCTGTGCAATATTTTCCGCTGCTGCTTCAACACT 189

Qy	591	GCAGGCAGAGTCAATGGTGGACATCATGTGAAGAGTAAACAATGACCTAATGATACGCCGT	650
Dd	190	CCAGCCCCGCCCATGCTCGATATATGTCAAGGCTTACAACTGACTTACGTCTCGCCCT	249
Qy	651	AACACACAGAAAGCACTATGAGAAAGTGGAGATGAGACTTCAAAAGATATGTCAAGCGAA	710
Dd	250	GCACACTGAAGGAATTTACGGGGAAAGTGGATGGAAGGCTTCAAAAGACTGGCTGGCCA	309
Qy	711	GGAAAGGATTTGCAATCGCCCACTCTTACAAAATCTACAGTAATGACAGGGAGACAGACTT	770
Dd	310	AGAGGGCCCTGCAATTTGCTCATTTCTGAACAAGATCTATAGCAATGCTGGGGAGAAAAAGCTT	369
Qy	771	TGATTAAGTGTCTGAAGAAGACTCACAAAGTCACTTGGCCCAAGGCCGGGTGTGTGGCTACTT	830
Dd	370	TGATGGCTGTGCCCGCAAGCTCCGAAAGATTACCCCAAGGCTAGAGTGTGTGTGGCTT	429
Qy	831	CTGTAGAGGGCATGAGCGTGAAGGATCTGTGATGTGCCAATGAGCGCTGTGGTCTAATGGG	890
Dd	430	CTGTAGAGGCATGACGATGAGGGGGAATCTCATCTGTATGAGACGCTGTGGAGTGCCTTGG	489
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Dd	490	GGAGTTCCTGCTAATTGGAGATGA	513

RESULT 12	LOCUS	DEFINITION
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BU939781		linear
60380338001	CSEQCCH57	Gallus gallus CDNA clone CHS5T778020 5', mRNA

ACCESSION	BU933781
VERSION	BU933781.1
KEYWORDS	GI:25762820
SOURCE	EST.
ORGANISM	Gallus gallus (chicken)
	Gallus gallus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

1 (bases 1 to 669)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Butt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken CDNA  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
Contact: Simon Hubbard  
12445392

University of Manchester Institute of Science and Technology (UMIST)  
)  
PO Box 88, Manchester, M60 1QP, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
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source

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FEATURES
source
location/Qualifiers
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/lab_host="DH10B"
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/note="Organ: brain; Vector: pluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dt) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with EcoRII
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pluescript (KS+) vector. The library was normalized in 2

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rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Query Match	25.4%	Score 281.6	DB 13	length 669
Best Local Similarity	72.4%	Pred. No. 1.4e72		
Matches 365, Conservative	0	Mismatches 139	Indels 0	Gaps 0

411 CCCTCCAGAGCCATAGTAGGGGTATTGGGCTGGTTCCAGTTCTTTAGCATTC 470

471 GGTGAGAAATTGACTGAGCTTTTCAATACCCAGATTGCTTACCTGAGGACCAATCAT 510

Db 82 GGTGAGAACTCTGAGCTTTTGACATCCCA<sup>CAAA</sup>TGGCTTCTGCGACACGAT 141

531 GGATCGAGTCAACAGACTCTGTTCAAAATTTCATGAGGGTTCGCCCTTCAGATGCTCA 590

[illegible]

Db 202 CCAAGCCCGGCATGCTCGATTGTCTAAGCGTTACACTGACTTACGTCGCCCGT 261

651 ACACACAGAAAGCAACTATGAGAAAGTGGATGGAGCCTTCAAGATATGTCACGAA 710

DB 262 GCACACCTGAGGAAATTACCGGGAAAGTGGAAATGAGGCCCTTCAAGAGAGCTGGCTGCCCA 321

Db 322 AGAGGCGCTCTGCATTGCTCATTTGACAAGATCTATAGCAATGCTGGGGAGAAAAGCTT 381

771 TGATAAGCTGCTGAAGAAGCTCAAGATCACTTCCCAAGGCCCGGGTGGTGGCTACTT 830

Db 382 TGATCGCCTGCTCCGCAAGCTCGGAGAAAGTATCCCAAGGCTAAGTGTGCTTCTT 441

442 CTGTGAGGGCA TGA CCGTGA GGGGAACTCA TTGCTA TGA GACCTT GGGAGT GCTTGG 501

891 AGAATTTCTGCTTCTGGGACAGGA 914

Db 502 GGAGTTCCTGCTAATTGGAAGTGA 525

RESULT 13		
LOCUS	T78107	
DEFINITION	T78107 392 bp mRNA linear EST 07-MAR-1995	
DESCRIPTION	<p>Y688a01.r1 Soares infant brain IN1B Homo sapiens cDNA clone              IMAGE:23998 5' similar to SP.JC132 JC132 METABOTROPIC GLUTAMATE              RECEPTOR 5 A - 1, mRNA sequence.</p>	

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VERSION      T78107.1  GI:696616
KEYWORDS     EST.

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SOURCE	ORGANISM
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Pharmacia - Veterinary	Overdose: Great Dane; Underdose: Dutch Shepherd

REFERENCE  
1 (bases 1 to 392)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Holtzman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, J., Rohlfing, T., Soares, M., Tan, P., Trevaaskis, R., Waterson

TITLE  
R., Williamson, A., Wohldmann, P. and Wilson, R.  
The Washu-Merck BST Project

**COMMENT**  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810



REFERENCE 1 (bases 1 to 673)  
AUTHORS Boardman, P. E., Sanz-Eguero, J., Overton, I. M., Burt, D. W., Bosch, E.,  
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.  
TITLE A Comprehensive Collection of Chicken CDNA  
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
MEDLINE 22335534  
PUBMED 12445392  
COMMENT Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology (UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

## FEATURES

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EcoRI; Site\_2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
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compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

BASE COUNT 165 a 173 c 180 g 155 t  
ORIGIN

Query Match 22.7%; Score 252.2; DB 13; Length 673;  
Best Local Similarity 72.1%; Pred. No. 8.6e-64;  
Matches 341; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

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DB 56 GGCGTGGTCCAGTCTTTAGCCATTCAGGT-CCAGATTGCTCCAGCTTTCAACATA 115  
OY 502 CCTCAGATTGCTTACTCAGCAACCATCATGATCTGAGTGAACAAGACTCTTCAATAT 561  
DB 116 CCACAAATTGCTTACTCAGCAACCATCATGATCTGAGTGAACAAGACTCTTCAATAT 175  
OY 562 TTCATGAGGTTGTGCTTCAAGTGTCTCAGCAGGCAAGTCCATGCTGACATAGTGAAG 621  
DB 176 TTTCTCGTGTGCTTCCCTCTGACACATCCAGCCCGCCCAATGCTCATATATTCAG 235  
OY 622 AGGTACAACTGCACTATGATCATGCGGTACACAGAAAGCAACTATGAGAAAGTGGG 681  
DB 236 CGTTACAACTGCACTATGATCATGCGGTACACAGAAAGCAACTATGAGAAAGTGGG 295  
OY 682 ATGGAAGCTTCAAGATATGTCAGCGAAAGAAAGGATTTGCATCGCCCACTTTACAA 741  
DB 296 ATGGAAGCTTCAAGATATGTCAGCGGTACAGCGAAAGGATTTGCATCGCCCACTTTACAA 355  
OY 742 ATCTAAGTAATGACAGGAGGACAGCTTTGATTAAGTGTGTAAGAAGCTCACAACTCAC 801  
DB 356 ATCTAAGTAATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415  
OY 802 TTGCCCAAGGCGCGGCTGAGCTTACTTCTGAGAGGCGATGACGGTGAAGGTCGCTG 861

DB 416 TTACCCAGCTAGAGTGTGTTGCTTCTGTGAGGGCATGACGCTGAGGGGATCTTC 475  
OY 862 ATGGCCATGAGGCGCGCTGGGTCTAGTGAAGAAATTTCTGCTTCTGGGACAGGA 914  
DB 476 ATGTATGAGACGTGTGGAGTCTTGGGAGTTCTCTTAATTTGAAGTGA 528

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